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Human monkeypox diagnose (HMD) strategy based on data mining and artificial intelligence techniques

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A B S T R A C T

In May 2022, monkeypox re-emerged as a rare zoonotic disease that is an important viral disease for public health. Monkeypox can be transmitted from animals to humans, between humans through close contact with an infected human, or with a virus stained substance. Through this paper, a new detection strategy based on artificial intelligence techniques is provided to early detect monkeypox patients. This strategy is called Human Monkeypox Detection (HMD) strategy and mainly consists of two main phases, which are; (i) Selection Phase (SP) and (ii) Detection Phase (DP). While SP tries to select the best features, DP tries to introduce fast and accurate detection based on valid data from SP. In SP, an Improved Binary Chimp Optimization (IBCO) algorithm as a new feature selection algorithm is introduced to select valuable features before learning an Ensemble Diagnosis (ED) model as a new diagnostic algorithm in the next phase called DP. In fact, the proposed IBCO algorithm is a hybrid selection algorithm that includes both filter and wrapper methods. IBCO consists of a filter layer called Filter Selection Layer (FSL) and a wrapper layer called Wrapper Selection Layer (WSL). At first, monkeypox dataset is entered into FSL to quickly select meaningful features by using 'm' filter selection techniques. Then, 'm' sets of selected features are fed into WSL to construct the initial population of Binary Chimp Optimization (BCO) algorithm to precisely choose the best set of features for the next phase (DP). Finally, the ED model will be correctly trained on the filtered data from FSL. This model consists of three diagnostic algorithms called Weighted Naïve Bayes (WNB), Weighted K-Nearest Neighbors (WKNN), and deep learning which are combined using a new weighted voting method to provide the best diagnostic results. The weighted values of WNB algorithm are determined by measuring the impact of each feature on the class categories while the Grey Wolf Optimization (GWO) algorithm is used to determine the weighted values of WKNN. Experimental results illustrated that the suggested feature selection algorithm called IBCO outperforms other modern feature selection methods and also the proposed ED model outperforms other modern diagnostic models. At the end, the HMD strategy gives the best results compared to other modern strategies with accuracy, precision, and recall values equal 98.48%, 91.1% and 88.91% respectively. Also, the HMD gives 92.56%,89.01%,88.01%,85.01%, 83.9%, and 5.4 s for micro-average precision, micro-average recall, macro-average precision, macro-average recall, F1-measure, and implementation time values respectively.

1. Introduction

Monkeypox is a rare zoonotic disease caused by monkeypox virus that belongs to the genus Orthopoxvirus in the family Poxviridae [1–5]. Two outbreaks of a pox-like disease appeared in colonies of monkeys preserved for research in 1958, hence, monkeypox was discovered [1]. In 1970, the first human patient of monkeypox was reported in the Democratic Republic of Congo and then the virus spread to other central and western countries in Africa [1]. Accordingly, the number of reported infected cases has increased. Although monkeypox virus has appeared since ancient times and no longer exists, the World Health Organization (WHO) and Centers for Disease Control and Prevention (CDC) have announced that the monkeypox virus has re-emerged now in May 2022 [2–4]. WHO and CDC announce that monkeypox is a self-limited disease. Additionally, symptoms of monkeypox last from 2 to 4 weeks [2–4]. The symptoms of human monkeypox are fever, body aches, headache, lymphadenopathy (lymph nodes to swell), Pustular Rashes, and exhaustion [1,2,4]. Recently, the case-fatality ratio was about 3–6%

[4]. Early monkeypox detection is an essential process to reduce the spread of this infection around the world, isolate infected cases, and follow appropriate treatment of infected cases (see Table 4).

Nowadays, Artificial Intelligence (AI) methods are used in many medical system applications such as end-to-end drug discovery and development, transcribing medical documents, patients diagnosis, pre-processing of medical data such as feature selection, and enhancing contact between physician and patient [6,7]. In fact, patients diagnosis and pre-processing processes based on AI techniques are the core of modern medical systems. That is because pre-processing techniques enable the medical system to filter data from useless data and diagnostic techniques can automatically diagnose patients without direct contact to medical staff. Thus, these techniques can reduce the efforts of medical staff, reduce patient waiting for examination, and reduce cost [6,7]. The importance of applying AI techniques to diagnose diseases is especially important in the event of a global pandemic resulting from new diseases that human expertise cannot diagnose with the required accuracy and speed. This may lead to a worsening of the health situation in the affected countries, threatening a catastrophe that the medical systems may be unable to absorb. Recently, serious and rapidly spreading diseases and epidemics have begun to appear in the world, such as Covid-19 disease and other diseases that have begun to appear, such as monkeypox. Therefore, diagnostic methods using AI techniques for serious diseases, that may be difficult for a human to diagnose quickly and accurately, are very important for the early, rapid and accurate detection of the disease to limit its spread.

Nowadays, many diagnostic models need to select the informative features before starting to diagnose patients for their correct class category [6–8]. Feature selection is a pre-processing of data that is used to provide valuable features that enables diagnostic models to perform well. Thus, feature selection process aims to prevent overfitting. Two main classes called filter and wrapper can be used to classify feature selection techniques [6,7]. To diagnose disease like monkeypox, diagnostic models based on AI such as neural network, fuzzy inference system, Naïve Bayes, and Association Rules can be applied [6,7]. In fact, most researchers have diagnosed monkeypox patients based on Polymerase Chain Reaction (PCR) and manually. PCR test is fast, sensitive, and reliable but has the risk of getting false-negative and false-positive results. A negative PCR test result does not negate the possibility of monkeypox infection, so PCR test doesn't capture all infections. Hence, PCR test should not be taken into account as the only criterion for diagnosing monkeypox cases. Additionally, manual diagnosis is accurate but time-consuming. On the other hand, automatic diagnosis based on AI techniques can provide fast and accurate results and can also prevent the spread of infection between humans. Accordingly, it is an important to introduce a new strategy based on AI techniques to accurately and quickly diagnose monkeypox patients based on blood tests rather than relaying only on PCR test.

During this paper, a new Human Monkeypox Detection (HMD) strategy has been presented to give rapid and more precise detection of monkeypox patients. HMD includes two main phases, which are; SP and DP. After selecting the most effective features of monkeypox patients using a new selection method in SP, the diagnostic process will be performed using a new ensemble diagnostic model in DP for early detection of monkeypox patients. The main objective of SP is to remove irrelevant features from the used dataset before beginning to learn the ED model in DP to enable it to introduce fast and precise diagnosis.

- This paper provides two main contributions, which are; IBCO algorithm as a new feature selection method in SP and ED model as a new diagnostic model in DP.
- The first contribution called IBCO is a hybrid selection algorithm that composes of two layers, namely; FSL and WSL. The main idea of IBCO is that it can solve the problems of the original version of BCO algorithm by determining the population size and initial values of

search agents using many filter selection methods through FSL before implementing the BCO in WSL.
- Hence, many filter selection methods are used in FSL to quickly select different sets of features. Then, these sets of features is passed to WSL to produce the initial population of BCO algorithm for accurately selecting the best set of features. At the last, the best set of features is utilized to correctly learn the ED model as a new diagnostic model in DP to provide rapid and precise diagnosis.
- The second contribution called ED model is a hybrid diagnostic model that contains three new and different algorithms called WNB using the effect of each feature on the class categories to calculate the weighted values, WKNN using GWO to calculate the weighted values, and deep learning that are combined using a new weighted voting method. While WNB is a modified probabilistic method, WKNN is a modified distance method and deep learning is a machine learning method which are combined to give accurate results.
- WNB algorithm is a new diagnostic model that modifies the classical NB model to take in the consideration the effective impact of each feature on the classifier by calculating the weights of features.
- WKNN algorithm is a new diagnostic model that modifies the classical KNN model to use the best value of K and the best weights of features obtained from the GWO algorithm before implementing KNN algorithm.
- Long Short-Term Memory (LSTM) model as a deep learning structure is used to diagnose monkeypox patients.
- Then, the results of WNB, WKNN, and LSTM are combined by a new weighted voting method called Confusion Based Voting (CBV) to accurately take correct decisions.

Experimental results showed that the proposed IBCO can provide the best subset of features compared to other recent methods and also the proposed ED model can provide the best results compared to its components based on the features selected by IBCO. Finally, the HMD strategy is superior other recently used strategies because it has the ability to give the best values of accuracy, precision, recall, micro-average, macro-average, F1-measure, and implementation time.

The structure of this paper is organized as follows; segment 2 shows the problem definition but segment 3 provides the research motivation. Segment 4 reviews the previous research efforts about medical diagnostic techniques while the human monkeypox detection strategy will be discussed in segment 5. Segment 6 describes the experimental results while segment 7 depicts the conclusions and future directions.

2. Problem definition

As the world is trying to get back to normal ignoring new record numbers of Covid-19, a new threat has been suddenly emerged, which is already spreading in the world known as Human MonkeyPox (HMP). Although HMP, which is a zoonotic viral disease, occurs predominantly in the rainforests of central and western Africa, it has recently appeared in the United States in wild rodents imported from Africa. The only escape for any potential pandemic that may arise from an outbreak of monkeypox is the accuracy and speed of diagnosis, so that it can be dealt with in the appropriate way. Accordingly, it is of utmost importance to find a way to accurately diagnose patients to give them the appropriate treatment at the right time.

However, there are many challenges to the accurate and rapid diagnosis of HMP, including; (i) HMP is clinically almost identical to ordinary smallpox as both belong to the same group of viruses called orthopoxviruses [9]. They have similar clinical presentation including headache, fever, flulike symptoms, malaise, back pain, and characteristic rash, (ii) HMP is difficult to manage due to the limited knowledge of it among both patients and health staff as well as the huge lack of diagnostic tools and treatment protocols, (iii) the risk of the disease is not only limited to the advanced level of care that should be offered to the affected individuals but may also put other patients and health

personnel at risk of infection. This paper keeps raising attention to an urgent need for an AI based methodology for fast and accurate diagnosing the disease [9–14]. Fig. 1 depicts some considerations for HMP, where Fig. 1 (A) depicts 156 Occurrence locations of HMP into Central African (red), West Africa (blue), and unclassified (green) HMP genotypes, on the other hand, Fig. 1(B) illustrates the Overall predicted distribution of HMP based on ecological niche modeling [15]. the model shows the high capacity and speed of spread that characterizes the disease. Dark shades indicate regions with the greatest model agreement in predicting HMP fit, while green dots indicate input occurrences used in model development [15]. Fig. 1(C) shows the number of recorded HMP cases per country (May 26, 2022) and where disease is endemic based of WHO recent reports, finally, Fig. 1(D) presents some cases of HMP patients and what does the disease look like on the skin of the infected people.

3. Research motivation

Currently, in light of the sudden emergence of infectious diseases that are rapidly spreading among humans, such as Covid-19 and monkeypox, it was necessary to find an early and rapid diagnosis of patients without contact with the medical staff. We are motived to work in this area of research to:

- Introduce a complete diagnostic strategy for new and rapidly spreading infectious diseases.
- Provide early and accurate diagnoses to new emerging diseases such as monkeypox based on AI and machine learning.
- Prevent the spread of infection with newly emerged diseases by preventing direct contact between the patient and the medical staff.
- Determine the appropriate treatment methods for the patient based on the correct diagnosis.
- Reduce the risk of transmission of infection, whether from patients to non-patients or to the treating medical staff.

4. The previous efforts

The previous efforts about the diagnostic methodologies in medical systems will be discussed in this segment. In Ref. [9], four diagnostic models called Random Forest (RF), Naïve Bayes (NB), Support Vector Machine (SVM), and Decision Tree (DT) were used to early identify diabetes. Experimental results showed that RF outperformed SVM, NB, and DT based on using two different datasets where RF provided the maximum accuracy, recall, and F-measure values. Although RF proved its effectiveness for diagnosing diabetes, it has not been tested on monkeypox. Additionally, RF is based on the original dataset without initially selecting the most effective features. As depicted in Ref. [1], a Neuro-Fuzzy based technique was provided to early diagnose monkeypox patients. This technique combines the benefits of fuzzy logic and artificial neural network techniques. In fact, fuzzy logic gave Neuro-Fuzzy the ability to handle uncertainty while neural network gave Neuro-Fuzzy the learning capability. In experimental results, Neuro-Fuzzy can effectivity diagnose monkeypox patients but it lacked to use all symptoms in the input. It also lacks the use of feature selection approach before implementing the diagnostic algorithm to enhance its performance further.

As introduced in Ref. [8], an Ensemble Learning based Genetic Algorithm (ELGA) method was provided to early diagnose heart disease patients. ELGA method begins to select the most effective features and then diagnose heart disease. According to experimental results, ELGA provided the maximum accuracy value compared to other diagnostic models. Despite the benefits of ELGA, it has not been combined with many common diagnostic models, namely; NB, DT and SVM which may enable ELGA to improve its performance further. It also has not been tested on many different diseases such as breast cancer, lung cancer, Covid-19, and monkeypox.

In [6], Distance Based Classification (DBC) strategy was introduced as a new diagnostic model to classify people vulnerability to Covid-19 infection. In fact, the DBC strategy consists of three stages; outlier rejection, feature selection, and classification. Hybrid outlier rejection approach that includes standard division and enhanced particle swarm optimization methods was implemented to reject noise data. Hybrid
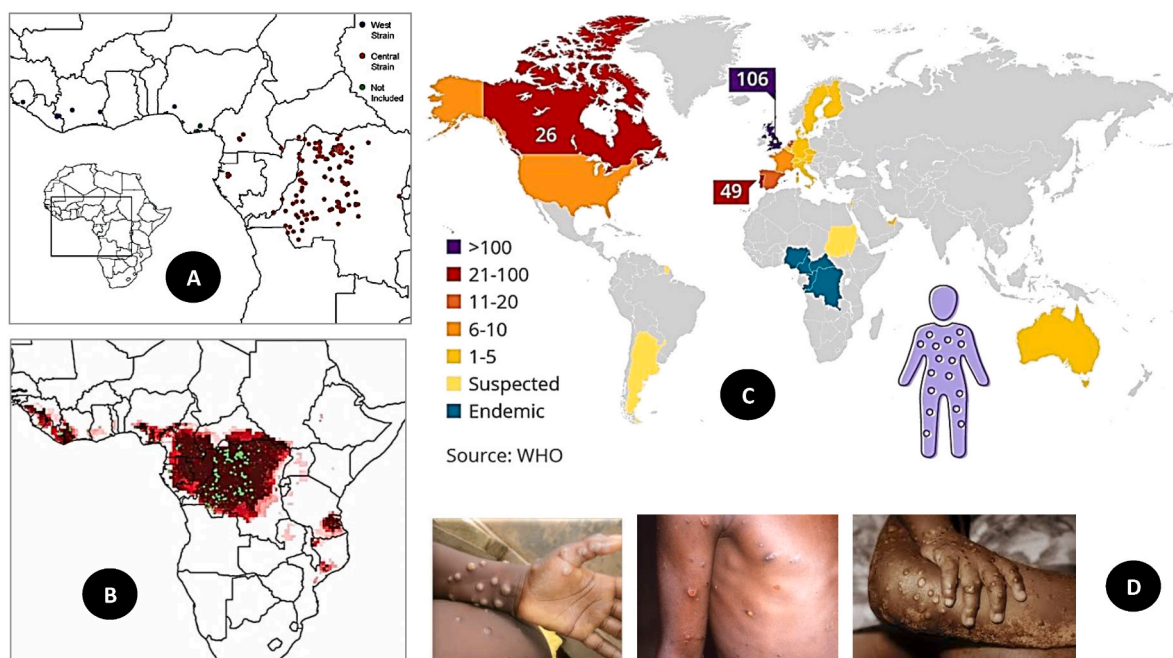

Fig. 1. (A) 156 Occurrence locations of human monkeypox into Central African (red), West Africa (blue), and unclassified (green) monkeypox genotypes, (B) the Overall predicted distribution of HMP based on ecological niche modeling, (C) Number of recorded HMP cases per country (May 26, 2022) and where disease is endemic, (D) Some cases of HMP patients.

feature selection approach that includes chi-square and enhanced grey wolf optimization methods has been used to select valuable features. At the last, the filtered data has been passed to a diagnostic method called accumulative K-nearest neighbors to introduce fast and precise results. The description of experimental results showed that DBC provided the maximum accuracy and the minimum error and implementation time. Despite the benefits of DBC, it has not been combined with many heuristics models such as fuzzy logic and deep learning. Additionally, DBC has not been tested on other diseases such as monkeypox.

