Pattern Recognition 119 (2021) 108110

Contents lists available at ScienceDirect

Pattern Recognition

journal homepage: www.elsevier.com/locate/patcog

Accurate detection of COVID-19 patients based on distance biased Naïve Bayes (DBNB) classification strategy

Warda M. Shaban[a,*], Asmaa H. Rabie[b], Ahmed I. Saleh[b], M.A. Abo-Elsoud[c]

[a] Nile higher institute for engineering and technology, Egypt
[b] Computers and Control Dept. faculty of engineering Mansoura University, Egypt
[c] Electronics and Communication Dept. faculty of engineering Mansoura University, Egypt

ARTICLE INFO

Article history:
Received 3 August 2020
Revised 9 March 2021
Accepted 19 May 2021
Available online 16 June 2021

Keywords:
COVID-19
Classification
NB
Feature selection
Wrapper
Optimization
Particle swarm

ABSTRACT

COVID-19, as an infectious disease, has shocked the world and still threatens the lives of billions of people. Early detection of COVID-19 patients is an important issue for treating and controlling the disease from spreading. In this paper, a new strategy for detecting COVID-19 infected patients will be introduced, which is called Distance Biased Naïve Bayes (DBNB). The novelty of DBNB as a proposed classification strategy is concentrated in two contributions. The first is a new feature selection technique called Advanced Particle Swarm Optimization (APSO) which elects the most informative and significant features for diagnosing COVID-19 patients. APSO is a hybrid method based on both filter and wrapper methods to provide accurate and significant features for the next classification phase. The considered features are extracted from Laboratory findings for different cases of people, some of whom are COVID-19 infected while some are not. APSO consists of two sequential feature selection stages, namely; Initial Selection Stage (IS^2) and Final Selection Stage (FS^2). IS^2 uses filter technique to quickly select the most important features for diagnosing COVID-19 patients while removing the redundant and ineffective ones. This behavior minimizes the computational cost in FS^2, which is the next stage of APSO. FS^2 uses Binary Particle Swarm Optimization (BPSO) as a wrapper method for accurate feature selection. The second contribution of this paper is a new classification model, which combines evidence from statistical and distance based classification models. The proposed classification technique avoids the problems of the traditional NB and consists of two modules; Weighted Naïve Bayes Module (WNBM) and Distance Reinforcement Module (DRM). The proposed DBNB tries to accurately detect infected patients with the minimum time penalty based on the most effective features selected by APSO. DBNB has been compared with recent COVID-19 diagnose strategies. Experimental results have shown that DBNB outperforms recent COVID-19 diagnose strategies as it introduce the maximum accuracy with the minimum time penalty.

1. Introduction

The new coronavirus (also called COVID-19) has resulted in a global epidemic problem due to its quick spread from one individual to another in society [1]. The terrifying spread of COVID-19 is the greatest challenge humanity has faced since the Second World War. World Health Organization (WHO) declared COVID-19 as a global Pandemic in March 2020 [2]. The most common symptoms of COVID-19 are dry cough, sore throat, and fever [2,3]. Symptoms can progress to a severe form of pneumonia with critical complications, including septic shock, and pulmonary edema [1]. Unfortunately, clinical characteristics alone cannot determine the diagnosis of COVID-19, especially for patients at the early-onset of symptoms. According to the recent study, it is shown that once coronavirus begins to spread, it takes no time to make the medical system collapse (e.g., hospital) [4]. Hence, early detection of COVID-19 patients is a vital process to quarantine the infected people.

Machine learning is a fancy term used for the concept of software that learns automatically how to solve a problem or execute a task, and which becomes more and more accurate over time [5,6]. All machine-learning techniques work on the same principle [7,8]. They receive some training data as an input, build a mathematical model based on the input data, and then use the mathematical model to solve the problem in hand [9]. Several techniques have been introduced for COVID-19 diagnosis based on machine

* Corresponding author.
E-mail address: warda.mohammed2010@yahoo.com (W.M. Shaban).

https://doi.org/10.1016/j.patcog.2021.108110
0031-3203/

learning techniques [10]. However, they suffer from several drawbacks such as; (i) low diagnose accuracy, (ii) long prediction time, and (iii) high complexity.

Naive Bayes (NB) classifier is a simple but surprisingly powerful machine learning technique [11,12]. Despite its naive design and apparently oversimplified assumptions, NB has worked quite well in many complex real-world situations such as; real-time prediction, spam filtering, weather forecast, and medical diagnosis [13,14,15]. However, in some cases, the performance of NB is sometimes thumping due to the unrealistic assumption that all features are independent and equally important given the class value [11]. To overcome such hurdle, several solutions have been introduced such as; feature selection and weighting [11,12].

The originality of this paper is concentrated in introducing a Distance Biased Naïve Bayes (DBNB) classification strategy for accurate diagnosis of Covid-19 patients. DBNB consists of two phases, namely; Feature Selection Phase (FSP) and (ii) Classification Phase (CP). During the former (e.g., FSP), the input features that are extracted from patient's laboratory findings are collected, and then the effective features are selected from those extracted features by using advanced Particle Swarm Optimization (APSO). APSO is a new proposed method that combines between filter and wrapper approaches, in which it composes of two stages called IS^2 using many filter methods and FS^2 using Binary Particle Swarm Optimization (BPSO) as a wrapper method. APSO aims to utilize the benefits of both filter and wrapper methods for overcoming their drawbacks. In fact, filter methods can provide fast selection, but it cannot give high performance in which it ignores features dependencies.

On the other hand, BPSO as a wrapper method can provide accurate detection because it depends on features dependencies and the interaction with the used classifier, but it cannot provide fast selection. Consequently, APSO can select the most informative subset of features as; (i) it can provide fast selection by using filter methods, (ii) it can provide accurate selection by using wrapper method, and (iii) it takes in the consideration the feature dependencies and the interaction with the classifier.

During the second phase (e.g., CP), fast and accurate detection of COVID-19 patients based on the selected features is provided through a new classification model. The proposed classification model involves the benefits of the traditional NB and overcomes its problems. The proposed classification model aims to improve performance and overcome the drawbacks of traditional NB by (i) assigning weights to the elected features, hence, the result is a Weighted Naïve Bayes (WNB) classifier, and (ii) fine tuning the decision of WNB using distance based biasing between the input item to be classified and the center of the target classes in the employed feature space.

Consequently, the proposed classification model consists of two modules, namely; (i) Weighted Naïve Bayes Module (WBNM) in which WNB classifier takes the initial decision based on the belonging degree of the input item to be classified to each of the considered classes, and (ii) Distance Reinforcement Module (DRM) in which the final decision is taken. The proposed DBNB classification strategy has been compared against recent COVID-19 diagnose strategies. Experimental results have shown that DBNB outperforms all competitors as it introduced the maximum diagnose accuracy as well as the minimum error.

The rest of the paper is organized as follows; Section 2 describes a problem definition about COVID-19. Section 3 discuss DBNB applicability For COVID-19 diagnose. Section 4 discusses Naïve Bayes Haste problem. Section 5 introduces the previous efforts about COVID-19 patients' classification. Section 6 focuses on the proposed Distance Biased Naïve Bayes (DBNB) classification strategy. Section 7 depicts the experimental results. Finally, conclusions and future works are presented in section 8.

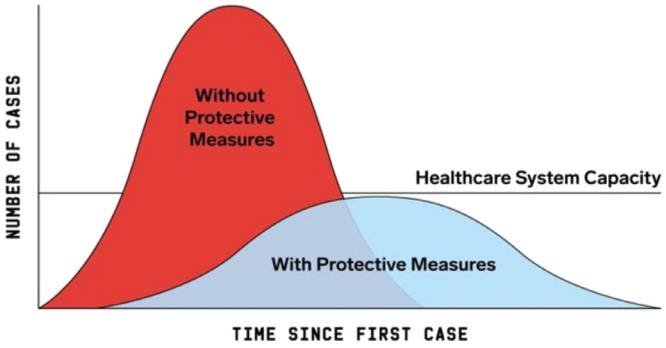

Fig. 1. A graphic representation of the rapid spike in infections.

2. Problem definition

Coronavirus pneumonia is a new species appeared in Wuhan, China, that subsequently termed COVID-19. Once coronavirus appeared, it grown at rapid rate around the whole world [16,17]. Detection and isolation of infected cases is the only solution for the healthcare system protection from becoming overwhelmed, and accordingly, it will flat the epidemic curve as shown in Fig. 1. Social and physical distancing measures aim to slow the spread of disease by stopping chains of transmission of COVID-19 and preventing new ones from appearing in order to keep hospitals and doctors' offices from becoming overcrowding with patients.

3. DBNB applicability for COVID-19 diagnose

What a pandemic represented by the terrifying spread of the COVID-19 virus. No doubt, it is the greatest challenge the humanity has faced since World War Two. However, COVID-19 is much more than a health crisis, it has the impact to create devastating economic, political, and social crises that will certainly leave deep scars [17]. Generally, COVID-19 diagnosis can be accomplished via three different treatments as illustrated in Fig. 2, which are; (i) Using Real-Time reverse transcriptase- Polymerase Chain Reaction (RT-PCR), (ii) using chest CT imaging scan, and (iii) using numerical laboratory tests Among nucleic acid tests, polymerase chain reaction (PCR) laboratory test, and more precisely, Real-time reverse transcriptase-PCR (RT-PCR) is currently used as the 'gold standard' for confirming COVID-19 positive patients.

RT-PCR tests are fairly quick, sensitive and reliable. A sample is collected from a person's nose or throat, chemicals are used to remove any fats, proteins and other molecules, leaving only RNA behind [3]. Such separated RNA is a mixture of a person's own genetic material and, if present, the coronavirus' RNA. However, RT-PCR test suffers from the risk of eliciting false-positive and false-negative results, and accordingly, it doesn't pick up all infections [18]. Thus, a negative result of RT-PCR test does not negates the possibility of COVID-19 infection. Due to COVID-19 exponential spread, such undiagnosed cases can cause catastrophic effects. Accordingly, RT-PCR should not be used as the only criterion for detecting COVID-19 patients [19].

