A Hybrid COVID-19 Detection Model Using an Improved Marine Predators Algorithm and a Ranking-Based Diversity Reduction Strategy

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ABSTRACT Many countries are challenged by the medical resources required for COVID-19 detection which necessitates the development of a low-cost, rapid tool to detect and diagnose the virus effectively for a large numbers of tests. Although a chest X-Ray scan is a useful candidate tool the images generated by the scans must be analyzed accurately and quickly if large numbers of tests are to be processed. COVID-19 causes bilateral pulmonary parenchymal ground-glass and consolidative pulmonary opacities, sometimes with a rounded morphology and a peripheral lung distribution. In this work, we aim to extract rapidly from chest X-Ray images the similar small regions that may contain the identifying features of COVID-19. This paper therefore proposes a hybrid COVID-19 detection model based on an improved marine predators algorithm (IMPA) for X-Ray image segmentation. The ranking-based diversity reduction (RDR) strategy is used to enhance the performance of the IMPA to reach better solutions in fewer iterations. RDR works on finding the particles that couldn’t find better solutions within a consecutive number of iterations, and then moving those particles towards the best solutions so far. The performance of IMPA has been validated on nine chest X-Ray images with threshold levels between 10 and 100 and compared with five state-of-art algorithms: equilibrium optimizer (EO), whale optimization algorithm (WOA), sine cosine algorithm (SCA), Harris-hawks algorithm (HHA), and salp swarm algorithms (SSA). The experimental results demonstrate that the proposed hybrid model outperforms all other algorithms for a range of metrics. In addition, the performance of our proposed model was convergent on all numbers of thresholds level in the Structured Similarity Index Metric (SSIM) and Universal Quality Index (UQI) metrics.

INDEX TERMS COVID-19 detection, marine predators algorithm, ranking-based reduction diversity, Kapur’s entropy, image segmentation.

I. INTRODUCTION

Due to the limited diagnosis tools available, many countries are only able to apply the COVID-19 [1], [2] test for a limited number of citizens. Despite the great efforts to find an effective way for COVID-19 detection, the required medical resources in many countries represent a big challenge. Accordingly, there is an urgent need to identify a low-cost and rapid tool to detect and diagnose COVID-19 effectively.

Many attempts have been conducted to find a suitable and fast way to detect infected patients in an early stage. After making chest CT scans of 21 patients infected with COVID-19 in China, Guan et al. [2] found that CT scan analysis included bilateral pulmonary parenchymal ground-glass and consolidative pulmonary opacities, sometimes with a rounded morphology and a peripheral lung distribution. Consequently, COVID-19 diagnosis can be represented as an image segmentation problem to extract the main features of the disease. This segmentation problem can be solved by developing an algorithm that has the ability to extract the smaller similar regions that can indicate infection with the COVID-19 virus.
Segmentation of an image, separating image regions from each other, is an essential step in image processing [3] and computer vision [4] to focus on a specific region thereby increasing the accuracy of image analysis techniques. The image segmentation problem (ISP) is present in many fields such as: medical diagnosis [5], [6], object recognition [7], satellite image processing [8], remote sensing [9], historical documents [10], and historical newspapers [11], [12].

Several techniques have been proposed to provide an effective image segmentation tool, such as region-based segmentation [13], edge-based detection [14], feature selection-based clustering [15], and threshold-based segmentation [16]. Due to its simplicity, speed, and accuracy, threshold-based segmentation is widely used for image segmentation [3], [17], [18] using either a bi-level threshold or a multi-level threshold. In bi-level thresholding, the image is segmented into two regions: object and background. Although the bi-level threshold is very useful in subdividing the image into only two parts, many applications are interested in more than two regions. In that case, another threshold technique called multi-level threshold has been used to segment the image into more than two regions. Although increasing the number of regions extracted from the image, the time needed to segment the image increases exponentially with the number of regions of interest.

Threshold techniques are based on two approaches: parametric and non-parametric [19]. In a parametric approach, some parameters for each class in the image need to be computed using a probability density function. However, in a non-parametric approach, the technique searches for the optimal threshold values based on maximizing an appropriate function (such as Kapur’s entropy [20], fuzzy entropy [21], and Otsu function [22]) without needing to calculate parameters at the outset.

Since processing time increases exponentially with increasing numbers of thresholds, traditional techniques will take considerable time to search for the optimal threshold. Consequently, meta-heuristic algorithms have been used as excellent stochastic meta-heuristic techniques to overcome the high processing time and accuracy problems [23]–[25]. Recently, many meta-heuristic algorithms have been proposed for image segmentation, such as genetic algorithm (GA) [26], particle swarm optimization (PSO) [27]–[29], ant-colony optimization algorithm [30], whale optimization algorithm (WOA) [31], honey bee mating (HBOM) optimization [32], multi-verese optimizer [33], cuckoo search (CS) [34], symbiotic organisms search (SOS) [35], Harris hawks optimization algorithm (HHA) [36], and moth-flame optimization algorithm (MFA) [31], flower pollination algorithm (FPA) [37], crow search algorithm [38], grey wolf optimizer [39], bee colony algorithm (BCA) [40], locust search algorithm (LSA) [41] and firefly optimization algorithm (FFA) [42].