As mentioned in Ref. [7], a new diagnostic model called Covid-19 Prudential Expectation (CPE) strategy has been provided to classify people vulnerability to Covid-19 infection. Outlier rejection, feature selection, and classification are the three main phases of CPE. Outlier rejection task was performed by executing improved grey wolf optimization algorithm while feature selection task has been performed by executing improved genetic algorithm. Finally, the filtered data has been passed to the statistical Naïve Bayes as a new diagnostic model to provide the best results. According to experimental results, CPE outperformed other strategies because it achieved the best accuracy and execution time values. Despite the effectiveness of CPE, it has not been implemented on other diseases such as monkeypox.

For the Diagnosis of Monkeypox Patients (DMP) in the UK, clinical features of humans monkeypox have been characterized in Ref. [16]. This study based on 197 patients who had confirmed monkeypox based on PCR test. All 197 patients were men with a mean age of 38 years and had mucocutaneous lesions whereby 111 patients had genital infection or 82 patients had infection in the perianal region. It is concluded that there are several clinical features of monkeypox in humans in the UK that can be used for the early diagnosis of monkeypox patients. Despite the accurate description and in-depth study of the characteristics of monkeypox patients, which help in the early and accurate diagnosis of patients, it takes a great deal of time for diagnosis. Therefore, it was better to rely on AI and machine learning methods for rapid and accurate diagnosis based on data collected from patients. Additionally, it is not sufficient to rely only the PCR test to diagnose patients. In Ref. [17], Monkeypox Diagnosis Process (MDP) in a sexual health center in London, UK, depended on demographic and clinical features of the patients. Confirmed cases were detected using PCR test as 54 cases were infected with the monkeypox virus. Despite the careful examination of the 54 cases, this process took a great deal of time with a small number of cases. Also, depending only on the PCR test reduced the efficiency of the diagnosis. Therefore, it is preferable to use AI techniques to make a quick and accurate diagnosis based on other characteristics in addition to the PCR test.

Table 1
The recent diagnostic strategies in medical system.

Technique	Description	Advantages	Disadvantages
Four diagnostic models [9]	Four diagnostic models called RF, NB, SVM, and DT were used to early identify diabetes.	RF outperformed SVM, NB, and DT based on using two different datasets where RF provided the maximum accuracy, recall, and F-measure values.	- RF has not been tested on monkeypox. - RF is based on the original dataset without initially selecting the most effective features.
Neuro-Fuzzy [1]	Neuro-Fuzzy based technique was provided to early diagnose monkeypox patients. This technique combines the benefits of fuzzy logic and artificial neural network techniques.	It can effectivity diagnose monkeypox patients.	- It lacked to use all symptoms in the input. - It lacks the use of feature selection approach before implementing the diagnostic algorithm to enhance its performance further.
Ensemble Learning based Genetic Algorithm (ELGA) [8]	ELGA was provided to early diagnose heart disease patients. ELGA method begins to select the most effective features and then diagnose heart disease.	It provided the maximum accuracy compared to other diagnostic models.	- It has not been combined with many common diagnostic models, namely; NB, DT and SVM which may enable ELGA to improve its performance further. - It has not been tested on many different diseases such as breast cancer, lung cancer, Covid-19, and monkeypox.
Distance Based Classification (DBC) strategy [6]	DBC was introduced to classify people vulnerability to Covid-19 infection. This strategy consists of three stages; outlier rejection, feature selection, and classification.	It provided the maximum accuracy and the minimum error and implementation time.	- It has not been combined with many heuristics models such as fuzzy logic and deep learning. - It has not been tested on other diseases such as monkeypox.
Covid-19 Prudential Expectation (CPE) strategy [7]	CPE has been provided to classify people vulnerability to Covid-19 infection. Outlier rejection, feature selection, and classification are the three main phases of CPE.	It outperformed other strategies because it achieved the best accuracy and execution time values.	- it has not been implemented on other diseases such as monkeypox.
Diagnosis of Monkeypox Patients (DMP) [16]	Clinical features of humans monkeypox for 197 patients who had confirmed monkeypox based on PCR test were characterized to diagnose patients.	It provided accurate description and in-depth study of the characteristics of monkeypox patients, which help in the early and accurate diagnosis of patients.	- Diagnosis takes a long time. - Diagnosis is done manually instead of using AI techniques. - It only relies on PCR testing to find confirmed cases.
Monkeypox Diagnosis Process (MDP) [17]	In a sexual health center in London, UK, demographic and clinical features of the patients were used to diagnose infected cases.	Careful examination of 54 cases was conducted to provide an accurate diagnosis.	- Diagnosis process took a great deal of time with a small number of cases. - Depending only on the PCR test reduced the efficiency of the diagnosis. - It only relies on PCR testing to find confirmed cases.
Diagnostic Method (DM) [18]	Humans diagnosis based on clinical features of 7 patients with monkeypox characterized in the UK between 2018 and 2021 was performed to accurately diagnose monkeypox patients.	The good description of the patients' condition and their diagnosis were provided.	- This study suffers from a small number of samples,. - It also suffers from the lack of use of AI methods. - Additionally, it is not sufficient to rely only the PCR test to diagnose patients.
Diagnose Monkeypox Individuals (DMI) process [19]	Based on several demographic and clinical features such as gay or bisexual men, human immunodeficiency virus infection, the median age, sexual activity, rash, anogenital lesions, and mucosal lesions, diagnosis was performed.	It can accurately diagnose monkeypox patients based on their clinical features.	- It takes a long time for diagnosing patients. - Diagnosis is done manually but AI techniques were not used. - It only based on PCR testing to determine confirmed patients.

As described in Ref. [18], the Diagnostic Method (DM) based on clinical features of 7 patients with monkeypox characterized in the UK between 2018 and 2021 was performed to accurately diagnose monkeypox patients. PCR test was performed on all patients to identify confirmed cases of monkeypox. The clinical features included clinical data (such as symptoms and signs, complications of illness, demographic variables, and any antiviral treatments received) and laboratory results (such as monkeypox virus PCR results and routine biochemical tests). Despite the good description of the patients' condition and their diagnosis, this study suffers from a small number of samples, as well as the lack of use of artificial intelligence methods. Additionally, it is not sufficient to rely only the PCR test to diagnose patients. Between April and June 2022, 528 cases of monkeypox were diagnosed in 16 countries as presented [19]. To perform Diagnose Monkeypox Individuals (DMI) process, there are many demographic and clinical features mentioned in Ref. [19]. These clinical features included gay or bisexual men, human immunodeficiency virus infection, the median age, sexual activity, rash, anogenital lesions, and mucosal lesions. PCR test was used to confirm the infected cases. Despite the benefits of this diagnosis, it lacks the use of AI technology to deal with a large number of cases and also to give fast and accurate results. Also, depending only on PCR test is not sufficient. The recent diagnostic methodologies in medical systems are presented in Table 1.

5. The human monkeypox detection (HMD) strategy

This segment describes the HMD strategy for early detection of monkeypox patients. The HMD strategy attempts to quickly and accurately diagnose patients who suffer from monkeypox. In fact, this strategy composes of two main phases which are named Selection Phase (SP) and Detection Phase (DP) as provided in Fig. 2. While SP aims to choose the most informative features in dataset without any useless features, DP aims to rapidly and accurately diagnose monkeypox patients depending on valid data from SP. Thus, feature selection task will be carried out at first to select valuable features and then the monkeypox detection model will be learned by valid dataset based on informative features to give the desired results. Feature selection algorithms can be categorized into two main classes called filter and wrapper [6,7]. Actually, filter techniques are faster than wrapper but less precise than wrapper [6,7].

Recently, optimization algorithms have been applied as wrapper selection algorithms to select valuable features [6,7,10]. Hence, a significant amount of time can be consumed by optimization algorithms versus providing an accurate set of features. Accordingly, a new feature selection methodology, namely; Improved Binary Chimp Optimization (IBCO) algorithm will be provided as a hybrid method that include both filter and wrapper algorithms to quickly and carefully choose the best features. Accurate set of features selected from SP allows ED model as a new diagnostic model in DP to be learned correctly and thus can give fast and accurate results. In fact, the ED model is a hybrid diagnostic model consisting of three techniques, which are; WNB, WKNN, and deep learning that are combined together by a new weighted voting method used to provide the best diagnostic results. In WNB, weighted values are calculated by measuring the effect of each feature on the class categories
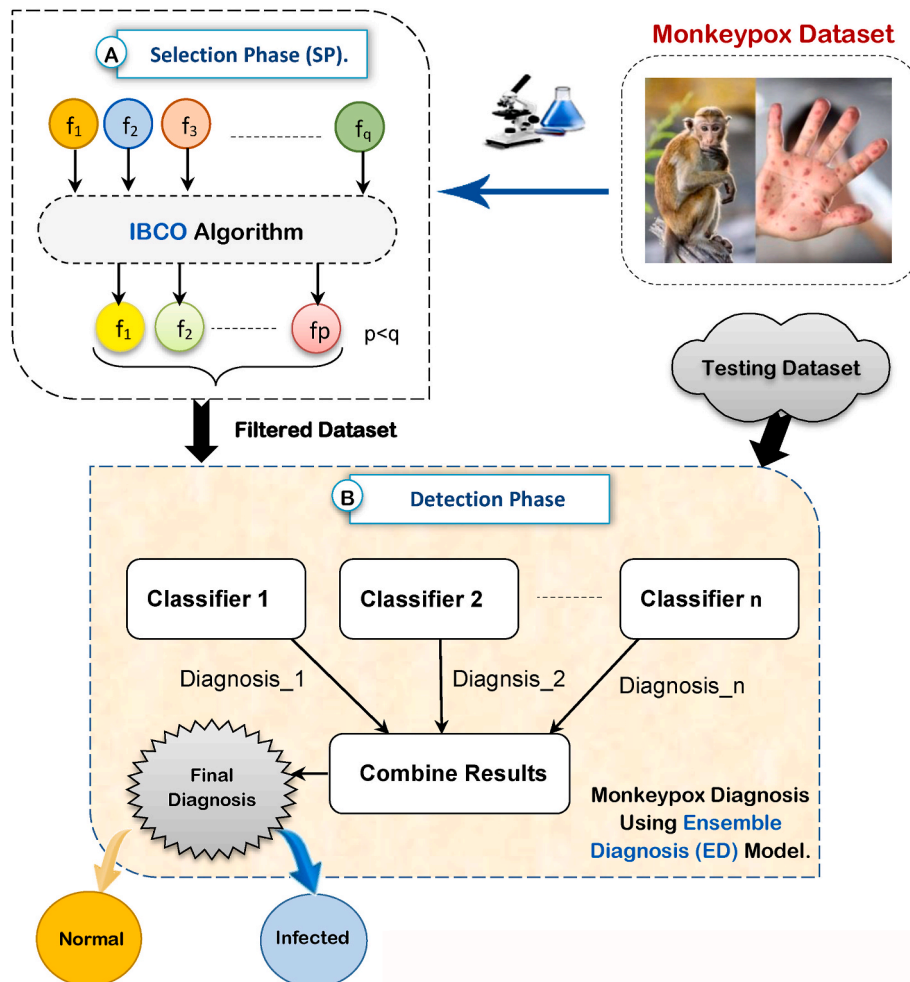

Fig. 2. The human monkeypox detection (HMD) strategy.

while the GWO is used to determine WKNN weighted values. In the following sub-segments, the IBCO as a new feature selection methodology in SP and the ED model as a new diagnostic model in DP will be explained in details.

5.1. Improved Binary Chimp Optimization (IBCO) algorithm

In this segment, the details of the proposed IBCO algorithm as a new selection algorithm in the first phase of the provided strategy called SP will be described. The IBCO algorithm is a hybrid selection method that includes filter and wrapper algorithms to provide fast and accurate group of features. It consists of two layers called Filter Selection Layer (FSL) and Wrapper Selection Layer (WSL) as illustrated in Fig. 3. FSL aims to quickly choose group of valuable features while WSL aims to accurately select the best subset of features. In fact, Binary Chimp Optimization (BCO) algorithm as a wrapper algorithm can give correct results but it is time consuming [12]. In addition to the fact that BCO is a slow technique, it lacks the determination of the exact number of search agents "chimps" in the population and their initial values. Thus, IBCO aims to enhance the performance of BCO by using FSL as a quick layer before using it in WSL. In FSL, 'm' filter selection techniques will be applied in parallel and each technique will separately provide a set of selected features. After that, the sets of features selected by 'm'

techniques in FSL will be passed to WSL as initial population of BCO. Hence, initial population of BCO consists of 'm' search agents that include initial values equal the sets of features selected by 'm' filter selection techniques in FSL. Based on this initial population, BCO tries to quickly select an accurate set of features that can give a diagnostic model the ability to introduce quick and correct monkeypox diagnoses.