Chest CT has become a critical diagnostic tool for COVID-19, which detects hazy, patchy, "ground glass" white spots in the lung, a telltale sign of Covid-19. Several studies observed that the sensitivity of CT in diagnosing COVID-19 is significantly higher than that of RT-PCR [20]. However, current evidence suggests that CT scans and x-rays are NOT specific enough to either diagnose or rule out COVID-19, this is due to the following reasons; (i) CT Scans sometimes fail to detect coronary lung tissue. Like ultrasounds, a CT scan is unable to differentiate coronary tissue from non- Coronary tissue. (ii) CT Scans Lack Detail as it cannot identify the most ag-

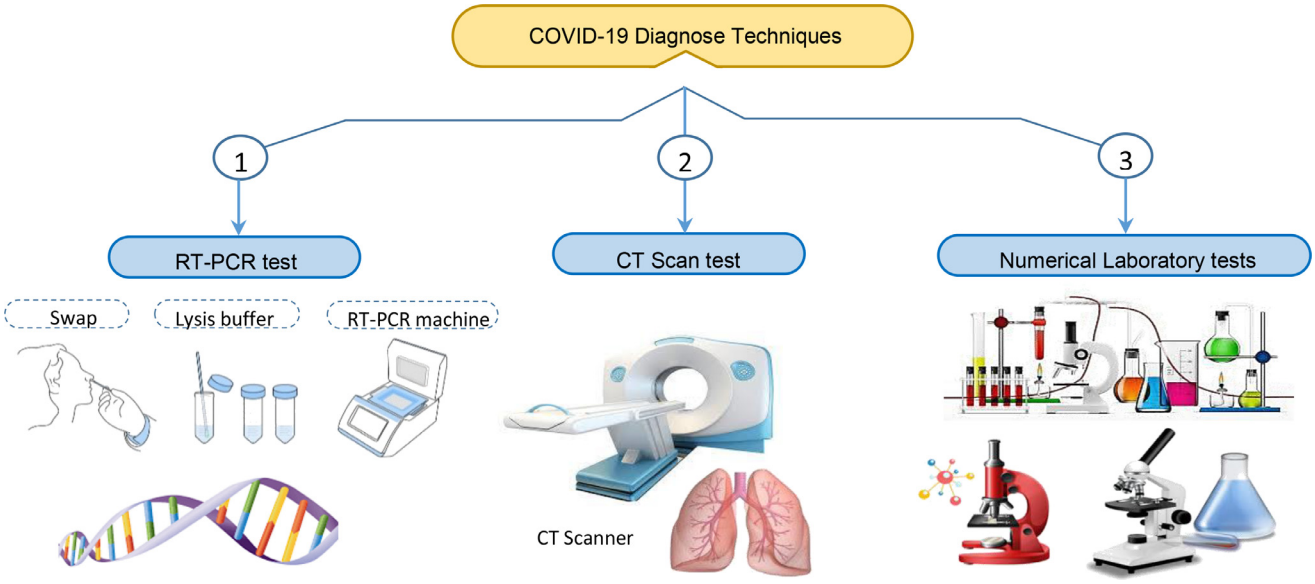

Fig. 2. Different COVID-19 diagnosis techniques.

gressive tumors, hence it is unable to differentiate between cancerous tissue, cysts (or fibroids), and coronary tissue, (iii) Although CT scan can result in rapid diagnose of COVID-19, rapid results mean rapid false-negatives and rapid false reassurance. This also means the rapid release of people with COVID-19, allowing them to mingle with people without the infection who may be potentially vulnerable.

Based on the above discussion, we claim that COVID-19 diagnoses and treatment plans based on a CT scan or RT-PCR are far less effective than those based on better accurate Numerical Laboratory Tests (NLTs). They are not recommended as primary screening tools. On the other hand, the use of NLTs can be considered as the most accurate method for diagnosing COVID-19. Recently, the use of NLTs is the only method that the Centers for Disease Control (CDC) currently endorses [21]. Hence, it makes perfect sense that the use of NLTs will provide more accurate diagnosis with less waiting time. To the best of our knowledge, Distance Biased Naïve Bayes (DBNB), the proposed diagnose strategy proposed in this paper, is the first to use NLTs as the main criteria for detecting COVID-19 patients. It relies on data mining techniques and more precisely on classification for diagnosing COVID-19. Although several classification techniques can be used, DBNB relies on Naïve Bayes (NB), which is a supervised learning classification method based on probability.

As a predictive model, we claim that NB is the best applicable classifier that can be used for COVID-19 diagnosis because of the following reasons; (i) NB is simple, flexible, fast, and appropriate to the real world scenarios, (ii) NB requires a small amount of training data to estimate the parameters necessary for building the classification model, hence, it can make accurate predictions even with small amount of training data, (iii) it is suitable for incremental training, which means that NB can train new samples in real time, (iv) NB is less sensitive to missing data, it is also resistive resistance to noisy data which avoids over-fitting the dataset, (v) it depends on a set of pre-computed probabilities, hence, the prediction time is very small, the classification of one instance has order O(1) when the model has been constructed, which makes it suitable for real time applications such as COVID-19 diagnoses [11,12]. DBNB is not only inherits the advantages of traditional NB, but also it has been enhanced by novel feature selection methodology as well as a distance biasing. The combination is done in a logical way, which is supposed to increase the performance over the traditional NB, and will be consistent in nature. As will be seen in the experimental results, the implementation of DBNB reflects this issue and proves the applicability of the proposed DBNB as the first COVID-19 diagnose strategy that completely relies on accurate NLTs rather than CT chest imaging or RT-PCR test.

4. Naïve Bayes haste problem

No doubt Naïve Bayes (NB) is a popular classifier in machine learning applications. It has been applied to the different domains such as; image and pattern recognition intrusion detection, weather forecasting, bioinformatics, and COVID-19 patients diagnosis. NB allows each feature to contribute towards the classification decision both equally and independently of other features. Although such simplicity promotes to computational efficiency, it sometimes makes NB incompatible with real world conditions.

Consider $F=\{f_1,f_2,f_3,\ldots f_n\}$ to be a set of feature vectors of a new item I_x to be classified and $C=\{c_1,c_2,c_3,\ldots.c_m\}$ be set of target classes. The probability of a new item being in class c_i using NB is given by (1).

$$Target\,(I_x) = \underset{c_i \in C}{\operatorname{argmax}}\,[P(c_i F)] = \underset{c_i \in C}{\operatorname{argmax}}\left[\frac{P(Fc_i) * P(c_i)}{P(F)}\right] \tag{1}$$

Where, $P(c_i\ |F)$ is the conditional probability of class c_i given the feature vector F (also called posterior probability), $P(F\ |c_i)$ is the conditional probability of class F given the class c_i (also called likelihood), and $P(c_i)$ is the prior probability of class c_i. Since features are independent, this yields;

$$\begin{aligned} P(F) &= P(f_1, f_2, f_3, \ldots f_n) = P(f_1) * P(f_2) * P(f_3) * \ldots.. * P(f_n) \\ &= \prod_{j=1}^{n} P(f_j) \end{aligned}$$

$$\begin{aligned} P(F|c_i) &= P(f_1, f_2, f_3, \ldots f_n|c_i) \\ &= P(f_1|c_i) * P(f_2|c_i) * P(\ f_3|c_i) * \ldots.. * P(f_n|c_i) \\ &= \prod_{j=1}^{n} P(f_j|c_i) \end{aligned}$$

Substitute in (1), this yields (2).

$$Target(I_x) = \underset{c_i \in C}{\operatorname{argmax}} \left[\frac{P(c_i) * \prod_{j=1}^{n} P\left(f_j | c_i\right)}{\prod_{j=1}^{n} P\left(f_j\right)} \right] \tag{2}$$

Since denominator in (2) remains constant for a given input for all target classes, it can be removed as illustrated in (3).

$$Target(I_x) = \underset{c_i \in C}{\operatorname{argmax}} \left[P(c_i) * \prod_{j=1}^{n} P\left(f_j | c_i\right) \right] \tag{3}$$

However, the performance of NB is sometimes poor due to the unrealistic assumption that all features are independent and equally important given the class value. The performance of NB can be improved by mitigating this assumption. Several enhancements have been proposed to resolve this problem including feature selection and feature weighting. Generally, feature selection can be applied to improve the performance of the traditional Naïve Bayes classifier. Hence, the target class can be identified by (4).

$$Target(I_x) = \underset{c_i \in C}{\operatorname{argmax}} \left[\begin{matrix} P(c_i) * \prod_{j=1}^{n} P\left(f_j | c_i\right)^{S_j} \\ where S_j \in \{0, 1\} \end{matrix} \right] \tag{4}$$

However, assigning equal weight to all considered features violates the nature of real-world applications. Accordingly, different weights can be assigned to each feature as a generalization of feature selection as illustrated in (5).

$$Target(I_x) = \underset{c_i \in C}{\operatorname{argmax}} \left[\begin{matrix} P(c_i) * \prod_{j=1}^{n} P\left(f_j | c_i\right)^{W_j} \\ where\ W_j \in \mathbb{R}^{+} \end{matrix} \right] \tag{5}$$

As depicted in (5), unlike traditional NB, each feature f_j has its own weight w_j, which can be any positive number representing the significance of the feature. However, both traditional and Weighted Naïve Bayes (WNB) classifiers depend mainly on probabilities, namely; the conditional probabilities of the input features given the considered target classes as well as the classes' prior probabilities. From another point of view, promoting the performance of WNB classifier can be achieved by compensating its performance with another heuristic beside conditional and prior probabilities. In this paper, distance based heuristic will be employed to derive a weighted Naïve Bayes classifier aiming to improve its performance.

5. Related work

In this section, the previous research efforts about COVID-19 patients classification will be reviewed. As depicted in [22], an automated COVID-19 diagnosis method using the implementation of a convolutional neural network (CNN) was introduced as a new classification method. The proposed CNN has been developed using EfficientNet architecture to be able to perform binary and multi-class classification using X-ray images. Experimental results in [22] showed that the average accuracy values for binary and multiclass are 99.62% and 96.70%, respectively.

As presented in [23], the Group Method of Data Handling (GMDH) was used as binary classification model. GMDH is a type of artificial neural networks that used to predict the number of confirmed COVID-19 cases in Hubei province. In fact, many different features were used as inputs to GMDH to predict the confirmed number of COVID-19 patients in the next 30 days. These features (factors) such as maximum, minimum, and average daily temperature, the density of city, humidity and wind speed. The results in [23] demonstrated that the proposed model introduced higher performance capacity in predicting the confirmed number of COVID-19 patients.

As presented in [24], a new Corona Patients Detection Strategy (CPDS) was introduced to detect COVID-19 patients. CPDS consists of two phase called Data Preprocessing (DP) and Patient Detection Phase (PDP). During DP, two main processes which are; feature extraction and feature selection were performed to extract and then select the most informative feature from CT images. On the other hand, during PDP, fast and accurate detection of COVID-19 patients based on the selected features was provided by the proposed Enhanced KNN (EKNN) classifier. Experimental results in [24] proven that CPDS outperforms recent ones in which it introduces the best detection accuracy with the minimum time penalty.

In [25], an automated COVID-19 detection model called DarkCovidNet was introduced as a new detection method based on using chest X-ray images. DarkCovidNet model represented a development of deep learning technique to be able to perform binary and multi-class classification. The experimental results in [25] proven that the proposed model could perform binary tasks better than multi-class tasks in which the accuracy of binary is higher than multi-class.

As presented in [26], a machine learning techniques were used to identify pneumonia caused by COVID-19 from other types and also healthy lungs using only chest X-ray (CXR) images on flat and hierarchical classification scenarios. The proposed Classification Schema (CS) consists of feature extraction process, the early fusion techniques, and the data resampling. According to the results in [26], the proposed approach achieved the best nominal rate obtained for COVID-19 identification in an unbalanced environment with more than three classes.

6. The proposed distance biased Naïve Bayes (DBNB) classification strategy

In this section, the proposed Distance Biased Naïve Bayes (DBNB) classification strategy will be explained in details. The main aim of DBNB is to quickly and accurately detect COVID-19 cases. Automatic medical diagnosis for COVID-19 patients has become very important, especially when rapid decisions are needed for such a serious infectious disease [27,28,29]. Quick detection of COVID-19 cases allow rapid treatment and isolation of patients and according breaks down the spread of infection of the disease. In this paper, an intelligent classification strategy called Distance Biased Naïve Bayes (DBNB) has been introduced in healthcare system to provide more accurate and rapid diagnostic results. As illustrated in Fig. 3, the proposed DBNB classification strategy composes of two phases, which are; (i) Feature Selection Phase (FSP), and (ii) Classification Phase (CP). The next subsections will be discussed.