Singla and Patra [43] investigated the bounds and the potential thresholds that contain the optimal threshold values by using the cluster validity measure, and then used the GA algorithm to search for the optimal thresholds from the discovered bounds. GA has also been proposed [44] for image segmentation based on a simulated binary crossover to maximize Kapur’s entropy for the medical image. Among swarm algorithms, PSO [45] has been proposed for image segmentation, in addition to improving its performance by cooperative and comprehensive learning to face the dimensionality curse and to reduce the premature convergence of the swarm, respectively. A modified PSO [46] has also been developed to improve its performance for solving ISP using adaptive inertia and the adaptive population. Ghamisi et al. [47] introduced fractional-order Darwinian PSO to solve the problem of the n-level threshold based on the Otsu function to maximize the variance between classes.

In [31], WOA and MFA were proposed for solving the image segmentation problem by maximizing Otsu’s criterion, although only for small threshold levels up to 6. FFA [42] has also been applied to image segmentation but does not perform well for multi-level thresholding, so the improved FFA (IFFA) [48] has been proposed using the Cauchy mutation and neighborhood strategy to avoid being trapped in local optima and to enhance the exploration operation.

CS [34] has also been proposed for tackling the ISP by maximizing the Tsallis entropy. SOS [35] has been proposed for segmenting the color images, improved by opposite-based learning in an attempt to enhance its performance (ISOS). ABC [49] has been used for segmentation of satellite imagery based on maximizing various fitness functions—the technique has been modified by initializing the population using a chaotic search and using differential evolution as a novel search technique to improve the exploitation phase.

The Bacterial Foraging Algorithm (BFA) [50], relying on fuzzy entropy to switch the bacterium between exploitation and exploration operators, has been adapted for gray-scale image segmentation. Also, BFA [51] has been modified by moving the best bacteria to the subsequent iterations to accelerate the convergence to the optimal solution. Furthermore, BFA [52] has been integrated with PSO to support the global search capability and accelerate the convergence rate. In addition, the weak bacterium in BFA chooses a strong bacterium from the healthiest bacteria, then it moves near to the location of this strong selection. WOA [53] has been proposed for tackling liver image segmentation. WOA divides the liver image into a predetermined number of clusters based on the prospect liver position in the abdominal image defined by a statistical image. The problem of multi-level threshold segmentation [54] is handled as a multi-objective problem that maximized both Kapur’s entropy and Otsu’s function.

Although there are many existing methodologies for medical image segmentation, none of the works exposed at the literature was validated on an image with high threshold levels to observe its ability to segment an image with many similar regions. Subsequently, those algorithms may not be the best choice for searching for smaller homogenous regions in medical images that may contain the features of a disease such as COVID-19. This challenge motivates us to observe
the performance of some state-of-art algorithms proposed in the literature for tackling ISP. In addition, it leads us to propose a robust meta-heuristic algorithm, namely the improved marine predators algorithm (IMPA), that has a good ability to segment an image into many similar regions.

The contribution of this paper is two-fold. First, we propose a hybrid model for COVID-19 detection using an improved marine predators algorithm (IMPA) for overcoming the multi-threshold image segmentation problems of chest X-Ray images. Second, a new method, namely ranking-based diversity reduction (RDR), has been proposed to improve the MPA by moving the positions of the worst solutions to be near to the best solution. The proposed RDR is compared with other well-known algorithms using a set of chest X-Ray images. The experimental results show that MPA and IMPA are better able to solve the image segmentation problem compared with state-of-art algorithms in terms of fitness value and standard metrics. Additionally, it is competitive with EO in low numbers of threshold levels in terms of peak signal-to-noise-ratio (PSNR), and signal-to-noise-ratio (SNR), but has significantly better performance for high numbers of threshold levels. Along with EO, the performance of our proposed algorithm is convergent using the structured similarity index metric (SSIM) and the Universal Quality Index (UQI).

The remainder of the paper is organized as follows. In section 2, we explain the Kapur’s entropy formulation. Then, section 3 provides a description of the marine predators algorithm. Section 4 describes the steps of adapting MPA for application to image segmentation. Section 5 provides the results and discussions and section 6 concludes the paper.