The second difference between the original BCO and the IBCO is that the IBCO depends on a better fitness function that is the average accuracy value produced by many diagnostic methods learned on the same set of features in dataset to produce the fitness of each chimp in the population. Thus, the evaluation values for chimps in IBCO will be generated by using many diagnostic methods rather than using only specific one. The main aim of that is to achieve the generality of selecting useful features that can adapt to any diagnostic model. Implementing IBCO requires many sequential steps as shown in Fig. 3. At first, monkeypox dataset will be passed to 'm' filter selection techniques in FSL to provide 'm' sets of selected features. Secondly, these sets of selected features will be used to generate the initial population of BCO in WSL. In fact, each chimp in the population will be represented in a q-dimensional space and also in a discrete form to represent a set of meaningful features in each chimp. Hence, each chimp's length equals the same number of features in the monkeypox dataset where the bits of each chimp includes either '0' or '1' value; 0 = not selected features and
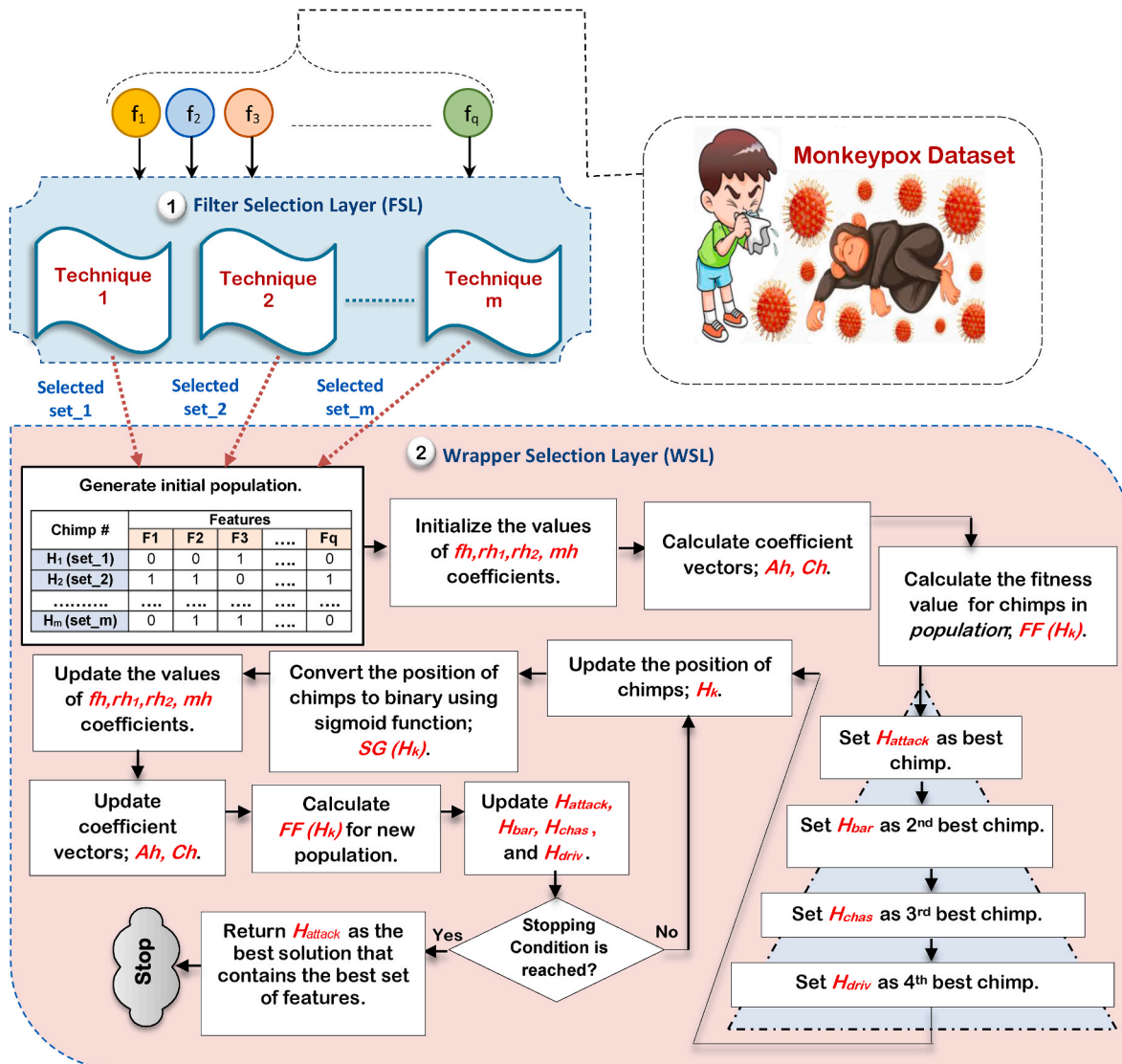

Fig. 3. The steps of IBCO as a feature selection method.

1 = selected features. Then, the steps of BCO will be continued until stopping condition (the maximum iterations number) is reached. After generating initial population from FSL as showed in Fig. 3, chimps will be evaluated by using the fitness function in (1).

$$FF(H_k) = \frac{\sum_{j=1}^{nd} Acc_j(H_k)}{nd} \tag{1}$$

Where $FF(H_k)$ represents the evaluation value of kth chimp, the accuracy value of jth diagnostic model based on the set of features in kth chimp is $Acc_j(H_k)$. j represents an index to the used diagnostic models; $j = 1,2, ..., nd$ where their number is nd. To illustrate the idea, it is assumed that the population size is two (two chimps) and three diagnostic models (nd = 3) will be applied to assess the picked features in every chimp as depicted in Table 2. In Table 2, the used diagnostic models are SVM [6], Deep Learning Method (DLM) [20–22], and K-Nearest Neighbors (KNN) [13]. It is noted that the maximum accuracy values of SVM and DLM are presented in H_1 while the maximum accuracy value of KNN is presented in H_2. Hence, the best chimp is the first solution (H_1) related on the average accuracy value to introduce a global solution because single diagnostic model cannot generally give the best set of features that can deal with any other diagnostic model (see Table 3).

After all chimps in the population are evaluated and their fitness values are calculated, the four leaders (H_{attack}, H_{bar}, H_{chas}, and H_{driv}) as the best solutions are determined. In the population, the positions of rest chimps (H_k) will be adjusted for the next iteration ($t+1$) based on the positions of leaders at the current iteration (t) by using (2-6) [12,14].

$$\vec{H}_1(t+1) = \vec{H}_{attck}(t) - \vec{Ah}_1.\vec{Dh}_{attck} \ , \ \vec{Dh}_{attck} = \left| \vec{Ch}_1.\vec{H}_{attcker} - mh * \vec{H}_k(t) \right| \tag{2}$$

$$\vec{H}_2(t+1) = \vec{H}_{bar}(t) - \vec{Ah}_2.\vec{Dh}_{bar} \ , \ \vec{Dh}_{bar} = \left| \vec{Ch}_2.\vec{H}_{bar} - mh * \vec{H}_k(t) \right| \tag{3}$$

$$\vec{H}_3(t+1) = \vec{H}_{chas}(t) - \vec{Ah}_3.\vec{Dh}_{chas} \ , \ \vec{Dh}_{chas} = \left| \vec{Ch}_3.\vec{H}_{chas} - mh * \vec{H}_k(t) \right| \tag{4}$$

$$\vec{H}_4(t+1) = \vec{H}_{driv}(t) - \vec{Ah}_4.\vec{Dh}_{driv} \ , \ \vec{Dh}_{driv} = \left| \vec{Ch}_4.\vec{H}_{driv} - mh * \vec{H}_k(t) \right| \tag{5}$$

$$\vec{H}_k(t+1) = \frac{\vec{H}_1 + \vec{H}_2 + \vec{H}_3 + \vec{H}_4}{4} \tag{6}$$

Where the current iteration number is t and the position of each chimp at t iteration is $H_k(t)$. Additionally, the distance between a prey and the chimp (H_k) is Dh, the positions of the best four chimps are $H_1, H_2, H_3,$ and H_4 respectively, and mh represents a chaotic value. In fact, mh includes value between [0,1] using quadratic map that refers to the effect of the agents' sexual motivation that can be calculated by using (7).

$$mh = H_k^2 - g \ , g = 1 \tag{7}$$

Coefficient vectors are Ah and Ch which are adjusted to determine

Table 2
Identify the best chimp depending on both every diagnostic model and the average accuracy value.

Diagnostic model #	Accuracy of every chimp		The best chimp (H_{attack})
	H_1	H_2	
D_1 = SVM	0.75	0.7	H_1
D_2 = DLM	0.9	0.7	H_1
D_3 = KNN	0.8	0.9	H_2
Average accuracy	0.816	0.767	H_1

Table 3
CM for WNB.

		Predicted Class		Total
		A	B	
Actual Class	A	550 = 92%	50	600
	B	240	160 = 40%	400
		790	210	1000

Table 4
CM for WKNN.

		Predicted Class		Total
		A	B	
Actual Class	A	370 = 62%	230	600
	B	180	220 = 55%	400
		550	450	1000

the nearest solution to the optimal. For each leader, Ah and Ch will be calculated by using (8-11).

$$Ah_1 = |2 * fh * rh_{11} - fh|, Ch_1 = 2 * rh_{12} \tag{8}$$

$$Ah_2 = |2 * fh * rh_{21} - fh|, Ch_2 = 2 * rh_{22} \tag{9}$$

$$Ah_3 = |2 * fh * rh_{31} - fh|, Ch_3 = 2 * rh_{32} \tag{10}$$

$$Ah_4 = |2 * fh * rh_{41} - fh|, Ch_4 = 2 * rh_{42} \tag{11}$$

Where fh is decreasing from 2 to 0 linearly. It can be calculated by using (12).

$$fh = 2 - 2 * \left(\frac{t}{MT} \right) \tag{12}$$

Where the maximum number of iterations represents MT and random factors between [0,1] which are calculated for each leader chimp are rh_1 and rh_2 using (13-20) [12].

$$rh_{11} = u_1d_1 * Rand(\ ), u_1d_1 = 1.95 - \left(\frac{2 * \left(t^{\frac{1}{4}}\right)}{MT^{\frac{1}{3}}} \right) \tag{13}$$

$$rh_{12} = u_2d_1 * Rand(\ ), u_2d_1 = \left(\frac{2 * \left(t^{\frac{1}{3}}\right)}{MT^{\frac{1}{3}}} \right) + 0.5 \tag{14}$$

$$rh_{21} = u_1d_2 * Rand(\ ), u_1d_2 = 1.95 - \left(\frac{2 * \left(t^{\frac{1}{3}}\right)}{MT^{\frac{1}{4}}} \right) \tag{15}$$

$$rh_{22} = u_2d_2 * Rand(\ ), u_2d_2 = \left(\frac{2 * (t^3)}{MT^3} \right) + 0.5 \tag{16}$$

$$rh_{31} = u_1d_3 * Rand(\ ), u_1d_3 = \left(\frac{-3 * (t^3)}{MT^3} \right) + 1.5 \tag{17}$$

$$rh_{32} = u_2d_3 * Rand(\ ), u_2d_3 = \left(\frac{2 * \left(t^{\frac{1}{3}}\right)}{MT^{\frac{1}{3}}} \right) + 0.5 \tag{18}$$

$$rh_{41} = u_1d_4 * Rand(\ ), u_1d_4 = \left(\frac{-2 * (t^3)}{MT^3} \right) + 0.5 \tag{19}$$

$$rh_{42} = u_2d_4 * Rand(\ ), u_2d_4 = \left(\frac{2 * (t^3)}{MT^3} \right) + 0.5 \tag{20}$$

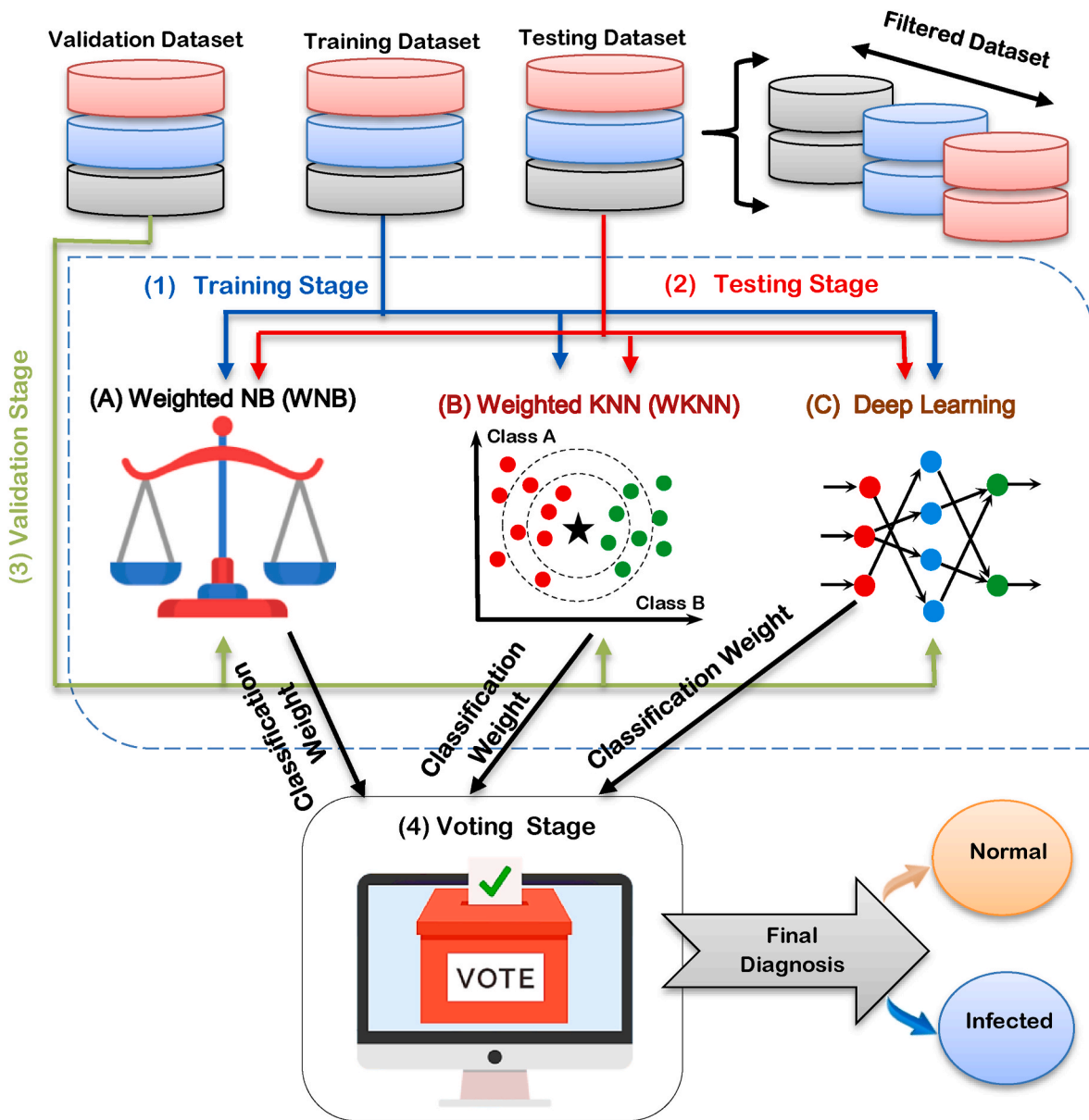Where uniform distribution between [0,1] is $Rand()$ and the dynamic

Fig. 4. The steps of Ensemble Diagnosis (ED) model.