6.1. Feature selection phase (FSP)

The existence of irrelevant features in the input dataset is one of the main causes of overfitting problem especially in the domain of medical diagnosis of COVID-19 patients [30,31,32]. The main issue during FSP in the proposed DBNB classification strategy is to select the most effective features for COVID-19 diagnosis. In fact, it is important to eliminate the least effected features on the output because it can decrease the accuracy of the diagnostic model. Accordingly, feature selection process should be performed before beginning to learn the diagnostic model to improve its performance to be a faster and more cost-effective model [33,34,35,36,37]. Initially, patient features should be extracted from the input dataset, and then feature selection process can be performed on those extracted features to select the most informative features. The extracted features from the input dataset such as white blood cell, lymphocytes, d-dimer, C-reactive protein …,etc. In this section, a simple but effective feature selection methodology called Advanced

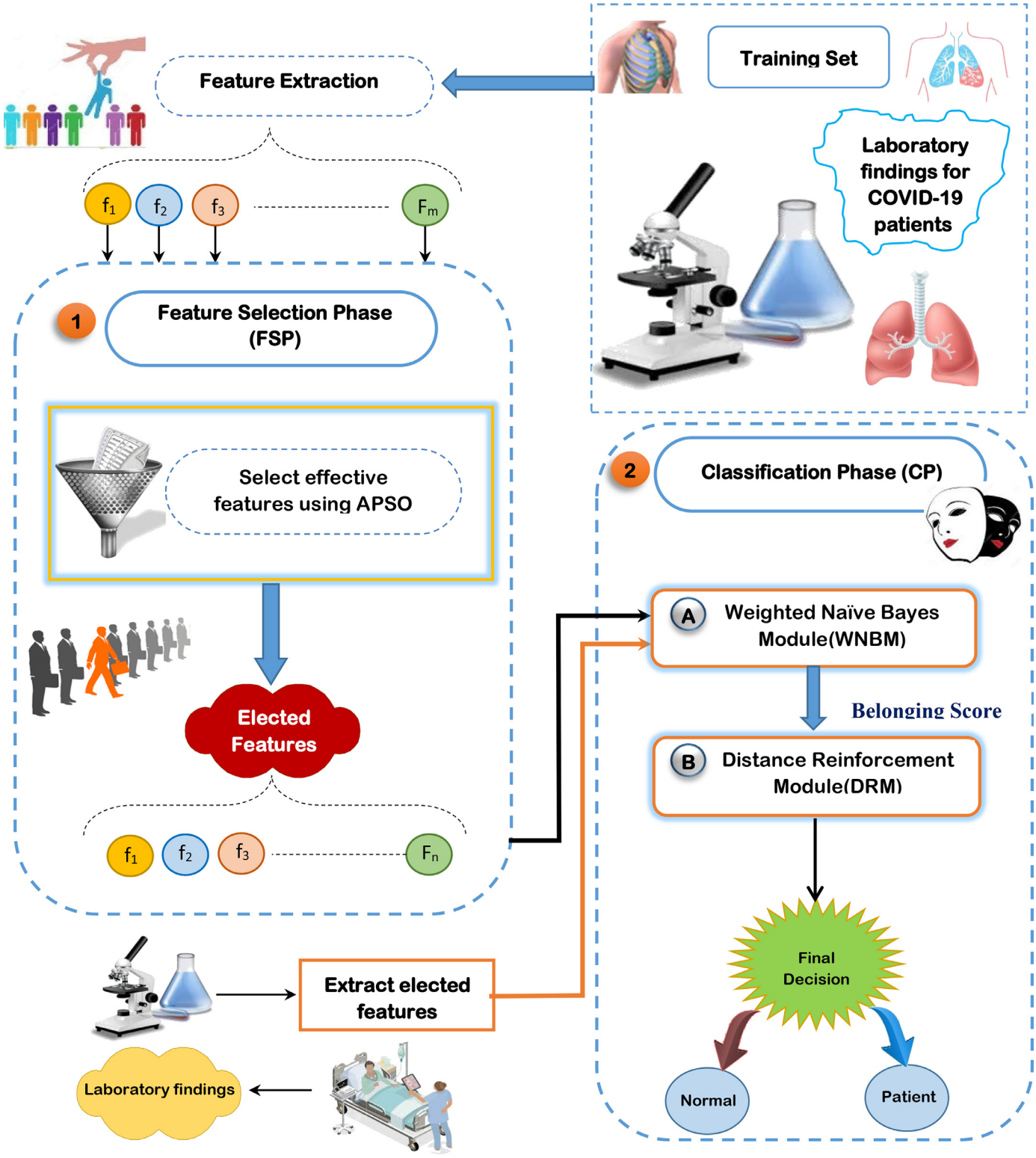

Fig. 3. The proposed DBNB classification strategy

Particle Swarm Optimization (APSO) method is provided as a new feature selection method.

APSO is a hybrid technique that integrates between filter and wrapper methods to quickly and accurately select the main subset of features that includes the most effective features for COVID-19 diagnosis. It mainly composes of two stages, called; (i) Initial Selection Stage (IS^2) using many filter methods as fast selection methods and (ii) Final Selection Stage (FS^2) using Binary Particle Swarm Optimization (BPSO) as a wrapper method that can accurately select the best subset of features. Although BPSO can accurately select the informative features, it suffers from the computational time and its convergence is very much dependent on the initial population of the particles in the swarm. For this reason, the main objective of IS^2 is to determine the initial population of

BPSO by using the results of fast selection methods in IS^2 as an initial population in FS^2 to reduce BPSO's computational time and to give it the ability to select an optimal subset of features. Finally, the best subset of features is used to improve the performance of COVID-19's classification model.

Particle Swarm Optimization (PSO) was initially designed to tackle problems in continuous numbers search space, but there are many optimization problems such as feature selection that occur in binary search spaces [38,39]. Consequently, PSO is modified to be Binary PSO (BPSO) to solve the discrete optimization problems. In fact, BPSO extended the original PSO by using the sigmoid transfer function that transforms the velocity's value from the continuous search space into discrete space. According to this transformation, velocity can indicate the probability of a particle in the position vector to take the value 1. Thus, particle's velocity in BPSO is still updated in the same manner as in the original PSO, but particle's current position, particle's best position, and global best position in the swarm can only have binary values (0 or 1). Although BPSO can accurately select the most significant features for COVID-19 diagnose in the binary space, it is so slow and randomly initializes the population of the particles in the swarm that makes its convergence difficult.

Accordingly, APSO is provided as a new selection method to speedily and optimally select the most effective features for COVID-19 diagnosis by utilizing the benefits of BPSO algorithm and tackling its problems. Before starting to implement the BPSO in FS^2, the number of the particles and their initial values in the initial population of the swarm are generated from the filter methods in IS^2. In other words, the particles have the same number of the filter methods and also have their results as initial values to enable BPSO in FS^2 to provide fast and accurate subset of informative features for COVID-19 diagnosis. Fig. 4 illustrates the sequential steps of APSO method using 'g' filter methods.

Firstly, COVID-19's dataset after performing feature extraction process on laboratory findings should be passed to IS^2 to implement 'g' filter methods on it in parallel manner. Then, the results of these filter methods will be passed to FS^2 to generate the initial population of BPSO. In Fig. 4, it is noted that the number of particles in the initial population of the swarm equals 'g' that is the same number of filter methods in IS^2. Additionally, the values of particles are the results of filter methods in IS^2. Secondly, BPSO iterations will be performed until a termination condition is satisfied. At the end, the global best position in the swarm provide the best subset of features that should be evaluated by using classifier such as Naïve Bayes (NB) as a standard classifier [34,40].

Generally, BPSO is a biologically-inspired optimization algorithm that was motivated by the social behavior of bird flocking or fish schooling to optimally solve the optimization problem depending on its fitness value [38,39]. Hence, BPSO can provide near-optimal solutions for fitness function of an optimization problem. Initially, BPSO begins with a group of particles (or "birds") as solutions called a Swarm (S).

In BPSO, each particle represents a potential solution (i.e. a subset of informative features) in an m-dimensional search space (e.g. m=12; the number of extracted features from the laboratory findings). Thus, a subset of features is represented in each particle as a binary string in which its length is the same number of features presented in the COVID-19's dataset. The value of particle bits may be zero or one. While zero in the j^{th} position in the particle denotes the elimination of the j^{th} feature in the particular subset, one denotes the selection of the j^{th} feature. An example for clarification, a single particle is represented in Table 1, assuming $m=12$, thus; $FS=\{f_1, f_2, f_3, \ldots, f_{12}\}$.

Each particle is represented in m-dimension (m= no. of features) as a vector, $(P_i, P_{Personal}, VP_i)$ where P_i represents the position of i^{th} particle; $P_i=(P_i^1, P_i^2, \ldots, P_i^m)$ and VP_i is the velocity of i^{th} particle; $VP_i=(VP_i^1, VP_i^2, \ldots, VP_i^m)$. Additionally, $P_{Personal}$ represents the best previous position of the i^{th} particle that possesses the best fitness value; $P_{Personal}=P_{pi}=(P_{pi}^1, P_{pi}^2, \ldots, P_{pi}^m)$. The global best position among all the particles determined by competition and cooperation among themselves in the swarm is called $P_{Global}=P_G=(P_G^1, P_{G2}, \ldots, P_G^m)$. Through iterations, particles adjust themselves based on its own flying experience ($P_{Personal}$) and its companions' flying experience (P_{Global}). Finally, the swarm converges to the global optimum solution.

Table 1
An example of single particle.

f_1	f_2	f_3	f_4	f_5	f_6	f_7	f_8	f_9	f_{10}	f_{11}	f_{12}
0	1	0	1	1	0	1	0	1	1	0	0

Hence, implementing BPSO as a feature selection technique requires many essential steps as shown in Fig. 4. In FS^2, 'g' particles are represented in S and then the fitness (evaluation) function of BPSO is implemented to measure the fitness degree of each particle P_i (subset of input features) based on an accuracy index of the classifier. Actually, fitness function represents an accuracy of the employed classifier such as NB classifier to select the most effective features for COVID-19 diagnosis. The fitness value of each particle can be calculated using (6).

$$Fit(P_i) = Accuracy\ (P_i) \tag{6}$$

Where $Accuracy(p_i)$ represents the classification accuracy according to a subset of features in i^{th} particle. The algorithm searches for the best particle with the aim of maximizing $Fit(p_i)$. According to fitness values for the particles in S, $P_{Personal}$ and P_{Global} in each particle memory will be updated using (7) and (8) [36].

$$P_{Personal}(P_i) = P_{pi} = \begin{cases} P_i & if(Fit(P_i) > Fit(P_{pi})) \\ P_{pi} & otherwise \end{cases} \tag{7}$$

$$P_{Global} = P_G = \begin{cases} P_{pi} & if(Fit(P_{pi}) > Fit(P_{pi+1})) \\ P_{pi+1} & otherwise \end{cases} \tag{8}$$

Where $P_{Personal}(P_i)$ represents the best solution of each i^{th} particle and P_i represents the current position of i^{th} particle. Additionally, P_{pi} represents the personal best position of i^{th} particle. $Fit(P_i)$ represents the fitness value of the i^{th} particle based on its current position. $Fit(P_{pi})$ represents the fitness value of the i^{th} particle based on its best position. P_{Global} is the best particle in whole swarm S and $Fit(P_{pi+1})$ represents the fitness value of the $(i+1)^{th}$ particle based on its best position. P_{pi+1} represents the personal best position of $(i+1)^{th}$ particle. Furthermore, $P_{Personal}$ and P_{Global} are used for updating every particle's velocity VP_i in the next iteration $(t+1)$ using (9) [36].

$$VP_i(t+1) = w * VP_i(t) + \left(c_1 r_1 \left(P_{pi}(t) - P_i(t)\right)\right) + (c_2 r_2 (P_G(t) - P_i(t))) \tag{9}$$

Where t represents the current iteration and $VP_i(t+1)$ represents the velocity of i^{th} particle at the next iteration. $VP_i(t)$ is the velocity of i^{th} particle at the current iteration and $P_{pi}(t)$ represents the personal best position of i^{th} particle at the current iteration; $P_{Personal}(P_i)$. Additionally, $P_G(t)$ represents the global best position in the swarm S at the current iteration; P_{Global}. $P_i(t)$ represents the current position of i^{th} particle at the current iteration. w is the inertia weight; $w \in [0.9\text{-}1.2]$ [36]. w is used to control the impact of the previous history of velocities on the current velocity. c_1 and c_2 are the cognitive and social acceleration constants; $c_1, c_2 \in [2\text{-}4]$. Additionally, r_1 and r_2 are uniformly distributed random numbers in the range [0,1]; $r_1, r_2 \in [0\text{-}1]$. Consequently, the adjusted velocity of

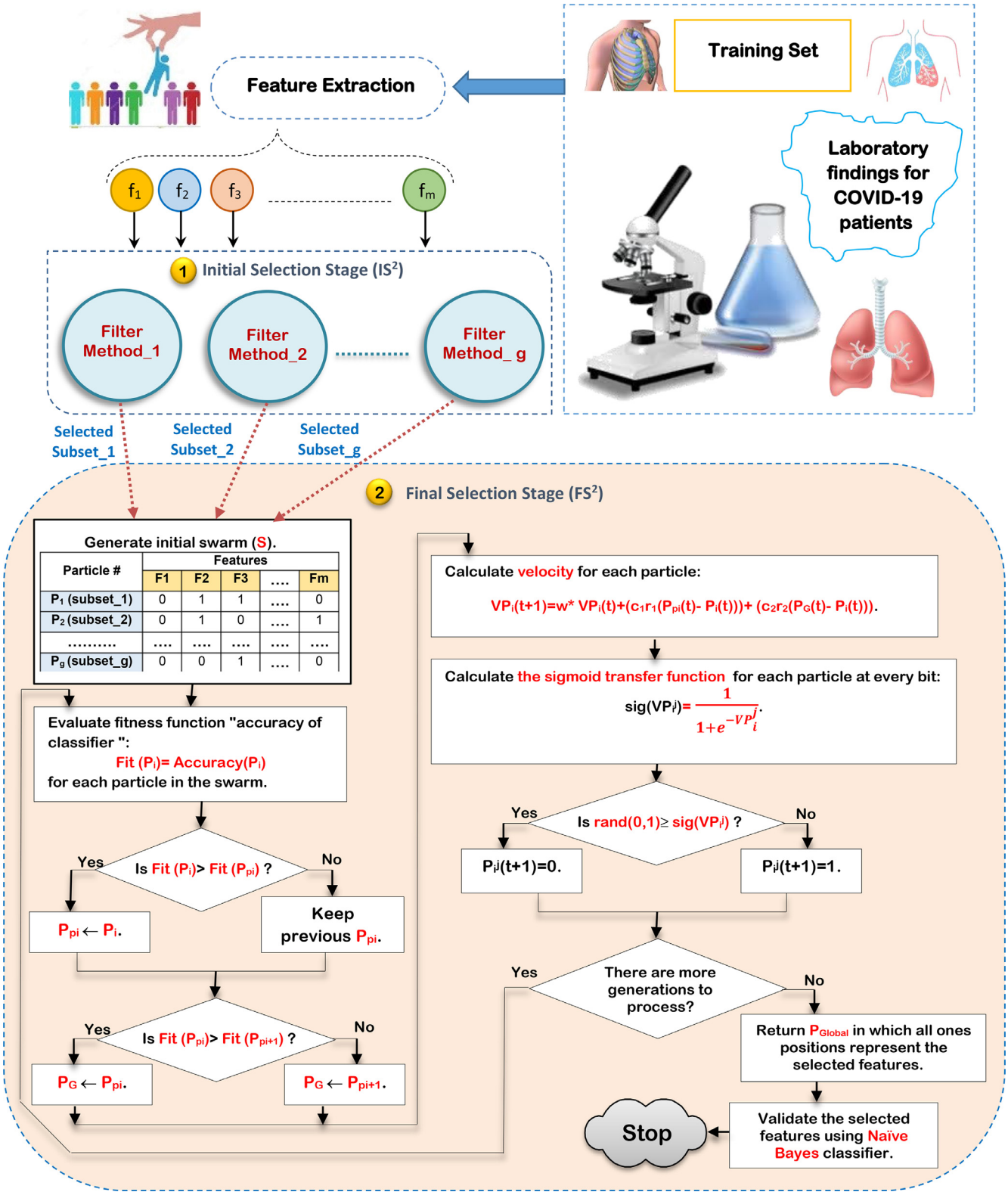

Fig. 4. The sequential steps of APSO method.

i^{th} particle $VP_i(t+1)$ depended on three main terms. The first term is $w^*VP_i(t)$ as a current motion term, the second term is $c_1r_1(P_{pi}(t)-P_i(t))$ as a cognitive term, and the third term is $c_2r_2(P_G(t)-P_i(t))$ as a social term. After calculating the velocity VP_i for every particle in S, the particle velocity can indicate the probability distribution with the main role to randomly produce the particle position. Hence, the particle position is adjusted by applying the sigmoid function that is used to identify new particle position based on binary values using (10).

$$P_i^j(t+1) = \begin{cases} 0 & if\ rand(0,1) \geq sig\left(VP_i^j\right) \\ 1 & otherwise \end{cases} \quad (10)$$

Where $P_i^j(t+1)$ represents the value of i^{th} particle at j^{th} position in the next iteration $t+1$. In other words $P_i^j(t+1)$ indicates to the value of j^{th} feature in i^{th} particle; $j=1,2,3,\ldots..,m$. $rand(0,1)$ is a random value between [0,1]. Additionally, $sig(VP_i^j)$ is the sigmoid transfer function that indicates the probability of j^{th} bit in which it takes 0 or 1 value. $sig(VP_i^j)$ is calculated by using (11).

$$sig\left(VP_i^j\right) = \frac{1}{1+e^{-VP_i^j}} \quad (11)$$

Where e is the base of the natural logarithm. Based on the new position $P_i(t+1)$ of every particle in S, every particle is evaluated using the fitness function in (6). Then, these calculations are continued until the number of generations is finished. At the end, the best particle of the whole swarm P_{Global} is the output and the algorithm terminates. All features donated by 1 in this particle represent the most effective features for COVID-19 diagnosis. After applying APSO algorithm on the COVID-19's dataset that contains the features, six different features will be selected as the best subset of features. These selected features are White Blood Cell (WBC), Lymphocyte (LYM), D-Dimer (D-D), C-Reactive Protein (CRP), Procalcitonin (PCT), and Locate Dehydrogenase (LDH).

To implement APSO, assume that there are 'm' dimensional Feature Space; $FS=\{f_1, f_{2,\ldots..}f_m\}$. Additionally, the input training data of 'n' patients can be expressed by $D=\{T_1, T_{2,\ldots..}, T_n\}$ and the testing data of 'q' patients can be expressed by $Q=\{E_1, E_{2,\ldots..}E_q\}$. Each item of $T_i \in D$ and $E_j \in Q$ is expressed as an ordered set of 'm' features; $T_i(f_1, f_2, f_3, \ldots., f_m)=[f_{1i}, f_{2i}, f_{3i}, \ldots, f_{mi}]$ and $E_j(f_1, f_2, f_3, \ldots., f_m)=[f_{1j}, f_{2j}, f_{3j}, \ldots, f_{mj}]$. Hence, each item T_i and E_j can be expressed in an 'm' dimensional space of features. For COVID-19 diagnosis, it is an important to reduce m-dimensions or eliminate non-informative features in COVID-19's dataset to avoid overfitting and enhance the performance of the classification model. The sequential steps of APSO method using 'g' filter methods is illustrated in Algorithm 1.

To illustrate the idea, assume that there are four filter methods in IS[2], which are; Information Gain (IG) [31,32], Chi-square (CHI) [41,42,43], Fisher score (F) [44], and Correlation Based Feature Selection (CBFS) [45]. Additionally, consider that the number of features in COVID-19's dataset is six (m=6); $FS=\{f_1, f_2, f_3, f_4, f_5, f_6\}$. After implementing IG, CHI, F, and CBFS on the dataset, it is assumed that the subset of selected features according to these methods are; $\{f_1, f_3, f_5, f_6\}$, $\{f_3, f_4, f_6\}$, $\{f_1, f_2, f_3, f_4, f_6\}$, and $\{f_1, f_2, f_5, f_6\}$ respectively. Hence, these four subsets of features are used as four particles (P_1, P_2, P_3, P_4) in the initial swarm (S) of BPSO in FS[2]. Then, BPSO is implemented related to many assumptions in Table 2.

According to these assumptions, it is assumed that BPSO is implemented through two iterations providing new swarm that includes new values at four particles; $P_1=\{0,1,1,1,1,0\}$, $P_2=\{1,1,0,1,1,1\}$, $P_3=\{0,0,0,0,1,1\}$, and $P_4=\{1,1,1,0,0,1\}$. After evaluating P_1, P_2, P_3, and P_4, it is considered that P_4 achieves the highest fitness value, thus, P_4 is the best particle in the swarm P_{Global} that provides the best subset of features. Finally, the most effected features in COVID-19's dataset are; $\{f_1, f_2, f_3, f_6\}$.

6.2. Classification phase (CP)

Due to its easiness as well as its good performance, Naive Bayes (NB) is widely employed to address classification problems in various real-world applications. However, NB sometimes suffers from degraded performance due to the unrealistic assumption that all features are independent and equally important. In order to alleviate such defectiveness, two issues will be considered to guarantee the maximum performance and to compensate the drawbacks of that robust classifier, which are; (i) assigning weights to the elected COVID-19 features, hence, the result is a Weighted Naïve Bayes (WNB) classifier, and (ii) fine tuning the decision of WNB using distance based biasing. Such biasing is based on the distance between the input item to be classified and the center of the target classes in the employed feature space [46].

The Classification Phase (CP) is divided into two modules. The first is the Weighted Naïve Bayes Module (WNBM) at which a WNB classifier is employed to take the initial decision of the degree of belonging of the input item to be classified to each of the considered classes. A feature weight vector is generated then employed to derive the decision taken by the WNB classifier. On the other hand, the second module is the Distance Reinforcement Module (DRM) at which the item belonging degree estimated by WNBM is finely tuned to take the final decision.

Hence, the new item can be easily classified to one of the considered target classes. The next subsections explain the details of both modules of the classification phase.

6.2.1. Weighted Naïve Bayes module (WNBM)

Despite its simplicity, NB classifier has exhibited surprisingly performance on a variety of data mining and machine learning problems for COVID-19 patients diagnose. However, due to the assumption that all features are independent and equally important, the predictions estimated by NB are sometimes poor. For illustration, for predicting whether a patient has a COVID-19 disease, his White Blood Cell count is supposed to be much more important than his height. The performance of NB can be improved by mitigating this assumption by giving a weight for each elected feature. In this subsection, an initial belonging score is assigned to the input item to be classified given each class label based on a WNB classifier.