coefficients applied to determine the values of rh_1 and rh_2 are u_1d_1, u_2d_1, u_1d_2, u_2d_2, u_1d_3, u_2d_3, u_1d_4, and u_2d_4. In the population, it is assumed a probability of 50% to select between either the normal updating position method or the chaotic model (*mh*) to update the positions of chimps by using (21).

$$H_k(t+1) = \begin{cases} \dfrac{H_1 + H_2 + H_3 + H_4}{4}, & if\,(\,y < 0.5) \\[2mm] mh\,, if\,(\,y \geq 0.5) \end{cases} \tag{21}$$

Where a random value between [0,1] is y. In fact, a new position value for each chimp H_k in the population is generated in a continuous form but this form cannot be applied to choose meaningful features. Hence, the converting function called sigmoid function should be applied to transform the continuous value to binary value. Accordingly, every chimp's position in the population; $H_k = (H_k^1, H_k^2, \ldots, H_k^q)$ will be modified by implementing the sigmoid function to calculate new chimp's position in a discrete form; $H_{bin\_k} = (H_{bin\_k}^1, H_{bin\_k}^2, \ldots, H_{bin\_k}^q)$ by using (22) [6,7].

$$H_{bin\_k}^i(t+1) = \begin{cases} 1 & if\quad RAND(0,1) \geq SG\big(H_k^i\big) \\[3mm] 0 & Else \end{cases} \tag{22}$$

Where the binary value of *k*th chimp in the next iteration *t+1* at *i*th position is $H_{bin\_k}^i(t+1)$ and *i* is a pointer to the current position (feature); $i = 1,2,3, \ldots,q$. Random value between 0 and 1 is *RAND(0,1)* and the sigmoid function is $SG(H_k^i)$. In fact, $SG(H_k^i)$ refers to the probability of *i*th bit that includes one or zero value measured by applying (23) [6,7].

$$SG\big(H_k^i\big) = \frac{1}{1 + e^{-H_k^i}} \tag{23}$$

Where *e* is the base of the natural logarithm. Related to $H_{bin\_k}^i(t+1)$ as a new position of every chimp in the population, the fitness value of every chimp is calculated by applying the fitness function in (1). The steps of BCO will be finished when the stopping condition is satisfied. At the last, the fittest chimp (H_1 or H_{attack}) is the best solution and the algorithm is finished. Then, all bits that includes 1 in H_1 are the most effective

features that will be used to enable the diagnosis model to correctly learned for providing quick and more accurate diagnosis. In other words, the filtered dataset without irrelevant features in the SP will be passed to the next phase of the provided strategy called DP to correctly learn the ED model in order to give quick and accurate diagnosis for monkeypox patients. The steps of IBCO algorithm are mentioned in algorithm 1.

Algorithm 1. Improved Binary Chimp Optimization (IBCO) Algorithm.

The ED model is a hybrid model consisting of three diagnostic algorithms called WNB, WKNN, deep learning implemented on the filtered dataset that is passed from the previous phase called SP without irrelevant features to be accurately diagnose monkeypox patients. The ED model aims to combine the results of these three diagnostic algorithms together through a new weighted voting method to provide more accurate results. The steps of implementing this model are showed in Fig. 4. As presented in Fig. 4, the filtered monkeypox dataset will be divided into training, testing, validating dataset before starting to implement the ED model. Then, the ED model implementation sequence will be passed through four main stages called training, testing, vali-

Improved Binary Chimp Optimization (IBCO) Algorithm

- **Inputs:**
  - F= Set of input features in both training and testing dataset; $F=f_1;......;f_q$.
  - $R= (Dn,F)$; Training dataset.
  - $E=(Q,F)$; Testing dataset.
  - $q=|F|$; No. of feature in dataset.
  - m=No. of filter techniques in FSL (or No. of chimps in population of BCO in WSL).
  - $H=H_1 H_2,....,H_m$; group of chimps in population.

- **Output:**
  - $Subset$= the selected features in the best chimp called attacker H_{attack} that introduces the maximum fitness value.

- **Steps:**

  /****** **Implement Filter Selection Layer (FSL)** ******/
  // Implement 'm' filter methods on training and testing dataset.
  1: **For each filter technique $a \in m$ do**
  2:     Assign the set of selected features for every technique as $Set (a)$.
  3: **Next**
  /****** **Implement Wrapper Selection Layer (WSL)** ******/
  // Construct initial population of BCO algorithm.
  4: Put the sets of 'm' filter techniques as the values of 'm' chimps in an initial Population with chimps symbolled by (H).
      // Initialize the values of fh, rh_1, rh_2, mh coefficients.
  5: Calculate mh as; $mh = H_k^2 - g$, $g = 1$
  6: Calculate fh as; $fh = 2 - 2 * \left(\frac{t}{MT}\right)$
  7: Calculate rh_1 and rh_2 using equations (13 to 20).
      // Calculate Ah and Ch vectors for $H_{attack}, H_{bar}, H_{chas}$, and H_{driv}.
  8: Calculate Ah and Ch using equations (8 to 11).
      // Calculate fitness value for every chimp.
  9: **For each agent $H_k \in H$ do**
  10:     Calculate the average accuracy value from 'nd' diagnosis method as;
  $$FF(H_k) = \frac{\sum_{j=1}^{nd} Acc_j(H_k)}{nd}$$
  11: **Next**
      // Determine the fourth leaders based on the maximum fitness values.
  12: H_{attack} = the 1st best (leader) chimp.
  13: H_{bar} = the 2nd best (leader) chimp.
  14: H_{chas} = the 3rd best (leader) chimp.
  15: H_{driv} = the 4th best (leader) chimp.
      // Adjust position of chimps based on $H_{attack}, H_{bar}, H_{chas}$, and H_{driv}.
  16: **For each agent $H_k \in H$ do**
  17:     $\vec{H}_k(t+1) = \begin{cases} \frac{\vec{H}_1 + \vec{H}_2 + \vec{H}_3 + \vec{H}_4}{4} & if(y < 0.5) \\ mh & if(y \geq 0.5) \end{cases}$
  18: **Next**
      // Apply the sigmoid function on every position of each chimp.
  19: **For each agent $H_k \in H$ do**
  20:     $SG\left(H_k^i\right) = \frac{1}{1+e^{-H_k^i}}$
  21: **Next**

  // Assign the new position of each chimp in binary form.
  22: **For each agent $H_k \in H$ do**
  23:     $H_{bin\_k}^i(t+1) = \begin{cases} 1 & if\ RAND(0,1) \geq SG(H_k^i) \\ 0 & Else \end{cases}$
  24: **Next**
  25: **If (T<MT) then**
  26:     Go to step 5.
  27:     **Else**
  28:     Return H_{attack} that achieve the highest fitness value in $Subset$, where all one's positions are the selected features.
  29: **End If**

Algorithm Parameters	
F	Set of input features in both training or testing dataset, F= {f₁;......;f_q }.
R	Training dataset that includes the training patients and its features, R= (Dn, F).
Dn	The training patients in the dataset.
E	Testing dataset that includes the testing items and its features, E= (Q, F).
Q	The testing patients in the dataset.
q	No. of features in dataset, q=|F|.
m	No. of filter techniques in FSL (or No. of chimps in population of BCO in WSL).
H	Group of chimps in population; H=H₁ H₂,....,H_m
Subset	The selected features in the best chimp called attacker H_attack that introduces the maximum fitness value.
mh	The chaotic value.
rh₁ and rh₂	Random vectors.
fh	Encircling coefficient vector.
t	Index refers to the current iteration.
MT	The maximum number of iterations.
Ah and Ch	Coefficient vectors for the leaders; H_attack, H_bar, H_chas, and H_driv.
H_attack, H_bar, H_chas, and H_driv.	The four best agents in the population called attacker, barrier, chaser, and driver chimps respectively.
H₁, H₂, H₃, and H₄.	The position of the four best agents respectively.
H_K(t+1)	The update position of kᵗʰ agent in the next iteration t+1.
FF(H_k)	Fitness value of kᵗʰ chimp.
Acc_j(H_k)	The accuracy of jᵗʰ diagnosis method based on the set of selected features in kᵗʰ chimp.
SG(H_k^i)	The sigmoid transfer function of kᵗʰ chimp at iᵗʰ position.
H_bin_k^i(t+1)	The position values of kᵗʰ agent in the next iteration t+1 in binary form.

5.2. The proposed Ensemble Diagnosis (ED) model

In this segment, the ED model as a new diagnostic model in the second phase of the HMD strategy called DP will be discussed in detail.

dation, and voting stages. At the training stage, the three diagnostic algorithms; WNB, WKNN, and deep learning will be trained in parallel on the same training dataset.

Secondly, these algorithms will be tested in parallel on the same

testing dataset during the testing stage. At the testing stage, the class categories will have different weight values according to each diagnostic algorithm, whether it is WNB, WKNN or deep learning. At the third stage called validation stage, each case in the validation dataset will be diagnosed by WNB, WKNN, and deep learning algorithms into different or similar class categories that have different weight values according to each diagnostic algorithm. In the fourth and final stage called voting stage, the weight value of the class category for each validate case will be passed from the three diagnostic algorithm to voting stage for determining the final diagnosis based on a new weighted voting method. In the next sub-segments, WNB, WKNN, deep learning, and weighted voting methods will be described in detail.

5.2.1. The Weighted Naïve Bayes (WNB) algorithm

In this segment, WNB is presented as an improved version of NB method to solve the NB problems. In fact, NB is a popular classification method that is characterized by simplicity and it can address real-time problems such as image and pattern recognition, medical diagnosis, and intrusion detection [23–25]. NB can give fast diagnoses rather than other diagnostic models and also it can be used for both small and large dataset. Additionally, NB has the ability to deal with the noise in the dataset as well as it is less sensitive to missing data [23–25]. Although NB is a sufficient technique for real-time applications such as medical

diagnosis application, it is considered all features equal and independent during the diagnosis process. Hence, NB should be modified to depend on the effective impact of each feature on the classifier to give more accurate results. In this paper, WNB is provided as a modification of the classical NB that takes into account the weights of features. In the WNB, the diagnosis of each patient in the dataset can be performed based on the different weights of features where each feature has its own weight according to its effectiveness on the class category using (24).

$$Diagnose(I_x) = \underset{cl_i \in cl}{\operatorname{argmax}} \left[Probability(cl_i) * \prod_{j=1}^{p} Weight_j * Probability\left(f_j|cl_i\right) \right]$$
$$where\ Weight_j \in \mathbb{R}^+$$

(24)

Where $Diagnose\ (I_x)$ is the diagnosis of patient I_x to the class category that give the highest probability value. $Probability\ (cl_i)$ is the prior probability of the class cl_i while $Probability\ (f_j|cl_i)$ is the conditional probability of the feature f_j according to the class cl_i. Additionally, $weight_j$ is the weight of the jth feature that represents the impact of this feature on the class category using (25).

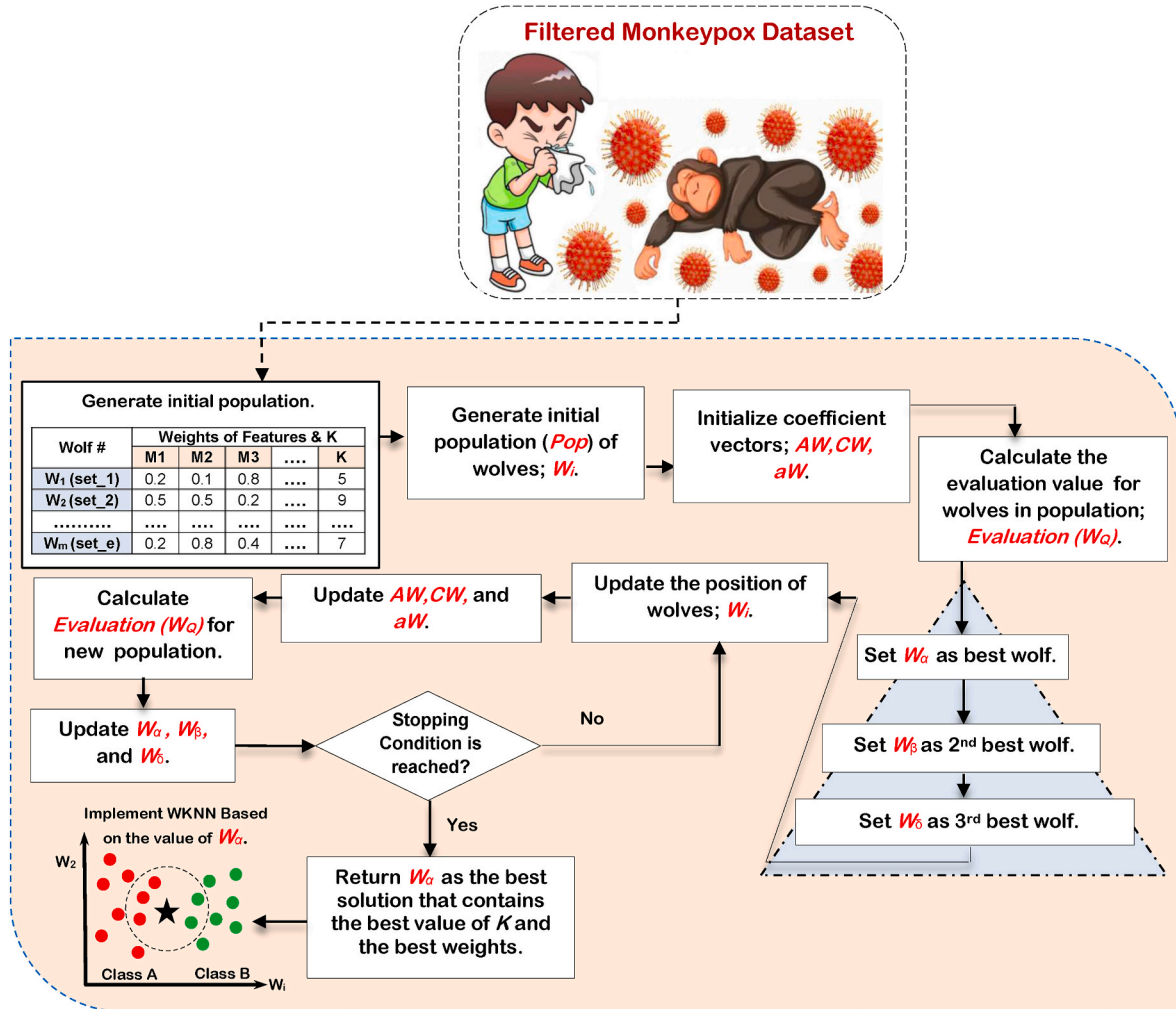$$weight_j = Acc\left(+f_j\right) - Acc\left(-f_j\right)$$

(25)

Fig. 5. The steps of implementing WKNN algorithm.

$$Evaluation\ (W_i) = WKNN\_Accuracy(W_i)$$

(26)

Where *weight_j* is the weight of the *j*th feature, the accuracy of the NB method based on the existence of the feature f_j in the feature set is *Acc (+f_j)*, and the accuracy of the NB method based on the absence of the feature f_j from the feature set is *Acc(-f_j)*.