As the efficiency is essential in COVID-19 disease diagnoses system, each elected feature will be weighted based on an efficiency of a base classifier. The weight of the feature f_y, denoted as; w_y is an indication to the feature impact and is defined as the degradation percentage of the model accuracy after discarding f_y from the input feature set. Several base classifiers can be used to implement the underlying model such as; classical Naïve Bayes (NB), K-Nearest Neighbors (KNN), and Support Vector Machines (SVM).

Feature weighting is a critical task that can promote the diagnose accuracy. The weight of a feature can be defined as the positive effect of the feature on the overall system accuracy. It can be modeled as the difference between the accuracy of the model in the presence of the feature and in its absence. The feature weight can be calculated by (12).

$$w_y = accuracy(+f_y) - accuracy(-f_y) \quad (12)$$

Where w_y is the weight (impact) of feature f_y, $accuracy(+f_y)$ is the accuracy of the model when the feature f_y is included in the feature set, and $accuracy(-f_y)$ is the accuracy of the model when f_y is removed. The normalized weight of each feature is calculated using (13).

$$Nw_y = \frac{w_y}{\max\limits_{\forall\ w_m} w_m} \quad (13)$$

Algorithm 1. Feature selection using APSO algorithm.

Feature Selection using APSO Algorithm

Inputs:

g=No. of particles in swarm "swarm size" equals no. of filter methods.
P=P_1....P_g; group of particles in swarm.
TRD= (D, FS); Training dataset.
TED=(Q, FS); Testing dataset.
m=|FS|; No. of features in training and testing dataset.
Initiate c_1,c_2∈[2-4]; the cognitive and social acceleration constants.
Initiate r_1,r_2∈[0-1]; uniformly distributed random numbers.
Initiate w∈[0.9-1.2]; inertia weight.
Initiate rand∈[0-1]; uniformly distributed random number.

Output:

O= the optimum particle of the whole swarm (P_{Global}).

Steps:

// Implement 'g' filter methods on training and testing dataset.

1: **For every filter method y ∈ g**
2: Determine the subset of selected features for every method as *Subset (y)*.
3: **End For**

// Construct initial population of the swarm.

4: Put 'g' Subsets as the values of 'g' particles in an initial population of swarm (S) with particles donated by (P).

// Evaluate fitness value of each particle.

5: **For every P_i∈P**
6: Fit (P_i)=Accuracy (P_i)
7: **End for**

// Update the optimum solution of each particle ($P_{Personal}$).

8: **For every P_i∈P**
9: $$P_{Personal}(P_i) = P_{pi} = \begin{cases} P_i & if(Fit(P_i) > Fit(P_{pi})) \\ P_{pi} & Else \end{cases}$$
10: **End for**

// Update the optimum particle of the whole swarm (P_{Global}).

11: **For every P_i∈P**
12: $$P_{Global} = P_G = \begin{cases} P_{pi} & if(Fit(P_{pi}) > Fit(P_{pi+1})) \\ P_{pi+1} & Else \end{cases}$$
13: **End for**

// Calculate the new velocity of each particle.

14: **For every P_i∈P**
15: $$VP_i(t+1) = w * VP_i(t) + \left(c_1 r_1 \left(P_{pi}(t) - P_i(t)\right)\right) + \left(c_2 r_2 \left(P_G(t) - P_i(t)\right)\right)$$
16: **End for**

Algorithm Parameters	
g	No. of particles in swarm "swarm size"= No. of filter methods.
P	Group of particles in swarm; P=P_1....P_g.
TRD	Training dataset contents of training items D and its features FS; TRD= (D, FS).
TED	Testing dataset contents of testing items Q and its features FS; TED= (Q, FS).
m	No. of features in training and testing dataset; m=|FS|.
c_1,c_2	The cognitive and social acceleration constants; c_1,c_2∈[2-4]; c_1+c_2=4.
r_1,r_2	Uniformly distributed random numbers; r_1,r_2∈[0-1].
w	Inertia weight; w∈[0.9 -1.2].
rand	Uniformly distributed random number; rand∈[0-1].
O	The optimum particle of the whole swarm (P_{Global}).
Subset (y)	The subset of selected feature at filter method y.
P	Group of particles in swarm; P=P_1,P_2,.....,P_g.
P_i	The i^{th} particle in the swarm.
Accuracy(P_i)	The classification accuracy according to the selected features in i^{th} particle.
Fit(P_i)	The fitness value of P_i particle.
$P_{Personal}$(P_i)	The optimum solution of P_i particle; P_{Pi}
P_{Global}	The optimum particle of the whole swarm; P_G.
VP_i(t+1)	The new velocity of particle P_i for iteration t+1.
sig(VP_i^j)	The sigmoid function of i^{th} particle velocity at j^{th} position.
P_i(t+1)	The new position of particle P_i for iteration t+1.

// Calculate the sigmoid function of each particle position.

17: **For every P_i∈P**
18: $$sig(VP_i^j) = \frac{1}{1+e^{-VP_i^j}}$$
19: **End for**

// Calculate the new position of each particle based on binary values.

20: **For every P_i∈P**
21: $$P_i^j(t+1) = \begin{cases} 0 & if(rand(0,1) > sig(VP_i^j)) \\ 1 & Else \end{cases}$$
22: **End for**
23: *Updating the values of w, c_1,c_2,r_1, and r_2 parameters according to their corresponding ranges.*

24: **if (there are more generations to process) then**
25: *Go to step5.*
26: **Else**
27: *Return P_{Global} in O, where all ones bits in this particle represents the best selected features.*
28: **End if**
29: Validated the selected features using NB classifier.

Table 2
The assumptions for employing BPSO in FS^2.

No.	Assumption	Value
1	No. of generations to process	2
2	Swarm size (no. of particles)	4"No of filter methods in IS^2"(g)
3	Initial $P_{personal}$(p_i)	P_i
4	Initial P_{Global}	0
5	Initial VP_i	0
6	Particle size "P"	6" No. of features" (m)
7	Fitness function	Accuracy of NB classifier
8	Initial swarm	P_1={1, 0, 1, 0, 1, 1}@@P_2={0, 0, 1, 1, 0, 1}@@P_3={1, 1, 1, 1, 0, 1}@@P_4={1, 1, 0, 0, 1, 1}
9	w	1.1
10	c_1=c_2	2
11	r_1=r_2	0.6

A feature weight vector is constructed that stores the normalized weight of all the elected features by the feature selection phase. The Belonging Score (BS) of an input item I_x to a class c_i can be calculated by (14).

$$BS(I_x,\ c_i) = P(c_i) * \prod_{\substack{j=1 \\ where\ w_j \in \mathbb{R}^+}}^{n} P\left(f_j|c_i\right)^{Nw_j} \tag{14}$$

Where $BS(I_x,c_i)$ is the belonging score for the input item I_x given the class label c_i, $P(c_i)$ is the prior probability of the class c_i, Nw_j is the normalized weight of the j[th] feature, $P(f_j|c_i)$ is the conditional probability of the feature f_j given the class c_i.

6.2.2. Distance reinforcement module (DRM)

To take the final decision, the input item should be classified to one of the target classes. To accomplish such aim, initially, all items (of different target classes) are projected into the considered n dimensional feature space. The center of each class containing t examples in n dimensional feature space for can be accomplished using (15).

$$C = \left\{ \frac{\sum_{q=1}^{t} V_q^1}{t}, \frac{\sum_{q=1}^{t} V_q^2}{t}, \ldots, \frac{\sum_{q=1}^{t} V_q^n}{t} \right\} \tag{15}$$

Where C is the class center in the considered n dimensional feature space, t is the number of examples within the class, and V_q^i is the value of the i^{th} dimension of the q^{th} example. The input item to be classified (e.g., I_x) is also projected into the n dimensional feature space. Then, the Affiliation Degree (AD) of the input item given each target class is determined using (16).

$$AD(I_x, c_i) = \frac{BS(I_x,\ c_i)}{Dis(I_x, Center\langle c_i \rangle)} \tag{16}$$

Where $AD(I_x,c_i)$ is the affiliation degree of the input item I_x given the class c_i, $BS(I_x,c_i)$ is the belonging score for the input item I_x given the class label c_i, $Dis(I_x,Center\ <c_i>)$ is the Euclidian distance between the input item I_x and the center of class c_i in the feature space. Calculating the distance between two points p_x and p_y in the n dimensional feature space can be calculated using (17):

$$Dis(p_x, p_y) = \sqrt{\sum_{i=1}^{n} \left(p_x^i - p_y^i\right)^2} \tag{17}$$

Where p_x^i and p_y^i is the value of the i^{th} dimension of the points p_x and p_y respectively in the n dimensional feature space as illustrated in Fig. 5 considering 3 target classes. Finally, the target class of the input item I_x, denoted as $Target(I_x)$, can be identified using (18).

$$Target\,(I_x) = \underset{c_i \in C}{\operatorname{argmax}} \left[AD(I_x,\ c_i) \right]$$

$$Target\,(I_x) = \underset{c_i \in C}{\operatorname{argmax}} \left[\frac{BS(I_x,\ c_i)}{Dis(I_x, Center\langle c_i \rangle)} \right]$$

$$Target\,(I_x) = \underset{c_i \in C}{\operatorname{argmax}} \left[\frac{P(c_i) * \prod_{\substack{j=1 \\ where\ w_j \in \mathbb{R}^+}}^{n} P\left(f_j|c_i\right)^{Nw_j}}{Dis(I_x, Center\langle c_i \rangle)} \right] \tag{18}$$

Where $P(c_i)$ is the prior probability of the class c_i, Nw_j is the normalized weight of the j[th] feature, $P(f_j|c_i)$ is the conditional probability of the feature f_j given the class c_i.

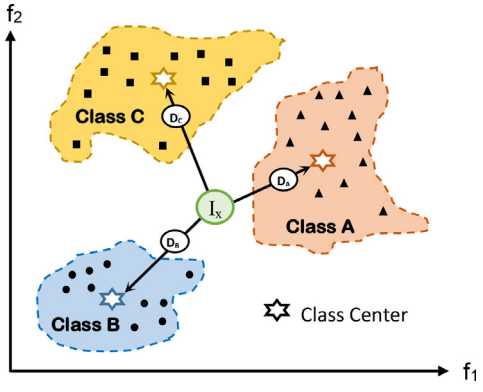

Fig. 5. Calculating the distance to class centers.

6.2.3. Illustrative example

In this subsection, an illustrative example showing how the diagnose decision can be taken in the classification phase of the proposed Distance Biased Naïve Bayes (DBNB) classification strategy. As illustrated in Table 3, consider a COVID-19 diagnose database for 10 persons considering 5 features labeled f_1, f_2, f_3, f_4, *and* f_5 and two target classes, namely; "True" and "False" diagnose. The symbols L, M, and H represents Low, Medium, and High respectively, while T and F represents True or False diagnose of COVID-19 virus. The weight of each feature is also reported in the last row of Table 3. On the other hand, the conditional probability for each feature value given different classes as well as the prior probability for each class are illustrated in (Tables 4–9).