5.2.2. The weighted K-nearest neighbors (WKNN) algorithm

WKNN is provided in this segment as an improved version of traditional KNN method to treat the KNN problems. KNN is a popular and straightforward method that is simple and easy to understand and use. It is used in many real-world applications such as electrical load forecasting, patient diagnosis, and traffic management [13]. Although KNN is simple, it is a lazy learning technique, depends on the value of *K*, and does not take into account the weight of each feature because each feature has different impact on the classification. Thus, KNN should be modified to use the best value of *K* and the best weights of features to provide the best classifications. In this paper, WKNN is presented as a new diagnostic algorithm based on using the optimal value of *K* and the best weight value for each feature obtained from the GWO algorithm before learning KNN algorithm. There are many steps to implement WKNN algorithm as shown in Fig. 5. The GWO will be implemented to select the best weight values for the features and the best *K* value and then the WKNN will be implemented on these best values. At first, initial population of GWO will be generated where each wolf includes weights of features and *K* value. Then, each wolf in the population will be evaluated using (26).Where *Evaluation (W_i)* is the evaluation value of *i*th wolf and *WKNN_Accuracy(W_i)* is the accuracy of implementing WKNN algorithm based on the values of genes in *i*th wolf. The best three wolves; W_α, W_β, and W_δ as leaders will be decided based on the high accuracy values. Depending on the position of these three wolves, the other wolves in the population including Omega (ω) will modify their position. Coefficient vectors *AW* and *CW* for the leaders must be calculated before starting to modify the positions of wolves in population using (27) and (28) [6,26].

$$\overrightarrow{AW} = \left| 2 * \overrightarrow{aW} * \overrightarrow{ran}_1 - \overrightarrow{aW} \right| \tag{27}$$

$$\overrightarrow{CW} = 2 * \overrightarrow{ran}_2 \tag{28}$$

Where $\overrightarrow{ran}_1$ and $\overrightarrow{ran}_2$ are random vectors in [0,1]. The encircling coefficient that is used to balance the tradeoff between exploration and exploitation is $\overrightarrow{aW}$. In fact, $\overrightarrow{aW}$ is linearly decreasing from 2 to 0 over iterations using (29) [6,26].

$$\overrightarrow{aW} = 2 - 2 * \left(\frac{itr}{M\_itr} \right) \tag{29}$$

Where the number of iterations is *itr* and the maximum number of iterations is *M_itr*. After calculating the coefficient vectors *AW* and *CW* for the leaders, each wolf (e.g., *i*th wolf) in population can modify its position in the next iteration (*itr+1*) based on W_α, W_β, and W_δ by using (30) [6,26].

$$\overrightarrow{W}_i(itr + 1) = \frac{\overrightarrow{W}_1 + \overrightarrow{W}_2 + \overrightarrow{W}_3}{3} \tag{30}$$

Where the positions of W_α, W_β, and W_δ are $\overrightarrow{W}_1, \overrightarrow{W}_2$, and $\overrightarrow{W}_3$ respectively based on the current wolf (W_i). In fact, $\overrightarrow{W}_1, \overrightarrow{W}_2$, and $\overrightarrow{W}_3$ can be calculated as in (31-33) [6,26].

$$\overrightarrow{W}_1 = \overrightarrow{W}_\alpha - \overrightarrow{AW}_1 \overrightarrow{D}_\alpha \tag{31}$$

$$\overrightarrow{W}_2 = \overrightarrow{W}_\beta - \overrightarrow{AW}_2 \overrightarrow{D}_\beta \tag{32}$$

$$\overrightarrow{W}_3 = \overrightarrow{W}_\delta - \overrightarrow{AW}_3 \overrightarrow{D}_\delta \tag{33}$$

Where the position of the leaders wolfs at iteration *itr* are $\overrightarrow{W}_\alpha$, $\overrightarrow{W}_\beta$, and $\overrightarrow{W}_\delta$. $\overrightarrow{A}_1$, $\overrightarrow{A}_2$, and $\overrightarrow{A}_3$ are calculated using (27) and $\overrightarrow{D}_\alpha$, $\overrightarrow{D}_\beta$, and $\overrightarrow{D}_\delta$ are calculated using (34-36) [6,26].

$$\overrightarrow{D}_\alpha = \left| \overrightarrow{CA}_1 . \overrightarrow{W}_\alpha - \overrightarrow{W}_i \right| \tag{34}$$

$$\overrightarrow{D}_\beta = \left| \overrightarrow{CA}_2 . \overrightarrow{W}_\beta - \overrightarrow{W}_i \right| \tag{35}$$

$$\overrightarrow{D}_\delta = \left| \overrightarrow{CA}_3 . \overrightarrow{W}_\delta - \overrightarrow{W}_i \right| \tag{36}$$

Where $\overrightarrow{C}_1$, $\overrightarrow{C}_2$, and $\overrightarrow{C}_3$ are calculated as in (28). Based on $\overrightarrow{W}_i(itr +1)$ as a new position of every wolf in population, the evaluation function will be implemented on every wolf using (26). Then, these steps continue until the maximum number of generations is reached. In the end, the algorithm terminates and the weights of features and the *K* value given in the best wolf W_α will be used as the best values to implement the steps of the WKNN algorithm to diagnose monkeypox patients. The implementation steps of WKNN are similar to the traditional KNN method but have a different distance method in which the WKNN distance depends on the weights of features. Additionally, WKNN is based on a predefined value of *K* but KNN is based on undefined value. In the WKNN algorithm, each testing case is passed through many steps to be diagnosed. In step 1, the distance between each testing case and each training case is calculated by using Euclidean distance in weighted form as presented in (37).

$$Distance(TE, TR) = \sqrt{\sum_{i=1}^{q} M_i(TE_i - TR_i)^2} \tag{37}$$

Where *Distance(TE,TR)* is the distance between the testing case *TE* and the training case *TR*. *q* is the number of features in the filtered dataset, M_i is the weight of *i*th feature, TE_i is the value of *i*th feature at the testing case *TE*, and TR_i is the value of *i*th feature at the training case *TR*. In step 2, the nearest *k* of neighbors which give the lowest distance between the testing case and everyone of training cases are assigned. In step 3, the diagnostics of *k* neighbors are used to determine the final diagnosis of the testing case by voting.

5.2.3. Deep learning algorithm

In this segment, Long Short-Term Memory (LSTM) model as a deep learning structure used to diagnose monkeypox patients will be described in detail. LSTM is an evolution of Recurrent Neural Network (RNN) to solve the gradient vanishing and exploding problem by replacing the hidden vectors from RNN with memory cells equipped with gates [20–22]. Thus, LSTM represents a special type of RNN that has the ability to learn long-term dependencies. It also can by default remember information for long periods of time. Accordingly, LSTM is a popular deep learning tool because it has the ability to learn from sequential data [20–22]. LSTM is a sufficient model for several real-time applications such as sequence-to-sequence predictions, medical diagnosis, various tagging problems, language modeling, and classification of sentences. In this paper, the designed model is based on a many-to-one LSTM structure to handle multi-label diagnostics as shown in Fig. 6.

According to Fig. 6, the input dataset that contains values of 'p' features is passed to 'p' LSTM cells where the cell state (c_i) and the current output state (h_i) of *i*th LSTM are used as inputs for the next LSTM or $(i+1)^{th}$ LSTM. In other words, the outputs of each LSTM are used as inputs to the next LSTM and then the last LSTM gives the definitive diagnosis. Each LSTM cell consists of three gates called input, forget, and output gates used to update the output value and maintain the cell state as illustrated in Fig. 7. These gates are intended to control the flow of information from one cell state to another. To give a decision to control
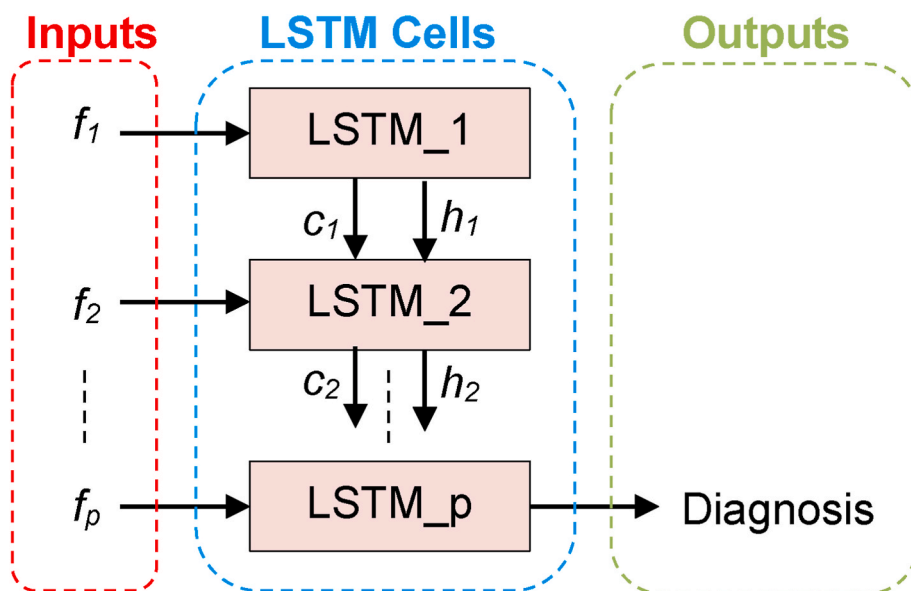
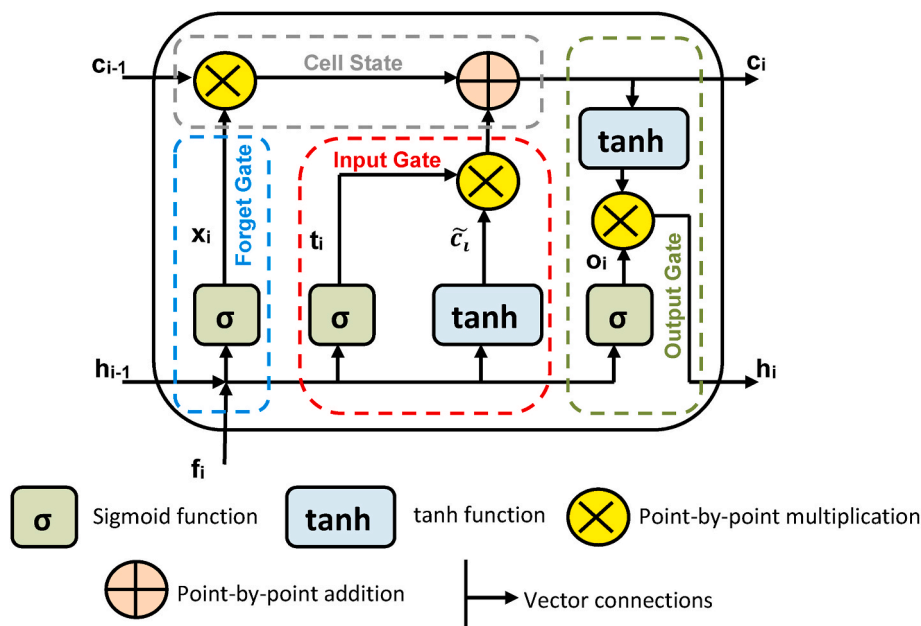**Fig. 6.** A many-to-one LSTM structure for multi-label diagnostics.

Fig. 7. The structure of LSTM cell.

the flow information, sigmoid activation (σ) is used by all three gates. In fact, information does not change in cell state but it can be added or omitted via each gate. The input values that should be used to change the cell state are determined by the input gate. The useless information that should be omitted from the cell state is determined by the forget gate while the amount of output is determined by the output gate [20–22].

To construct the LSTM, three main steps are required. Initially, LSTM begins to identify undesired information and then remove it from the cell by the forget gate. In the forget gate, current input (f_i) and previous output (h_{i-1}) in the cell state (c_{i-1}) are used to give output (x_i) between zero and one. Completely forget the information is represented by one while completely retaining it is represented by zero. In the second step, a decision about storing information in the current cell state (c_i) is provided by the input gate by multiplying its output (t_i) with the output of *tanh* activation layer ($\tilde{c}_i$). In the third and final step, the flow of fraction

Table 5
CM for deep learning.

		Predicted Class		Total
		A	B	
Actual Class	A	220 = 37%	380	600
	B	270	130 = 32%	400
		490	510	1000

of information(h_i) in the current cell state (c_i) is provided at the output of LSTM cell by the output gate by combining its output (o_i) with the output of another *tanh* activation layer. The operation of these three gates in an LSTM cell for giving output (h_i) in cell state (c_i) can be mathematically represented using (38-43) [20–22].

$$x_i = \sigma((w_x * h_{i-1}) + (w_x * f_i) + b_x) \tag{38}$$

Table 6
ED with confusion based voting.

Classifier	Predicted class	Vote for Class	
		A	B
WNB	A	0.92	0.40
WKNN	B	0.62	0.55
Deep Learning	B	0.37	0.32

$$t_i = \sigma((w_t * h_{i-1}) + (w_t * f_i) + b_t) \tag{39}$$

$$\widetilde{c_i} = \tanh((w_c * h_{i-1}) + (w_c * f_i) + b_c) \tag{40}$$

$$c_i = (x_i * c_{i-1}) + (t_i * \widetilde{c_i}) \tag{41}$$

$$o_i = \sigma((w_o * h_{i-1}) + (w_o * f_i) + b_o) \tag{42}$$

$$h_i = o_i * \tanh \ c_i \tag{43}$$

Where w_x, w_t, w_c, and w_o are the weight matrices. b_x, b_t, b_c, and b_o are bias factors for different gates of LSTM cell.

5.2.4. The weighted voting method

During this segment, Confusion Based Voting (CBV) is provided as a new weighted voting method for combining the ensemble classifier (see Table 5). Based on the validation dataset, the Confusion Matrices (CMs) of the applied three classifier of the ensemble called WNB, WKNN, and Deep Learning are illustrated in tables (3, 4, and 5) respectively. The general accuracy for WNB, WKNN, Deep Learning are; 71%, 59%, and 35% as depicted from such figures. On the other hand, Table 6 presents the output of classifying a new case depending on the used three classifiers. Based on the majority voting, if class B gets two votes and class A votes gets one vote only, the target class will be class B. However, class A gets a weight of 0.92 and class B gets $0.55 + 0.32 = 0.87$ based on CBV. Accordingly, the input case belongs to class A.

6. The description of experimental results

Through this segment, the HMD strategy that includes SP and DP will be implemented to early detect monkeypox cases. The implementation of HMD starts with the implementation of the IBCO algorithm as a feature selection method in SP to determine a valuable set of features. Then, the valid dataset without useless features is passed to ED as a diagnostic model in DP to give fast and more accurate diagnosis. In fact, ED model is a hybrid model that includes three methods called WNB, WKNN, and LSTM as a Deep Learning technique which are combined using a new weighted voting method called CBV. During this implementation, the fitness function of BCO depends on using SVM [6], DLM [20–22], NB [9], and KNN [13] to calculate the average accuracy of them. Three main scenarios will be followed to implement the HMD strategy. During the first scenario, the proposed IBCO algorithm will be tested and compared to other modern selection algorithms using NB algorithm as a standard method [9].

In the second scenario, WNB, WKNN, LSTM, and the combined model called ED will be tested and their results will be compared. In the third scenario, the HMD strategy that includes both the proposed IBCO as a new feature selection method and ED model as a diagnostic method will be implemented and compared to other modern strategies. This

Table 7
Confusion matrix which depicts how diagnostic on cases.

		Diagnosed Label	
		Positive	Negative
Known Label	Positive	True Positive (TP)	False Negative (FN)
	Negative	False Positive (FP)	True Negative (TN)

Table 8
Confusion matrix formulas.

Measure	Formula	Meaning
Precision	TP/(TP + FP)	The percentage of positive diagnostics those are already correct.
Recall	TP/(TP + FN)	The percentage of positive diagnostics that were diagnosed as positive.
Accuracy	(TP + TN)/(TP + TN + FP + FN)	The percentage of diagnostics those are correct.
Macro-average	$\sum_{i=1}^{c} P_i/c$ "for Precision" $\sum_{i=1}^{c} R_i/c$ "for Recall"	The average of the precision and recall of the system on different c classes.
Micro-average	(TP1 + TP2)/(TP1 + TP2 + FP1 + FP2) "for Precision" (TP1 + TP2)/(TP1 + TP2 + FN1 + FN2) "for Recall"	the summation up to the individual true positives, false positives, and false negatives of the system for different classes and the apply them to get the statistics.
F1-measure	2*PR/(P + R)	The weighted harmonic mean of Precision and Recall.

Table 9
The values of the used parameters.

Parameter	Description	Applied value
MT	The maximum iterations number in BCO	100
Rand ()	Uniform distribution value in BCO	Random ($0 \leq$ Rand () ≤ 1)
Y	The random value to choose between the chaotic model or the normal adjusting position method	Random ($0 \leq y \leq 1$)
K	The closed number of neighbors	$1 < K < 5$
r_1 and r_2	Two independent random numbers	Random ($0 \leq r_1$, $r_2 \leq 1$)
aW	Linearly decrease	[2,0]
M_itr	The maximum number of iterations for GWO	100

work is based on the use of monkeypox dataset that classifies patients into two classes called "Positive" as an infected case and "Negative" as an uninfected case [27]. In fact, negative or uninfected case does not mean health case but he/she does not suffer from monkeypox infection but may suffer from other diseases or not. The performance of the used methods can be calculated by using recall, accuracy, and precision measurements based on confusion matrix as presented in Table 7 [6,7]. Various formulas of confusion matrix are summarized in Table 8. The dataset is divided into 10 equal parts based on10-fold cross-validation. Training sets are represented in 9 of parts while a testing set is represented in the other part. Actually, 70% of the used dataset has been assigned as training data while 30% has been assigned as testing data. The values of used parameters are mentioned in Table 9.

6.1. The used hardware and software

The proposed HMD strategy has been implemented using hardware and software tools. The used hardware tools are Dell machine with 8 GB RAM and 1 TB hard disk while the used software tools are windows operating system and MATLAB_R2021b_win64. Based on the MATLAB libraries, the implementation codes for the used techniques are represented in m-files. Thus, the components of HMD, which are; IBCO, WNB, WKNN, LSTM, and CBV were established as source codes in m-files. In MATLAB, the original versions of the used methods are available as open source m-files codes. During this work, these m-files were downloaded and then modified to be new versions provided in this paper. Initially, the used dataset in spreadsheet (Excel sheet) has been read in the MATLAB and then stored in a matrix (m-dimensional vector). This dataset has been entered into IBCO code that consists of two m-files where the first m-file contains the filter selection methods that passes their results as initial population values in the second m-file that contains BCO algorithm. The dataset was filtered from irrelevant features and only includes the selected features. The filtered dataset was passed to three m-files include WNB, WKNN, LSTM algorithms. Diagnosis

ALT level,	ALP level,	Arthralgia	Albumin l	Hospitalis	Date_confi	RT-PCR	HIV co-inf	Outcome	Diagnosin	Diagnosed disease	
37	147	10	2.5	yes	5/6/2022	yes	positive	Full recov	positive	Monkeypox	
37	145	9.8	1.9	yes	8/31/2022	no	positive	Full recov	positive	Monkeypox	
42	149	11	2.8	yes	5/12/2022	yes	negative	Full recov	positive	Monkeypox	
41	143	6.6	2	yes	8/13/2022	yes	positive	Full recov	positive	Monkeypox	
38	143	7	2.7	yes	5/15/2022	no	unknown	Full recov	positive	Monkeypox	
39	141	7.6	2.9	yes	5/15/2022	yes	positive	Full recov	positive	Monkeypox	
38	141	6.8	2.7	yes	6/19/2022	no	positive	Full recov	positive	Monkeypox	
41	145	11	2.4	yes	6/19/2022	yes	unknown	Full recov	positive	Monkeypox	
40	148	9.8	2.1	yes	6/17/2022	yes	positive	Full recov	positive	Monkeypox	
6	89	8	4.5	yes	6/1/2022	unknown	positive	Full recov	negative	normal	
38	145	7	2.9	yes	6/2/2022	yes	positive	Full recov	negative	acne	
40	141	10	2.6	yes	8/3/2022	unknown	positive	Full recov	positive	Monkeypox	
38	144	11	2.3	yes	6/2/2022	yes	negative	Full recov	positive	Monkeypox	
38	141	6.6	2.9	yes	6/25/2022	yes	positive	Full recov	positive	Monkeypox	
38	144	8	3.4	yes	7/5/2022	no	positive	Full recov	negative	psoriasis	
20	46	7	4	yes	7/17/2022	yes	positive	Full recov	negative	normal	
43	148	9.8	2.3	yes	7/17/2022	no	positive	Full recov	positive	Monkeypox	
11	124	8	5.3	yes	8/11/2022	yes	positive	Full recov	negative	normal	
7	140	7	5.3	yes	7/14/2022	yes	positive	Full recov	negative	normal	
40	144	10	2.6	yes	7/25/2022	unknown	positive	Full recov	positive	Monkeypox	
43	142	10	2.4	yes	7/26/2022	yes	positive	Full recov	positive	Monkeypox	
37	144	8	2.9	yes	5/18/2022	no	positive	Full recov	negative	alopecia	
17	116	7	4	yes	5/19/2022	yes	positive	Full recov	negative	normal	

Fig. 8. A snapshot of monkeypox dataset.

results from these three algorithms were passed to CBV m-file to define the final diagnosis.

6.2. The monkeypox dataset description

Monkeypox dataset is an internet data collected from 6-5–2022 to 19-9-2022 [27]. This dataset is a blood test dataset collected from patients of different ages and genders in different regions in different countries such as Nigeria, Spain, UK, etc. Monkeypox dataset contains 500 cases who were classified into two class categories called "Positive" and "Negative". While the positive cases are patients with monkeypox, the negative cases are patients without monkeypox. In fact, negative case does not mean health case but he/she does not have monkeypox but may or may not have other diseases. This dataset was collected from patients suffering from different diseases, which are; monkeypox, acne, alopecia, normal, psoriasis, and small pox as shown in Fig. 8 that is a snapshot of monkeypox dataset. Monkeypox is a class category of positive cases but normal is a class category of negative cases who are health cases. On the other hand, acne, alopecia, normal, psoriasis, and small pox are classes of negative cases who are uninfected with monkeypox but suffer from other diseases. In fact, this dataset consists of 47 features that include demographic features and features of laboratory blood tests as presented in Table 10. These features are used to describe causative conditions based on the blood test that gives each patient's status. In fact, the selected features after applying IBCO are 34. According to the 500 cases in the dataset, 296 of them had monkeypox as presented in Table 11. In fact, monkeypox dataset was divided into 350 cases as a training set of data and 150 cases as a testing set of data.

6.3. Testing the Improved Binary Chimp Optimization (IBCO) algorithm

Through this segment, IBCO will be executed as a new feature selection algorithm and compared to other modern selection methods to ensure its effectiveness in identifying valuable features in the monkeypox dataset. These selection methods are Genetic Algorithm (GA) [8], Improved Genetic Algorithm (IGA) [7], Adjusted Brain Storm Optimization (ABSO) algorithm [28], Hybrid Feature Selection Method (HFSM) [6], and BCO [12]. After implementing these feature selection methods, the NB is used as a diagnostic model to be trained on the filtered dataset using the selected features from each feature selection method separately and then it will be tested to calculate the diagnostic

efficiency according to each selection method [9]. Accuracy, precision, and recall calculations are illustrated in Figs. 9-11. Implementation time measurement also is provided in Fig. 12. Actually, IBCO provides the best performance values, thus, it outperforms other methods.

Figs. 9-11 show that IBCO outperforms GA, IGA, ABSO, HFSM, and BCO as it introduced 98.05% accuracy value that represents the maximum value at number of training data = 350. At the maximum number of training dataset, the accuracy values of GA, IGA, ABSO, HFSM, BCO, and IBCO are 62.4%, 65.65%, 76.05%, 83.74%, 90.1%, and 98.05% respectively. Based on these results, it is noted that GA gives the lowest accuracy value while IBCO outperforms all methods because it gives the highest accuracy. Additionally, IBCO provides the maximum precision and recall values equal 89.16% and 90.09% respectively. The precision values of GA, IGA, ABSO, HFSM, and BCO are 62.12%, 65%, 73%, 82.5%, and 84.06% respectively but their recall values are 58.2%, 64.99%, 78%, 86%, and 87.9% at the maximum number of training data. From these measurements, it is noted that GA provides the worst results while IBCO provides the best results.

According to implementation time in Fig. 12, it is noted that IBCO takes a short execution time but GA takes a long execution time with values reach to 2.51 s and 8.2 s respectively at the number of training data = 350. In fact, BCO is faster than GA, IGA, ABSO, and HFSM but slower than IBCO as it takes 3.1 s to be executed. Hence, IBCO can determine valuable features that can accurately diagnose monkeypox patients. At the last, it is concluded that the performance of IBCO method is superior to GA, IGA, ABSO, HFSM, and BCO. Based on experimental results, the second best feature selection method after IBCO is BCO algorithm because it can provide the maximum accuracy, precision, and recall values and the minimum implementation time. Thus, IBCO can improve the diagnostic performance more than BCO because IBCO can solve two main problems of BCO which are the number of search agents in population and the initial values of each search agents are were randomly generated. This solution is provided by using FSL that contains 'm' of filter methods which give the BCO 'm' of search agents which include the selected features from filter methods as initial values of these 'm' agents.

At the end, the selected features from GA = *{Age, Transmission rank, Smallpox vaccination history,Fever, Dysuria, Myalgia, headache, Approximate maximum number of concurrent lesions, Monkeypox viral DNA detected in Blood, Day of illness treatment commenced, AST level, Duration of hospitalization with monkeypox, Outcome of monkeypox infection}*. The

Table 10
Descriptions about the features of Monkeypox.

Feature	Normal Range	Selected Feature
Age (>2)	–	Yes
Sex (Male/Female)	–	No
Transmission rank	–	Yes
Country of acquisition	–	No
Smallpox vaccination history	–	No
HIV, hepatitis B, and hepatitis C status (Negative/Positive)	Negative	Yes
Fever (Yes/No/None)	No	Yes
Rectal pain or pain on defecation (Yes/No/None)	No	Yes
Dysuria (Yes/No/None)	No	Yes
Bleeding/discharge *per rectum* (Yes/No/None)	No	No
Conjunctivitis (Yes/No/None)	No	Yes
Oropharyngeal manifestations	–	Yes
Back pain (Yes/No/None)	No	Yes
Myalgia (Yes/No/None)	No	Yes
headache (Yes/No//None)	No	Yes
Sexually transmitted infections	–	No
Lymphadenopathy (Yes/No/None)	No	Yes
Approximate maximum number of concurrent lesions	–	Yes
Distribution of lesions	–	Yes
Complications of illness		No
Monkeypox viral DNA detected in Blood (Yes/No/None)	No	Yes
Monkeypox viral DNA detected in Nose or throat swab (Yes/No/None)	No	Yes
Monkeypox viral DNA detected in Urine (Yes/No/None)	No	Yes
Antivirals received	–	No
Day of illness treatment commenced	–	No
Complications of treatment	–	No
Duration of hospitalization with monkeypox (days)	–	No
Sore throat (Yes/No/None)	No	Yes
Chills (Yes/No/None)	No	Yes
White Blood Cell (WBC) count, cells/mm³	400–9000	Yes
Hematocrit, %	For men (39–49) & For woman (35–45)	Yes
Platelet count * 10⁹ platelets/L.	150–400	Yes
Sodium level, mmol/L	136–145	Yes
Potassium level, mmol/L	3.5–5.0	Yes
Blood urea nitrogen level, mg/dL	10–20	Yes
Creatinine level, mg/dL	<1.5	Yes
Calcium level, mmol/L	9–10.5	Yes
Total bilirubin level, mg/dL	0.3–1	Yes
Aspartate aminotransferase (AST) level, U/L	0–35	Yes
Alanine aminotransferase (ALT) level, U/L	0–35	Yes
Alkaline phosphatase (ALP) level, U/L	40–140	Yes
Arthralgia	6.7–15.8	Yes
Albumin level, mg/dL	3.5–5.5	Yes
Hospitalized (Yes/No/None)	–	No
Date_confirmation	–	No
Reverse transcription polymerase chain reaction (RT-PCR) (Yes/No/None)	–	Yes
Outcome of monkeypox infection	–	No

Table 11
Distribution of people in dataset based on infection.