Assume an input case I_x that represents a probable COVID-19 patient. Such input case can be expressed as a point in the n-dimensional feature space using its numerical values of those considered features. The distance from the input case to the centers of "True Diagnosed" and "False Diagnosed" classes are assumed to be 6.3 and 12.7 respectively. The features numerical values of I_x can be expressed by the following feature vector F_x=<*M, H, L, M, H*>,

Table 3
An example of single particle.

Case number	f_1	f_2	f_3	f_4	f_5	Diagnose
1	L	L	H	M	L	T
2	H	H	H	M	L	F
3	M	L	L	L	H	T
4	L	H	L	L	H	T
5	M	L	L	L	H	T
6	H	H	H	M	L	F
7	M	H	L	H	H	F
8	L	L	H	L	L	F
9	M	H	L	H	L	T
10	H	L	L	L	H	T
Normalized Weight	1	0.7	0.8	0.5	0.6	

Table 4
Conditional probabilities for feature f_1.

Values	Classes		P(f_1|T)	P(f_1|F)
	T	F		
L	2	1	2/6	1/4
M	3	1	3/6	1/4
H	1	2	1/6	2/4
Total	6	4	100%	100%

Table 5
Conditional probabilities for feature f_2.

Values	Classes		P(f_2|T)	P(f_2|F)
	T	F		
L	4	1	4/6	1/4
H	2	3	2/6	3/4
Total	6	4	100%	100%

Table 6
Conditional probabilities for feature f_3.

Values	Classes		$P(f_3\|T)$	$P(f_3\|F)$
	T	F		
L	5	1	5/6	1/4
H	1	3	1/6	3/4
Total	6	4	100%	100%

Table 7
Conditional probabilities for feature f_4.

Values	Classes		$P(f_4\|T)$	$P(f_4\|F)$
	T	**F**		
L	4	1	4/6	1/4
M	1	2	1/6	2/4
H	1	1	1/6	1/4
Total	6	4	100%	100%

Table 8
Conditional probabilities for feature f_5.

Values	Classes		$P(f_5\|T)$	$P(f_5\|F)$
	T	F		
L	2	3	2/6	3/4
H	4	1	4/6	1/4
Total	6	4	100%	100%

Table 9
Prior probabilities of the target classes.

Diagnose	Count	Prior probability
T	6	P(T)=6/10
F	4	P(F)=4/10
Total	10	1

which represents the corresponding linguistic values for features f_1, f_2, f_3, f_4, and f_5 respectively. It is needed to detect the corresponding target class of I_x. Initially, the belonging score to each class (e.g., "T" or "F") is determined as following;

$$BS(I_x,\ T) = P(T) * \prod_{j=1}^{5} P\left(f_j|T\right)^{Nw_j}$$
$$= 0.6 * \left[\left(\frac{3}{6}\right)^{1.0} * \left(\frac{2}{6}\right)^{0.7} * \left(\frac{5}{6}\right)^{0.8} * \left(\frac{1}{6}\right)^{0.5} * \left(\frac{4}{6}\right)^{0.6}\right]$$
$$= 0.0383$$

$$BS(I_x,\ F) = P(F) * \prod_{j=1}^{5} P\left(f_j|F\right)^{Nw_j}$$
$$= 0.4 * \left[\left(\frac{1}{4}\right)^{1.0} * \left(\frac{3}{4}\right)^{0.7} * \left(\frac{1}{4}\right)^{0.8} * \left(\frac{2}{4}\right)^{0.5} * \left(\frac{1}{4}\right)^{0.6}\right]$$
$$= 0.0083$$

Then, the Affiliation Degree (AD) of the input item given "True" and "False" diagnose classes is determined, which are found to be 0.006 and 0.00065 as shown below. Since, $AD(I_x,T) > AD(I_x,F)$, then the input case for a COVID-19 infected patient.

$$AD(I_x, T) = \frac{BS(I_x,\ T)}{Dis(I_x, Center\langle T\rangle)} = 0.0383/6.3 = 0.006$$

$$AD(I_x, F) = \frac{BS(I_x,\ F)}{Dis(I_x, Center\langle F\rangle)} = 0.0083/\ 12.7 = 0.00065$$

Table 10
. The applied parameters with the corresponding used values.

Parameter	Description	Applied value
m	No. of extracted features	12
w	Inertia weight	1.1
c1	The cognitive acceleration	2
c2	The social acceleration	
r1	Uniformly distributed	0.6
r_2	random number	

7. Experimental results

In this section, the proposed Distance Biased Naïve Bayes (DBNB) classification strategy will be evaluated. DBNB is implemented through two sequential phases, which are; Feature Selection Phase (FSP), and Classification Phase (CP). In FSP, APSO was proposed as a new feature selection method to select the most significant features extracted from patients laboratory findings. Then, those elected features are weighted during feature weighting module using classical NB classifier as a base classifier to assign a weight to each identified feature based on its effect on the classification accuracy to determine the importance of each feature. Those weighted features used to enable WNB classifier to take the initial decision. Then, depending on the distance between the testing item and the class center in DRM, the final decision is taken. During the following experiments, four evaluation criteria called accuracy, precision, sensitivity, and the inference time will be used to evaluate each part of the proposed strategy [36]. Our implementation is based on a set of laboratory findings for COVID-19 patients collected from Mansoura University Hospital in Egypt. This collected data (patients dataset) has been employed to allow reproduction of the results introduced in this paper. Due to the small number of available dataset, cross-validation is used to validate the classification model. In this paper, 10-fold cross-validation is used to divide the dataset into 10 equal partitions in which it uses one of these sets as a testing set and the remaining nine as training sets. Hence, the number of training and testing patients are 2700 (90%) and 300 (10%) respectively. The applied parameters with the corresponding implemented values are depicted in Table 10.

To implement the proposed DBNB in the training phase, (i) the number of patients in the dataset is 3000 patients including both COVID-19 and non COVID-19 patients, and (ii) the number of used features in both training and testing dataset is twelve features routine blood exams. These features are; {*White Blood Cell (WBC), Aspartate aminotransferase (AST), Alanine Aminotransferase (ALT), Locate Dehydrogenase (LDH), C-reactive protein (CRP), Procalcitonin (PCT), Creatinine (Cr), Fibrinogen (FIB), Neutrophils (NEU), Lymphocytes (LYM), Interleukin-6 (IL-6), D-Dimer (D-D).* To select the most effective features, APSO is used to select the most significant features extracted from patients routine blood exams. Firstly, the patients laboratory findings pass in parallel manner through a set of filter methods which are; Information Gain (IG) [31,32], Chi-square (CHI) [41,42,43], Fisher score (F) [44], and Correlation Based Feature Selection (CBFS) [45]. After implementing IG, CHI, F, and CBFS on the patients laboratory findings, the subset of selected features according to these methods are; *{WBC, LDH, CRP, Albumin, NEU, IL-6}, { WBC, AST, ALT, PCT}, { WBC, LDH, LYM, NEU, D-D}, and {WBC, LDH, LYM, NEU, D- D}* respectively. Hence, these four subsets of features are used as the initial swarm (S) of BPSO in FS^2 to select the best subset of features. These features are six features, which are; *{WBC,LDH, LYM,CRP, NEU, D- D}*.

Table 11
Dataset description.

Criteria	Value / Description						
Total number of cases	male				female		
	1969				1031		
Not sick (ordinary) cases	410						
Sick cases	COVID-19				Other		
	1990				600		
COVID-19 patients	<15	15-25	25-35	35-45	45-55	55-65	>65
	20	98	170	287	395	420	600

7.1. Dataset description

Dataset represents medical records of data collected on patients from Mansoura University Hospital in Egypt [47]. These records contain results of laboratory findings from various cases who have different ages, sex (male or female), and diseases. The number of the collected dataset equal to 3000 cases. In fact, the cases in the collected dataset are categorized into COVID-19 patients, and non COVID-19 patients as presented in Table 11. COVID-19 patients are people who suffer from COVID-19 disease. On the other hand, non COVID-19 patients are people who do not suffer from COVID-19 disease, but they may suffer from other diseases. Thus, the cases of non COVID-19 patients have been categorized into normal people who do not suffer from any disease, patients who suffer from other lung diseases, and patients who have chronic diseases such as diabetes and pressure diseases. The distribution of the used cases in the collected dataset has been represented according to "Age", "Sex", and "type of disease", as shown in (Figs. 6–8).

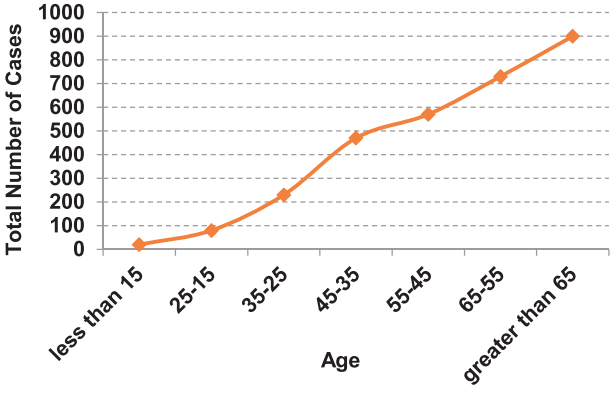

Fig. 6. The total number of cases according to age.

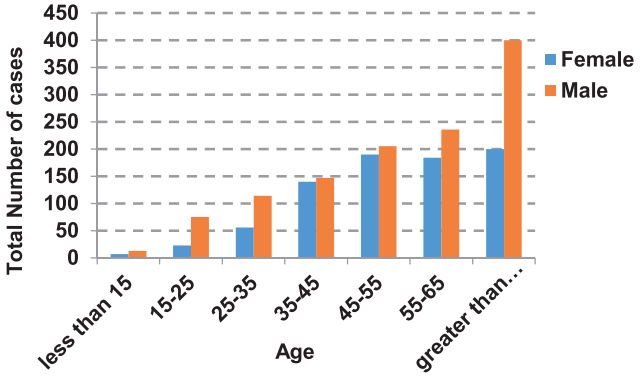

Fig. 7. The total number of COVID-19 cases according to age and sex.

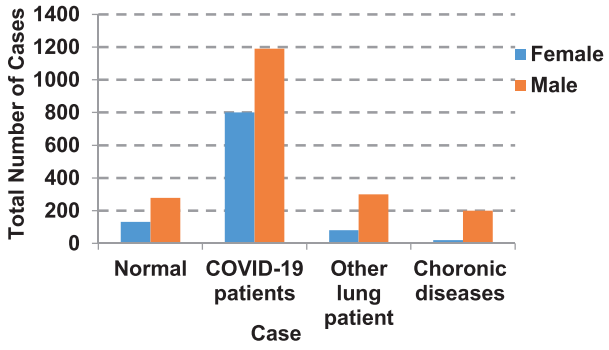

Fig. 8. The presentation of COVID-19 patient and non COVID-19 patient distribution.

Table 12
Clinical laboratory data for 1990 COVID-19 patients.

Features	Normal Range	Severe group n=696	Mild group N=1294
WBC, x109 per L	3.5-9.5	4.96 ± 1.85	4.26 ± 1.64
AST, U/L	15-40	33.21 ± 18.24	27.80 ± 11.42
ALT, U/ L	9-50	24.50 (15.75, 37.75)	27.00 (21.00, 41.00)
LDH, U/L	120-250	360–540	183–360
CRP, mg/L	0-10	18.76 ± 22.20	39.37 ± 27.68
PCT, ng/ml	<0.1	0.02 (0.01, 0.04)	0.04 (0.02,0.09)
FIB, g/L	2-4	3.11 ± 0.83	3.84 ± 1.00
Cr, µmol/L	74.3-107	66.96 ± 13.38	65.33 ± 15.55
NEU, x109 per L	1.8-6.3	3.43 ± 1.63	2.65 ± 1.49
LYM, x109 per L	1.1-3.2	1.07 ± 0.40	1.20 ± 0.42
IL-6, pg/L	≤ 20	10.60 (5.13, 24.18)	36.10 (23.00, 59.20)
D-D, μg/ L	0-0.55	0.21 (0.19, 0.27)	0.49 (0.29, 0.91)

Table 13
Performance of APSO in terms of accuracy, precision, and recall.

Fold	Accuracy	Precision	Recall
1	93.4%	91.68%	92.28%
2	94.5%	95.5%	95.5%
3	92.63%	94.2%	94%
4	94.72%	95.01%	94%
5	95.52%	95.8%	94%
6	95.36%	94.54%	95.76%
7	94.52%	94.98%	95.61%
8	94.52%	95.98%	96.79%
9	93%	91.5%	95.29%
10	94.54%	94.6%	91.5%
Average	94.271%	94.379%	94.473%

7.1.1. Statistical analysis

COVID-19 Patient characteristics were compared by using *t* tests for continuous variables and chi-squared or Fisher exact tests for categorical variables. Descriptive statistics are expressed as *mean* ± *standard deviation* (SD). $P \leq .05$ was considered statistically significant. All statistical analyses were performed using SPSS, version 23.0, software (SPSS, Chicago, IL). Table 12 shows the statistical analysis of COVID-19 patients laboratory findings.

7.2. Testing the proposed advanced particle swarm optimization (APSO)

In this section, the proposed Advanced Particle Swarm Optimization (APSO) will be evaluated based on NB classifier as a standard classifier. Results are shown in Table 13. Also, to prove the effectiveness of the proposed method, many features selection techniques are compared to the proposed features selection technique APSO. The most recent feature selection techniques used for evaluation are Hybrid Fuzzy ARTMAP and Brain Storm Optimiza-

Table 14
Comparison between APSO and the existing feature selection techniques in terms of accuracy, precision, recall, and inference time.

Used Technique	Accuracy	Precision	Recall	Inference time (Sec)
FAM-BSO	92.8%	92%	92.2%	14
OCS	89%	89.234%	89.98%	11
FWFSS	91.12%	90.58%	90.8%	12.5
HFS	93.3%	92.89%	92.5%	12
APSO	94.271%	94.379%	94.473%	9

Table 15
Performance of WNBM in terms of accuracy, precision, and recall.

Fold	Accuracy	Precision	Recall
1	96.5%	95.2%	96.6%
2	95.98%	94.9%	93.98%
3	97.5%	96.8%	96.99%
4	97.5%	96.8%	96.99%
5	95.36%	94.6%	93.6%
6	96.365%	95.87%	94.12%
7	97%	96.8%	94.2%
8	95.98%	94.6%	93.9%
9	96.78%	95%	94.9%
10	96.89%	95.5%	94.99%
Average	96.585%	95.607%	95.027%

Table 16
Comparison between WNBM and the existing classification techniques in terms of accuracy, precision, recall, and inference time.

Used technique	Accuracy	Precision	Recall	Inference time (Sec)
EKNN	93.5%	90.9%	92.3%	18
NB-PKC	94.02%	91.68%	90.78%	13
WOA-SVM	92.6%	90.89%	91%	14
WNBM	96.585%	95.607%	95.027%	11

tion (FAM-BSO) [48], Opposition-based Crow Search (OCS) algorithm [49], Filter-Wrapper Feature Subset Selection (FWFSS) [50], and parallelized Hybrid Feature Selection (HFS) [51]. Results are depicted in Table 14.

As shown in Table 13, the results are presented for each fold, and the average values are also calculated. According to Table 13, the average accuracy, precision, and recall for APSO are 94.271%, 94.379%, and 94.473% respectively. APSO can provide fast and efficient feature selection method as shown in Table 14. Consequently, APSO is much better than FAM-BSO, OCS, FWFSS, and HFS.

7.3. Testing the proposed weighted Naïve Bayes module (WNBM)

During this subsection, the proposed Weighted Naïve Bayes Module (WNBM) will be evaluated. WNBM is compared against the most recently used classification methods which are; (i) Enhanced K-Nearest Neighbors (EKNN) [52], (ii) Naïve Bayes-Probabilistic Kernel Classifier (NB-PKC) [53], and (iii) Whale Optimization Algorithm-SVM (WOA-SVM) [54]. Results are shown in Tables 15 and 16.

Table 15, presents the accuracy, precision, and recall results for WNBM. As shown in Table 15, the lower performance values of WNBM are reported for 2, 5 and 8-fold, while the best values are reported for 1, 3, 4, 6, 7, 9, and 10 fold. The average accuracy, precision, and recall for WNBM are 96.585%, 95.607%, and 95.027% respectively. As illustrated in Table 16, it is concluded that WNBM is much better and faster than EKNN, NB-PKC, and WOA-SVM.

Table 17
Performance of DBNB in terms of accuracy, precision, and recall.

Fold	Accuracy	Precision	Recall
1	97.78%	96%	96.5%
2	96.86%	95.9%	95%
3	96.86%	95.5%	95.5%
4	97.78%	96%	96.5%
5	97.78%	96%	96.5%
6	97.78%	96.6%	96.85%
7	96.86%	95.86%	95%
8	97.78%	96.5%	96.5%
9	97.78%	96%	96.85%
10	97.78%	97.1%	97.2%
Average	97.504%	96.146%	96.24%

Table 18
Comparison between DBNB and the existing classification techniques in terms of accuracy, precision, and recall.

Used technique	Accuracy	Precision	Recall
CNN	84.2%	85.3%	82.12%
GMDH	92.4%	93%	91%
CPDS	94.6%	90.06%	91.63%
DarkCovidNet	85%	87.2%	85.21%
CS	90.2%	89.19%	89.4%
DBNB	97.504%	96.146%	96.24%

7.4. Testing the proposed distance biased Naïve Bayes (DBNB) classification strategy

Through this subsection, it is the time to test the proposed DBNB. All capabilities proposed are used in our DBNB, hence, APSO is employed for feature selection, and the proposed classification model that contains two modules called WNBM and DRM is used for classification. Results are shown in Table 17. Also, to argue the effectiveness of our proposed strategy for diagnosing COVID-19 patients, it is compared against some of the recently used COVID-19 classification methods which are; CNN [22], GMDH [23], CPDS [24], DarkCovidNet [25], and CS [26]. Results are shown in Table 18.

Table 17 presents the accuracy, precision, and recall, for DBNB to detect COVID-19 patient. The lower performance values of the DBNB model are presented for 2, 3, and 7-fold, while the best values are presented for 1, 4, 5, 6, 8, 9,and 10-fold. The average accuracy, precision, and recall are 97.504 %, 96.146%, and 96.24% respectively. According to Table 18, it is concluded that the performance of DBNB is much better than CNN, GMDH, CPDS, DarkCovidNet, and CS. The reason is that DBNB gives fast and accurate detection for the infected COVID-19 patients based on using the proposed modules in CP which are; WNBM and DRM depending on the most effective and significant features for COVID-19 diagnosis which are selected through FSP. Finally, DBNB is much better than other recent methods according to many metrics of measurement as it has the ability to quickly and accurately diagnose COVID-19 patients. Also, DBNB is also more simple, flexible and able to detect any disease. DBNB has proven to be a safe decision-making system for detecting COVID-19 patients. Consequently, it protects the healthcare system from exhaustion.

8. Conclusions and future work

COVID-19 infection was grown at rapid rate and still threatens the lives of billions of people. Therefore, early detection of COVID-19 patients is a vital for disease cure and control. The literature review work shows that no optimal technique can be determined yet. In this work, we have presented an accurate and intelligent classification strategy which can potentially provide smart medical

diagnosis. In our classification strategy, DBNB is built upon two essential parts, which are; features selection, and new classification model. The proposed feature selection methodology is called APSO which combines between the benefits of both filter and wrapper selection methods. APSO elects the most informative and effective features from the extracted features from patients laboratory findings. Then, the elected features are weighted to feed the proposed classification model that contains two modules called WNBM and DRM to make accurate and correct decision. Experimental results showed that the proposed DBNB provides fast and accurate results comparing to other recent methods in terms of accuracy, precision, sensitivity, and inference time.

In spite of its effectiveness in diagnosing COVID-19 patients, the proposed DBNB relies only on numerical data. However, nominal data such as the data extracted by analyzing CT images may be valuable for confirming the infection. With regard to future research, more work can be done to combine the proposed diagnose strategy (e.g., DBNB) with other diagnose strategies that depend on nominal data. This may promote the diagnose accuracy. Moreover, test-cost should be performed on the proposed APSO to achieve the maximum accuracy as well as the minimum cost.

Declaration of Competing Interest

The authors declare that they have no conflict of interest. “This paper does not contain any studies with human participants or animals performed by any of the authors.”

Acknowledgments

The authors are so pleased to introduce their great thanks to all staff members of Nile higher institute for engineering and technology for the great support. Most of the work introduced in this paper has been done in the laboratories of that great institution in Egypt. Special thanks of gratitude to doctor Salah Abd Elghafar Mansour for his endless support and kindness.