Criteria	Value/Description		
Total number of cases	Monkeypox Patients 297	Normal People **95**	Cases with other Diseases **108**
Type of other Diseases	Acne **18**	Alopecia **9**	Psoriasis **15**
	small pox **29**	other **37**	
Sex	**Male**	**Female**	
Monkeypox	**152**	**145**	
Normal	**48**	**47**	
Other Diseases	**57**	**51**	
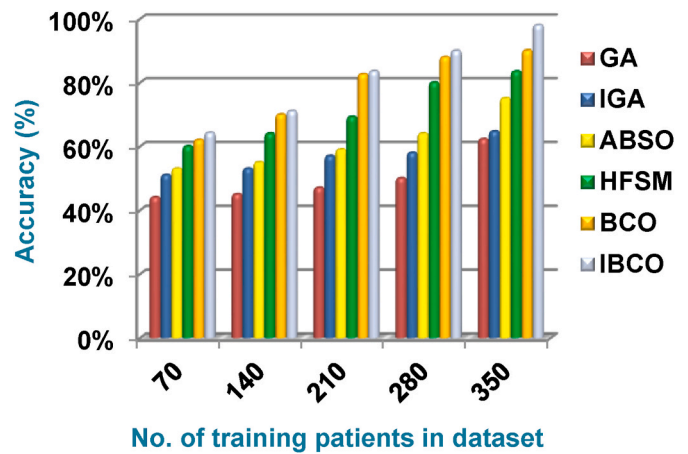
Fig. 9. Accuracy of selection techniques using NB.
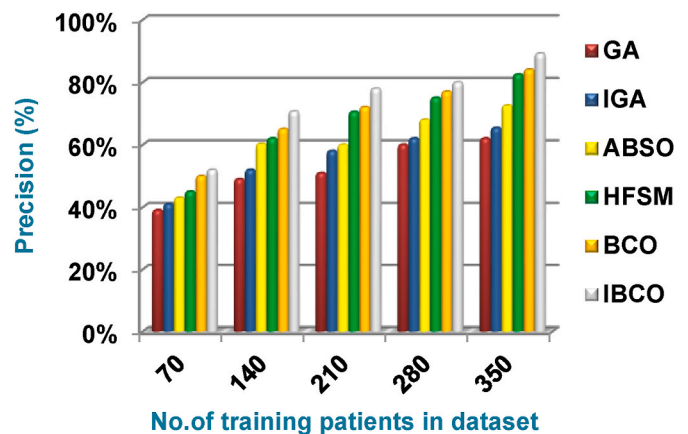
Fig. 10. Precision of selection techniques using NB.

selected features from IGA = *{Transmission rank, HIV, hepatitis B, and hepatitis C status, Fever, Dysuria, Myalgia, headache, Monkeypox viral DNA detected in Blood, Day of illness treatment commenced, AST level, Hematocrit, Arthralgia, Outcome of monkeypox infection }*. The selected features from ABSO = *{Sex, Transmission rank, HIV, hepatitis B, and hepatitis C status, Dysuria, Bleeding/discharge per rectum, Myalgia, headache, Monkeypox viral DNA detected in Blood, Monkeypox viral DNA detected in Nose or throat swab, Day of illness treatment commenced, Hematocrit, AST level, Arthralgia, RT-PCR, Outcome of monkeypox infection}*. The selected features from HFSM = *{Age, Transmission rank, HIV, hepatitis B, and hepatitis C status, Dysuria, Bleeding/discharge per rectum, Myalgia, headache, Monkeypox viral DNA detected in Blood, Monkeypox viral DNA detected in*

Nose or throat swab, Oropharyngeal manifestations, Hematocrit, AST level, ALT level, RT-PCR, Outcome of monkeypox infection}. The selected features from BCO = *{Age, Transmission rank, HIV, hepatitis B, and hepatitis C status, Dysuria, Bleeding/discharge per rectum, Monkeypox viral DNA detected in Blood, Monkeypox viral DNA detected in Nose or throat swab, Oropharyngeal manifestations, Sore throat, Chills, WBC counts, Hematocrit, Platelet count, Sodium level, Potassium level, AST level, ALT level, RT-PCR, Outcome of monkeypox infection}*. The selected features from IBCO are presented in the last column in Table 10. Accordingly, monkeypox dataset with the best subset of features selected from IBCO will be passed to the next segments to train and then test the proposed ED model on the correct dataset without irrelevant features.
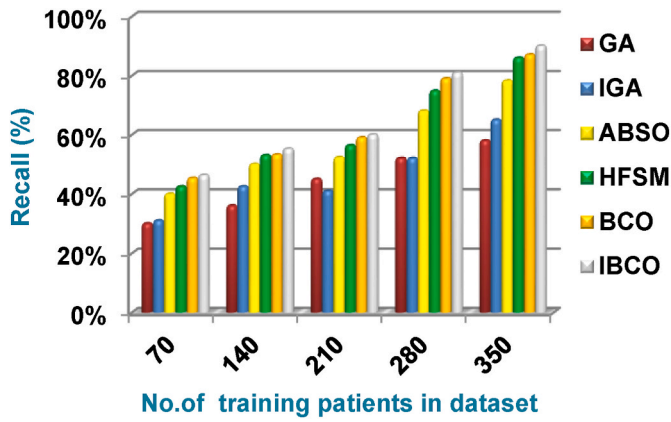
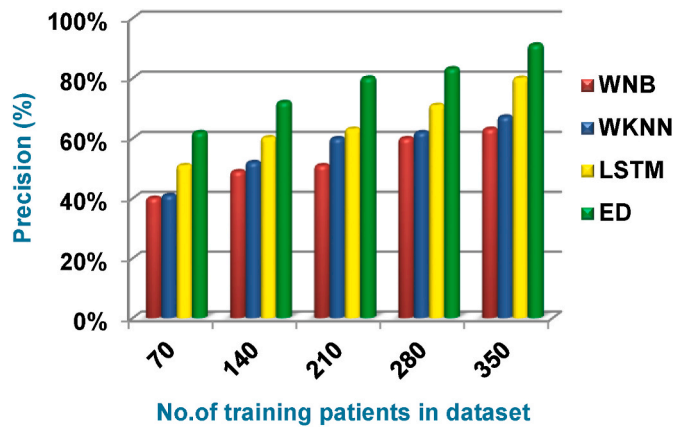**Fig. 11.** Recall of selection techniques using NB.

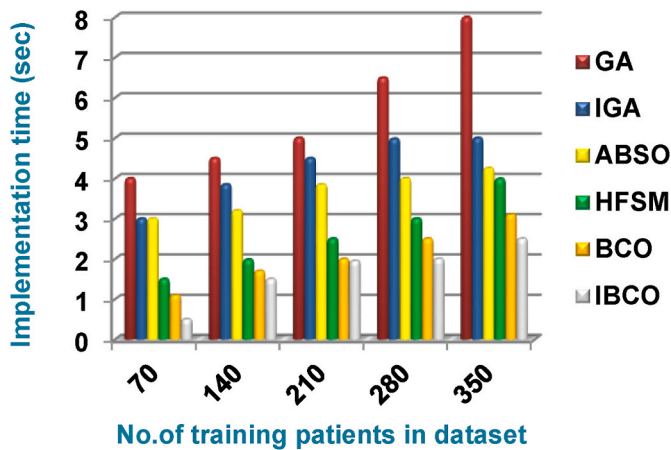**Fig. 14.** Precision of different diagnostic models.

Fig. 12. Implementation time of selection techniques using NB.
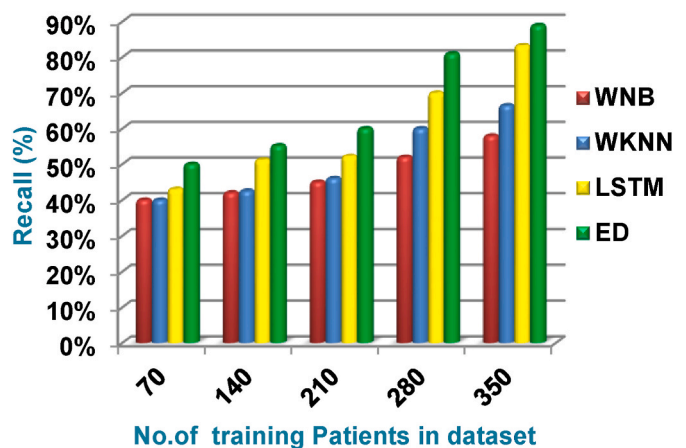

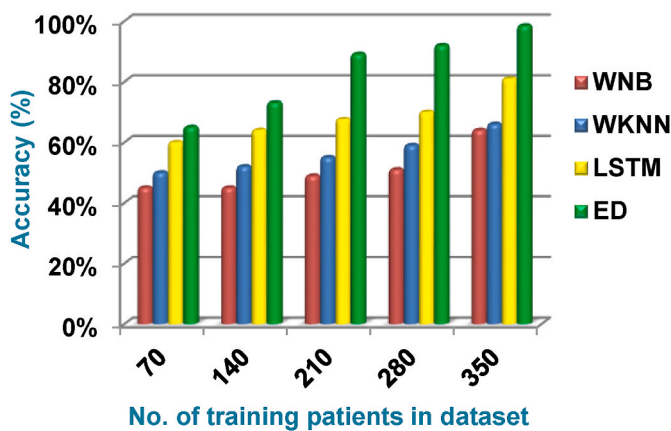**Fig. 15.** Recall of different diagnostic models.

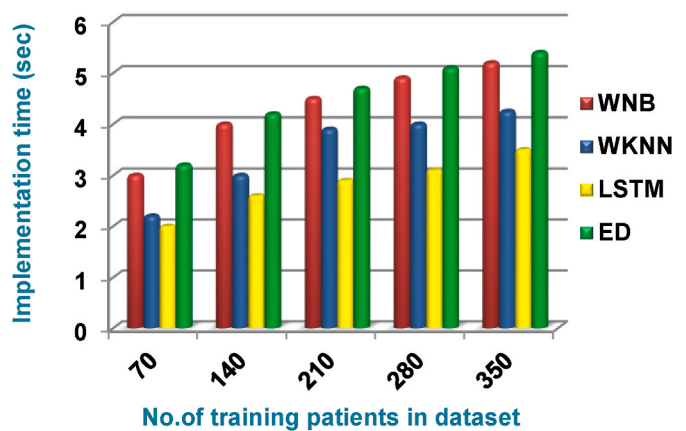**Fig. 13.** Accuracy of different diagnostic models.

Fig. 16. Implementation time of different diagnostic models.

6.4. Testing the Ensemble Diagnosis (ED) model

In this segment, ED model will be tested against its components which are WNB, WKNN, and deep learning algorithm called LSTM to ensure the effectiveness of the combined model called ED is higher than its component separately. At first, the monkeypox dataset after selecting the most significant features using IBCO will be divided into training, testing, and validation datasets. Then, WNB, WKNN, LSTM, and ED will be trained by using the same training dataset. After that, these algorithms will be tested by using the same testing dataset. Finally, these

algorithms will be validated by using validation dataset to measure their performance metrics which are accuracy, precision, and recall as presented in Figs. 13-15. Additionally, the implementation time measurement is provided in Fig. 16. In fact, ED model gives the best results, hence, it is superior WNB, WKNN, and LSTM.

According to figures (13 → 15), ED model outperforms WNB, WKNN, and LSTM with accuracy values reach to 98.48%, 64%, 66.01%, and 80.99% respectively at the maximum value at number of training data = 350. On the other hand, WNB algorithm introduced the lowest accuracy

value while ED model outperforms all methods because it gives the maximum accuracy value. According to precision and recall measurements, ED model provides the maximum precision and recall values equal 91.1% and 88.91% respectively. WNB, WKNN, and LSTM algorithms provide precision values reach to 63.12%, 67.2%, and 80.04% respectively but their recall values are 58%, 66.5%, and 83.25% at the maximum number of training data. From these calculations, it is noted that WNB algorithm provides the worst results while ED model provides the best results.

In Fig. 16, LSTM model takes a short execution time but ED takes a long execution time with values reach to 3.5 s and 5.4 s respectively at the maximum number of training data. In fact, WKNN algorithm is faster than WNB and ED but slower than LSTM model as it takes 4.25 s to be executed but WNB takes 5.2 s. It is noted that ED model requires a large diagnostic time because it has to wait for the decision-making time of the three classifiers. Therefore, the time of ED diagnosis is the highest time taken from the three classifiers, in addition to the voting time. However, this time spent does not affect the efficiency of the diagnostic system, as the goal of diagnostic systems is the efficiency of diagnosis and not the time taken for diagnosis, in addition to the combined time for the three classifiers is small and can be neglected in the case of diagnosis. Hence, ED model can accurately diagnose monkeypox patients because it combines three different algorithms to insure the maximum diagnose accuracy. These three algorithms are WNB as a probabilistic classifier, WKNN which combined a distance based classifier (traditional KNN) with one of the most effective bio-inspired optimization technique, which is GWO, and LSTM which the most recently used machine learning method and introduces excellent results. Finally, it is concluded that the performance of ED model is superior to WNB, WKNN, and LSTM. In the next segment, the proposed HMD strategy that includes IBCO to select the best subset of features and ED model as a diagnostic model to provide accurate diagnosis will be tested against many recent strategies.

6.5. Testing the human monkeypox detection (HMD) strategy

In this segment, HMD strategy will be executed and compared to other modern diagnostic strategies to ensure that HMD can provide fast and accurate diagnosis. These strategies are RF [9], Neuro-Fuzzy [1], ELGA [8], DBC [6], CPE [7], and Ensemble Diagnosis Strategy (EDS) [29]. In fact, HMD strategy takes many steps to be implemented where it begins with implement IBCO as a new feature selection method. After that, ED model is applied depending on valid data without useless features to give a quick and correct results. Based on Table 8, accuracy, precision, recall, micro-average precision, micro-average recall, macro-average precision, macro-average recall, and F1-measure calculations are illustrated in figures (17→24). In fact, micro-average precision, micro-average recall, macro-average precision, macro-average
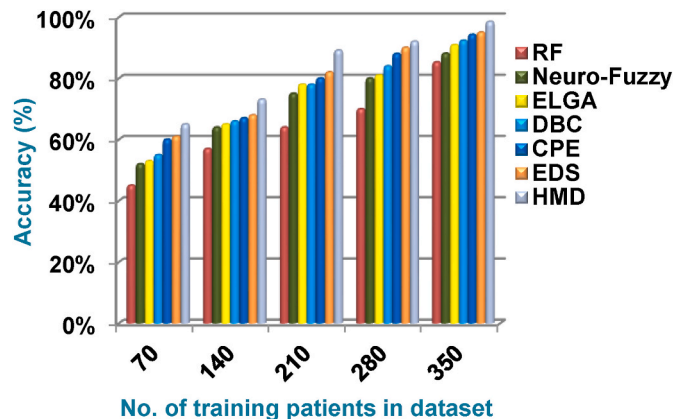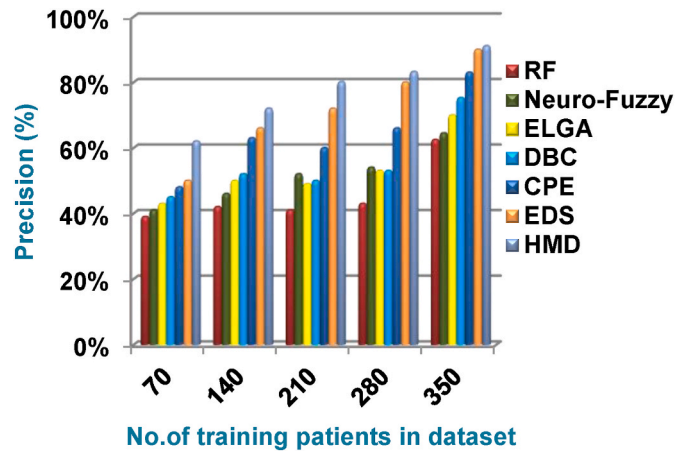

Fig. 18. Precision of monkeypox diagnostic strategies.

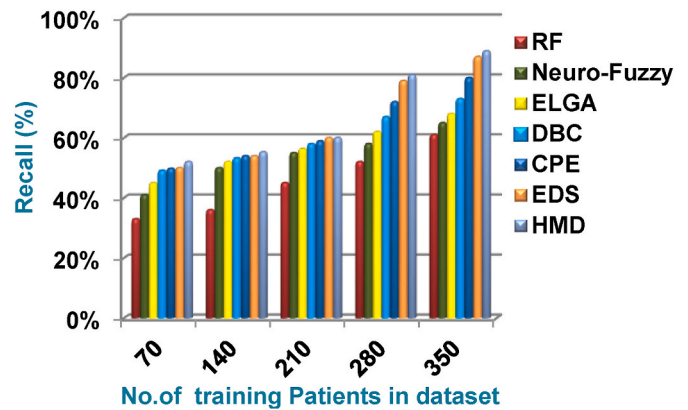**Fig. 19.** Recall of monkeypox diagnostic strategies.

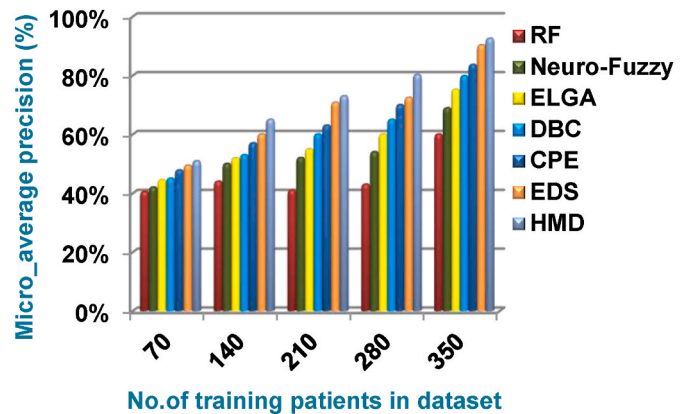**Fig. 20.** Micro_average precision of monkeypox diagnostic strategies.

Fig. 17. Accuracy of monkeypox diagnostic strategies.

recall, and F1-measure will be used to measure the performance of algorithms based on unbalanced data. The implementation time measurement also is provided in Fig. 25. At the end, the diagnosing time according to testing dataset is illustrated in Fig. 26 to prove the computational efficiency of the proposed HMD strategy against other strategies. Actually, HMD provides the best performance values, thus, it outperforms other strategies.

Fig. (17-24) show that HMD outperforms RF, Neuro-Fuzzy, ELGA, DBC, CPE, and EDS as it introduced the best results at the number of training data = 350. In Fig. 17, HMD algorithm provides the maximum
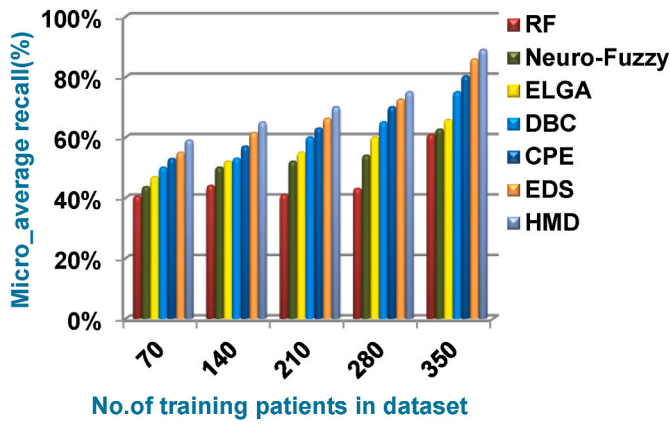
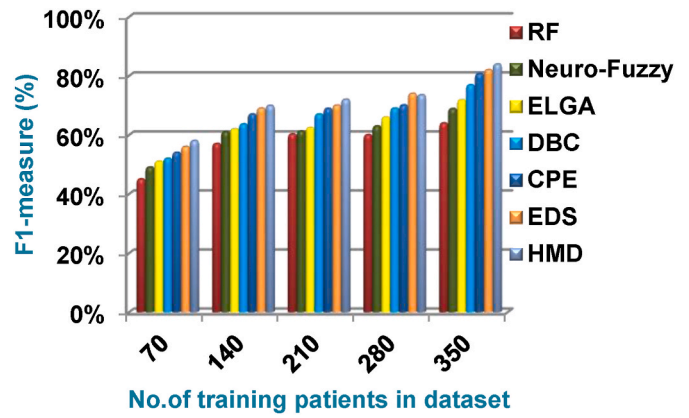**Fig. 21.** Micro_average recall of monkeypox diagnostic strategies.

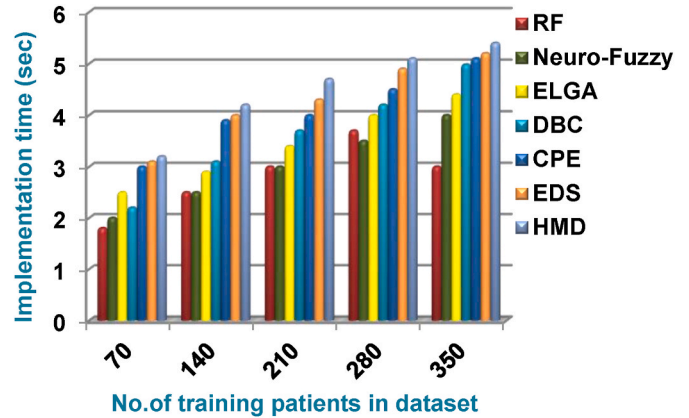**Fig. 22.** Macro_average precision of monkeypox diagnostic strategies.

accuracy value while RF provides the minimum value with values 98.48% and 85.26% respectively at the maximum number of training data. Additionally, the accuracy values of Neuro-Fuzzy, ELGA, DBC, CPE, and EDS are 88.12%, 90.9%, 92.3%, 94.25%, and 95% respectively. According to precision and recall results in Figs. 18 and 19, it is noted that HMD introduces the maximum precision and recall values reach to 91.1% and 88.91% respectively at the number of training data = 350. In fact, RF, Neuro-Fuzzy, ELGA, DBC, CPE, and EDS provide precision values reach to 62.5%, 64.5%, 70%, 75.25%, 83%, and 90% respectively at the number of training data = 350. On the other hand, these strategies provide recall values in the same order reach to 61%,
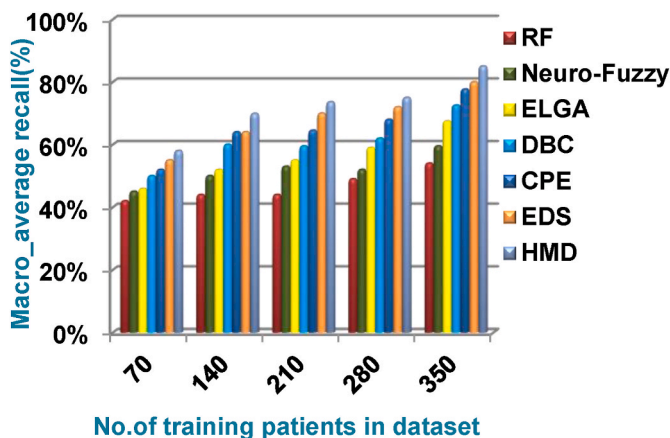

Fig. 23. Macro_average recall of monkeypox diagnostic strategies.

Fig. 24. F1-measure of monkeypox diagnostic strategies.
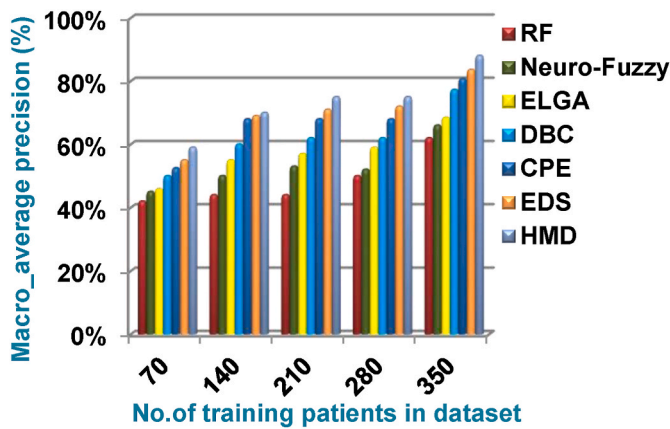
Fig. 25. Implementation time of monkeypox diagnostic strategies.
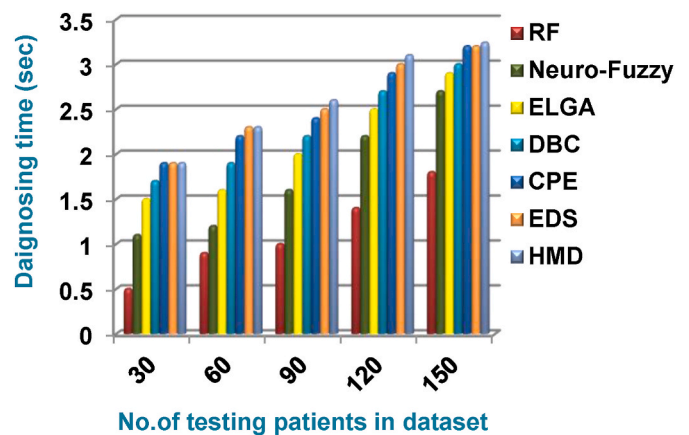

Fig. 26. Diagnosing time of diagnostic strategies.

65%, 68.01%, 73.02%, 80.05%, and 87% respectively. From these measurements, it is noted that RF provides the worst results while HMD provides the best results. The reason is that RF is implemented on the original dataset without selecting informative features before starting to be learned but HMD begins with selecting the best subset of features using IBCO before learning the diagnostic model. Additionally, EDS can provide the best results after HMD.

In Figs. (20-24), micro-average, macro-average, and F1-measure are measured to test the ability of diagnostic strategies to handle unbalanced data and provide the best performance. As presented in Fig. 20, HMD gives the maximum micro-average precision value but RF gives the

minimum value with values 92.56% and 59.99% respectively. The micro-average precision of Neuro-Fuzzy, ELGA, DBC, CPE, and EDS are 68.9%, 75.25%, 79.85%, 83.65%, and 90.32% respectively at the maximum number of training data. Micro-average recall values in Fig. 21 are 60.85%, 62.6%, 65.8%, 75%, 80.25%, 85.9%, and 89.01% for RF, Neuro-Fuzzy, ELGA, DBC, CPE, EDS, and HMD respectively at the number of training data = 350. Thus, RF provides the minimum micro-average recall value while HMD provides the maximum value. Fig. 22 shows that the maximum macro-average precision is provided by HMD while the minimum value is provided by RF with values reach to 88.01% and 62% respectively at the number of training data = 350. The macro-average precision of Neuro-Fuzzy, ELGA, DBC, CPE, and EDS reach to 66.01%, 68.5%, 77.25%, 80.65%, and 83.6% respectively. Hence, the best macro-average precision is provided by HMD but the worst value is provided by RF. The macro-average recall of HMD is the maximum value but the minimum value is given by RF at the number of training data = 350 as shown in Fig. 23. The macro-average recall of RF, Neuro-Fuzzy, ELGA, DBC, CPE, EDS, and HMD are 54%, 59.5%, 67.5%, 72.85%, 77.68%, 80% and 85.01% respectively.

In Fig. 24, F1-measure of RF, Neuro-Fuzzy, ELGA, DBC, CPE, EDS, and HMD are 64%, 68.85%, 71.85%, 76.9%, 80.65%, 82%, and 83.9% respectively at the maximum number of training data. Based on Figs. (17-24), the proposed HMD strategy outperforms other diagnostic strategies because it provides the maximum accuracy, precision, recall, micro-average, macro-average, and F1-measure values. In fact, it is noted that EDS outperforms other strategies after HMD strategy. As shown in Fig. 25, the implementation time of HMD takes a long execution time but RF takes a short execution time with values reach to 5.4 s and 3 s respectively at the number of training data = 350. As presented in Fig. 26, the diagnosing time of HMD is larger than other strategies. The diagnosing time of RF, Neuro-Fuzzy, ELGA, DBC, CPE, EDS, and HMD are 1.8, 2.7, 2.9, 3, 3.2, 3.2, and 3.24 s respectively at the maximum number of testing data = 150. Accordingly, EDS can provide the best results and takes a long execution time after HMD strategy. Hence, HMD can accurately diagnose monkeypox patients which consumes a long execution time but this time was neglected compared to accurate diagnosis. At the last, it is concluded that the performance of HMD method is superior to RF, Neuro-Fuzzy, ELGA, DBC, CPE, and EDS.

7. Conclusions and future directions

The main core of this paper is to provide a robust strategy using AI techniques to accurately detect monkeypox patients to limit the spread of the virus. Hence, Human Monkeypox Detection (HMD) strategy has been introduced for early detection of infected persons quickly and accurately. This strategy includes two main phases called Selection Phase (SP) and Detection Phase (DP). In SP, monkeypox dataset has been filtered from useless features using Improved Binary Chimp Optimization (IBCO) algorithm that combines two layers called Filter Selection Layer (FSL) as a quick layer and Wrapper Selection Layer (WSL) as an accurate layer. After eliminating irrelevant features as possible in FSL using many filter methods, sets of features provided by these filter methods have been passed to WSL to accurately choose the useful features. The filtered dataset without any irrelevant features has been passed to DP to correctly learn Ensemble Diagnosis (ED) model to accurately diagnose monkeypox patients. ED model is a hybrid model that consists of Weighted Naïve Bayes (WNB), Weighted K-Nearest Neighbors (WKNN), and deep learning which are combined using a new weighted voting method to introduce the best diagnostic results.

Experimental results illustrated that the suggested IBCO as a new feature selection outperformed other selection techniques using NB algorithm as a standard diagnostic model. Additionally, the HMD strategy gives the best measurements compared to other strategies in terms of accuracy, precision, recall, micro-average, macro-average, F1-measure, implementation time, and diagnosing time. The HMD strategy provided 98.48%, 91.1% and 88.91% for accuracy, precision, and recall values at

the number of training data = 350. Additionally, the micro-average precision, micro-average recall, macro-average precision, macro-average recall, F1-measure, and implementation time of HMD strategy are 92.56%, 89.01%, 88.01%, 85.01%, 83.9%, and 5.4 s respectively at the number of training data = 350. At the number of testing data = 150, diagnosing time of HMD is 3.24 s. Thus, it is concluded that the HMD is superior other strategies because it provided the maximum accuracy. On the other hand, HMD provided the maximum execution time but this time was neglected compared to accurate diagnosis. According to future directions, the proposed HMD strategy should be tested on a large dataset and also should be tested on different datasets. Outlier rejection layer should be added to the proposed HMD strategy to reject noise data before learning ED model for improving the performance of this strategy.

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".

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