References

[1] S. Zaim, J. Chong, V. Sankaranarayanan, A. Harky, COVID-19 and multiorgan response, Curr. Probl. Cardiol. 45 (8) (2020) 1–21 Elsevier.
[2] Y. Wang, H. Kang, X. Liu, Z. Tong, Combination of RT-PCR testing and clinical features for diagnosis of COVID-19 facilitates management of SARS-CoV-2 outbreak, J. Med. Virol. 22 (6) (2020) 538–539.
[3] Y. Li, L. Yao, Jiawei Li, Lei Chen, et al., Stability issues of RT-PCR testing of SARS-CoV-2 for hospitalized patients clinically diagnosed with COVID-19, J. Med. Virol. (2020) 1–6 Wiley, doi:10.1002/jmv.25786.
[4] T. Conghy, B. Pon, E Anderson, When does Hospital Capacity Get Overwhelmed in USA? Germany? A model of beds needed and available for Coronavirus patients, trentst, 2020.
[5] G.Li S.Fong, N. Dey, R. Crespo, E. Viedma, Composite Monte Carlo decision making under high uncertainty of novel coronavirus epidemic using hybridized deep learning and fuzzy rule induction, Appl. Soft Comput. 93 (2020) 1–14 Elsevier.
[6] J. Suri, A. Puvvula, M. Biswas, et al., COVID-19 pathways for brain and heart injury in comorbidity patients: a role of medical imaging and artificial intelligence-based COVID severity classification: a review, Comput. Biol. Med. 124 (2020) 1–15.
[7] O. Albahri, A. Zaidan, A. Albahri, et al., Systematic review of artificial intelligence techniques in the detection and classification of COVID-19 medical images in terms of evaluationand benchmarking: taxonomy analysis, challenges, future solutions and methodological aspects, J. Infect. Public Health 13 (2020) 1382–1396 Elsevier.
[8] S. Toraman, T. Alakus, I. Turkoglu, Convolutional capsnet: a novel artificial neural network approach to detect COVID-19 disease from X-ray images using capsule networks, Choas, Solitons Fractals 140 (2020) 1–11 Elsevier.
[9] Y. Mohamadou, A. Halidou, P. Kapen, A review of mathematical modeling, artificial intelligence and datasets used in the study, prediction and management of COVID-19, Appl. Intell. 50 (2020) 3913–3925 Springer.
[10] T. Ozturk, M. Talo, E. Yildirim, et al., Automated detection of COVID-19 cases using deep neural networks with X- ray images, Comput. Biol. Med. 121 (2020) 1–11 Elsevier.
[11] L. Jiang, L.YuY. Zhang, et al., Class-specific attribute weighted naive Bayes, Pattern Recognit. 88 (2019) 321–330 Elsevier.
[12] N. Harzevili, S. Alizadeh, Mixture of latent multinomial naïve Bayes classifier, Appl. Soft Comput. 69 (2018) 516–567 Elsevier.
[13] Y. Kwon, A. Kwasinski, A. Kwasinski, Solar irradiance forecast using Naïve Bayes classifier based on publicly available weather forecasting variables, Energies 12 (8) (2019) 1–13, doi:10.3390/en12081529.
[14] M. Sharad, J. Bhavesh, Application of Naïve Bayes classification for disease prediction, Int. J. Manag., IT Eng. 9 (4) (2019) 80–87.
[15] B. Dedeturk, B. Akay, Spam filtering using a logistic regression model trained by an artificial bee colony algorithm, Appl. Soft Comput. J. 91 (2020) 1–18 Elsevier.
[16] T. Singhal, A review of coronavirus disease-2019 (COVID- 2019), Indian J. Pediatr. 87 (4) (2020) 281–286 Springer.
[17] S. Piva, M. Filippini, et al., Clinical presentation and initial management critically ill patients with severe acute respiratory syndrome coronavirus 2 (SARS–CoV-2) infection in Brescia, Italy, J. Crit. Care 58 (2020) 29–33 Elsevier.
[18] G. Youmin, L. Shiyuan, Radiological diagnosis of new coronavirus infected pneumonitis: expert recommendation from the Chinese society of radiology (First edition), Chin. J. Radiol. 54 (2020) 1–12.
[19] A. Tahamtan, A. Ardebili, Real-time RT-PCR in COVID-19 detection: issues affecting the results, Expert Rev. Mol. Diagn. 20 (5) (2020) 453–454 Taylor & Francis.
[20] Z. Ye, Y. Zhang, et al., Chest CT manifestations of new coronavirus disease 2019(COVID-19): a pictorial review, Eur. Radiol. 30 (2020) 4381–4389 Springer.
[21] https://www.cdc.gov/coronavirus/2019-ncov/
[22] G. Marques, D. Agarwal, I. Diez, Automated medical diagnosis of COVID-19 through EfficientNet convolutional neural network, Appl. Soft Comput. 96 (2020) 1–11 Elsevier.
[23] B. Pirouz, S. Haghshenas, S. Haghshenas, P. Piro, Investigating a serious challenge in the sustainable development process: analysis of confirmed cases of COVID-19 (new type of coronavirus) through a binary classification using artificial intelligence and regression analysis, Sustainability 2 (6) (2020) 1–22.
[24] W. Shaban, A. Rabie, A. Saleh, A new COVID-19 Patients Detection Strategy (CPDS) based on hybrid feature selection and enhanced KNN classifier, Knowl. Based Syst. 205 (2020) 1–18 Elsevier.
[25] T. Ozturk, M. Talo, E. Yildirim, et al., Automated detection of COVID-19 cases using deep neural networks with X-ray images, Comput. Biol. Med. 121 (2020) 1–11 Elsevier.
[26] R. Pereira, D. Bertolini, et al., COVID-19 identification in chest X-ray images on flat and hierarchical classification scenarios, Comput. Methods Programs Biomed. 194 (2020) 1–18 Elsevier.
[27] M. Allam, M. Nandhini, A study on optimization techniques in feature selection for medical image analysis, Int. J. Comput. Sci. Eng. (IJCSE) (9) (2017) 75–82.
[28] A. Cortegiani, G. Ingoglia, M. Ippolito, et al., A systematic review on the efficacy and safety of chloroquine for the treatment of COVID-19, J. Crit. Care (2020) 1–5 Elsevier, doi:10.1016/j.jcrc.2020.03.005.
[29] F. Felice, A. Polimeni, V. Valentini, The impact of Coronavirus (COVID-19) on head and neck cancer patients’ care, Radiother. Oncol. 147 (2020) 84–85 Elsevier.
[30] H. Lim, D. Kim, Pairwise dependence-based unsupervised feature selection, Pattern Recognit. 111 (2020) 1–12 Elsevier.
[31] S. Gu, R. Cheng, Y. Jin, Feature selection for high-dimensional classification using a competitive swarm optimizer, Soft Comput. 22 (3) (2018) 811–822 Springer.
[32] S. Ayyad, A. Saleh, L. Labib, A new distributed feature selection technique for classifying gene expression data, Int. J. Biomath. 12 (2) (2019) 1–34.
[33] R. Sheikhpour, M. Sarram, S. Gharaghani, et al., A Survey on semi-supervised feature selection methods, Pattern Recognit. 64 (2017) 141–158 Elsevier.
[34] A. Saleh, A. Rabie, K. Abo-Al-Ezb, A data mining based load forecasting strategy for smart electrical grids, Adv. Eng. Inf. 30 (3) (2016) 422–448 Elsevier.
[35] A. Rabie, S. Ali, A. Saleh, H. Ali, A new outlier rejection methodology for supporting load forecasting in smart grids based on big data, in: Cluster Computing, Springer, 2019, pp. 1–27. https://doi.org/10.1007/s10586-019-02942-0.
[36] A. Rabie, S. Ali, A. Saleh, H. Ali, A fog based load forecasting strategy based on multi-ensemble classification for smart grids, J. Ambient Intell. Humanized Comput. 11 (1) (2020) 209–236 Springer.
[37] A. Rabie, S. Ali, H. Ali, A. Saleh, A fog based load forecasting strategy for smart grids using big electrical data, Cluster Comput. 22 (1) (2019) 241–270 Springer.
[38] B. Nguyen, B. Xue, M. Zhang, A survey on swarm intelligence approaches to feature selection in data mining, Swarm Evol. Comput. 54 (2020) 1–27 Elsevier.
[39] N. Kushwaha, M. Pant, Link based BPSO for feature selection in big data text clustering, Fut. Gener. Comput. Syst. 82 (2018) 190–199 Elsevier.
[40] X. Feng, S. Li, C. Yuan, P. Zeng, Y. Sun, Prediction of slope stability using Naive Bayes classifier, KSCE J. Civ. Eng. 22 (3) (2018) 941–950.
[41] Y. Li, Text feature selection algorithm based on Chi-square rank correlation factorization, J. Interdiscip. Math. 20 (1) (2017) 153–160 Taylor& Francis Group.
[42] K. Rajab, New hybrid features selection method: a case study on websites phishing, Secur. Commun. Netw., Hindawi (2017) 1–10 2017.
[43] H. Vinutha, B. Poornima, An ensemble classifier approach on different feature selection methods for intrusion detection,", in: Information Systems Design and Intelligent Applications, 672, Springer, Singapore, 2018, pp. 443–451.
[44] H. Djellali, N. Zine, N. Azizi, Two stages feature selection based on filter ranking methods and SVMRFE on medical applications," modelling and implementation of complex systems, Lecture Notes Netw. Syst. (1) (2016) 281–293 Springer, Cham.
[45] R. Alyam, J. Alhajja, B. Alnajran, et al., Investigating the effect of correlation based feature selection on breast cancer diagnosis using artificial neural net-

work and support vector machines, in: Proceedings of the 2017 International Conference on Informatics, Health & Technology (ICIHT), IEEE, Riyadh, Saudi Arabia, 2017.
[46] L. Jiang, Ch. Qiu, Ch. Li, A novel minority cloning technique for cost-sensitive learning, Int. J. Pattern Recognit Artif Intell. 29 (4) (2015) 1–18.
[47] Mansoura University Hospital web site: www.muh.mans.edu.eg.
[48] F. Pourpanah, Y. Shi, Ch. Lim, et al., Feature selection based on brain storm optimization for data classification, Appl. Soft Comput. 80 (2019) 761–775 Elsevier.
[49] R. Raj, S. Shobana, I. Pustokhina, D. Pustokhin, D. Gupta, K. Shankar, Optimal feature selection-based medical image classification using deep learning model in internet of medical things, IEEE Access (8) (2020) 58006–58017.
[50] A. Shukla, P. Singh, M. Vardhan, A hybrid framework for optimal feature subset selection, J. Intell. Fuzzy Syst. 36 (2019) 2247–2259 IOS Press.
[51] L. Venkataramana, S. Jacob, R. Ramadoss, et al., Improving classification accuracy of cancer types using parallel hybrid feature selection on microarray gene expression data, Genes Genom. 41 (2019) 1301–1313 Springer,.
[52] N. Maleki, Y. Zeinali, S. Niaki, A k-NN method for lung cancer prognosis with the use of a genetic algorithm for feature selection, Expert Syst. Appl. 164 (2020) 1–7 Elsevier.
[53] N. KakhandakiM, S. Kulkarni, et al., Classification of brain hemorrhages in MRI using naïve Bayes- probabilistic kernel approach, J. Cases Inf. Technol. (JCIT) 21 (3) (2019) 1–15.
[54] S. Vijh, D. Gaur, Sushil Kumar, An intelligent lung tumor diagnosis system using whale optimization algorithm and support vector machine, J. Syst. Assurance Eng. Manag. 11 (2) (2020) 374–384 Springer.

Warda M. Shaban, received a B. Sc. in Electronics and Communication Engineering with general grade very good with honor. She got the master Degree in the area of image processing and artificial intelligent at Electronics and Communication Engineering dept., Mansoura University, Egypt. Her Interests (Programming Languages, Classification, Artificial intelligent), she is currently an assistant lecturer in the nile higher institute for engineering and technology

Asmaa H. Rabie, received a B. Sc. in Computers and Systems Engineering, with general grade Excellent. She got the master Degree in the area of load forecasting using data mining techniques at Computers eng. and system dept, Mansoura University, Egypt. Her Interests (Programming Languages, Classification, Big Data, Data Mining and Internet of Things), she is currently an assistant lecturer in the faculty of Engineering, Mansoura University.

Ahmed I. Saleh, received a B. Sc. in Computers and Systems Engineering, with general grade Excellent. He got the master Degree and PhD Degree in the area of Mobile agent ad Computing at Computers eng. and system dept, Mansoura University, Egypt. His Interests (Programming Languages, Networks and System Administration, and Database), he is currently professor in the faculty of Engineering, Mansoura University.

Mohy Eldin A. Aboelsoud received the M.Sc. degree in Electronics and Communication Engineering Department from Cairo University, Cairo, Egypt, in 1979, and the Ph.D degree from L'Institut National Polytechnique de Toulouze, Toulouze, France, in 1983. He has worked for Technical Research Center (TRC) from 1970 to 1990. During 1984 – 1990,he was a chairman with Electronics Department at TRC. From 1991 to 1996, he was an associated professor at Mansoura University. He is currently full professor with ECE Department of Mansoura University since 1996.He has authored and co-authored more than 103 in international journals and conferences. His research interests, analog/digital VLSI and FPGA circuit design, Sigma/Delta A/D techniques, switched-resistor networks, electronic systems and its applications of neural networks .