II. MULTILEVEL THRESHOLDING

As discussed earlier, image threshold techniques are categorized as bi-level or multilevel thresholding. In this work, optimal threshold values are obtained using a popular multilevel method, namely Kapur’s entropy, which determines the optimal threshold values based on the entropy of the segmented regions [20]. Assuming that \([t_0, t_1, t_2, \ldots, t_n]\) represents the threshold values that segment the image into multiple regions, then Kapur’s entropy method can be formulated in Eq. 1, Eq. 2, Eq. 3, Eq. 4, and Eq. 5.

\[
T(t_0, t_1, t_2, \ldots, t_n) = T_0 + T_1 + T_2 + \ldots + T_n
\]

where:

\[
T_0 = -\sum_{i=0}^{t_0-1} \frac{X_i}{W_0} * \ln \frac{X_i}{W_0}, \quad X_i = \frac{N_i}{W_0}, \quad W_0 = \sum_{i=0}^{t_0-1} X_i
\]

\[
T_1 = -\sum_{i=t_0}^{t_1-1} \frac{X_i}{W_1} * \ln \frac{X_i}{W_1}, \quad X_i = \frac{N_i}{W_1}, \quad T_1 = \sum_{i=t_0}^{t_1-1} X_i
\]

\[
T_2 = -\sum_{i=t_1}^{t_2-1} \frac{X_i}{W_2} * \ln \frac{X_i}{W_2}, \quad X_i = \frac{N_i}{W_2}, \quad T_2 = \sum_{i=t_1}^{t_2-1} X_i
\]

\[
T_n = -\sum_{i=t_n-1}^{L-1} \frac{X_i}{W_n} * \ln \frac{X_i}{W_n}, \quad X_i = \frac{N_i}{W_n}, \quad T_n = \sum_{i=t_n-1}^{L-1} X_i
\]

\(T_0, T_1, T_2, \ldots, T_n\) are the entropy of the distinct regions, and \(N_i\) indicates the number of pixels with a value of \(i\), the grey level. \(W_0, W_1, W_2, \ldots\), and \(W_n\) are the probabilities of the regions relative to the number of pixels W found in the whole image.

To obtain the optimal threshold values, the function at Eq. 6 must be maximized.

\[
F(t_0, t_1, t_2, \ldots, t_n) = \max\{T(t_0, t_1, t_2, \ldots, t_n)\}
\]

Here, Eq. 6 is used as a fitness function to obtain the optimal threshold values using the MPA illustrated in the next section.

III. MARINE PREDATORS ALGORITHM (MPA)

MPA has been proposed to simulate the optimal foraging mechanism for marine predators in finding their prey: predators use Lévy strategy when there is a low concentration of prey and Brownian movements when there is abundant prey [55]. The velocity ratio \(v\) from the prey to the predators represents the tradeoff between the Lévy and Brownian strategies:

1. At low-velocity, \(v < 0.1\), the best strategy for the predators is to move in Lévy steps regardless of whether the prey is moving in Brownian or Lévy.
2. At unit velocity, \(v = 1\), the predators should move in Brownian if the prey is moving in Lévy steps.
3. Finally, at high-velocity > 10, the best strategy for the predators is to remain motionless, regardless of whether the prey is moving in Brownian or Lévy.

The mathematical model of the MPA is as follows:

In the first stage, a group of the prey will be initialized within the search space using the following equation:

\[
\overrightarrow{X} = \overrightarrow{X}_{\text{min}} + \text{rand} (0, 1) * (\overrightarrow{X}_{\text{max}} - \overrightarrow{X}_{\text{min}})
\]

where \(\text{rand} (0, 1)\) is a random number in the range of \([0, 1]\), and \(\overrightarrow{X}_{\text{min}}\) and \(\overrightarrow{X}_{\text{max}}\) are the vectors including the upper and lower bounds for the search space of each dimension in the optimization problem.

After initializing the prey, the fitness of each predator is calculated. Then, the one that has the best fitness value is determined to be the top predator. Based on the survival of the fittest, the top predator is the best one in foraging, so it is used to construct a matrix known as \(\text{Elite}\). This elite matrix can be formulated as follows:

\[
\text{Elite} = \begin{bmatrix} X_{10}^1 & X_{10}^2 & \cdots & X_{10}^{d_1} \\ X_{20}^1 & X_{20}^2 & \cdots & X_{20}^{d_2} \\ \vdots & \vdots & \ddots & \vdots \\ X_{n0}^1 & X_{n0}^2 & \cdots & X_{n0}^{d_n} \end{bmatrix}
\]

where \(X_i^j\) represents the top predator vector and is replicated \(n\) times to build up an \(n \times d\) Elite matrix, where \(n\) is the number
of the individuals in the population, and \( d \) is the number of dimensions.

Another matrix, namely \( \text{Prey} \), has the same dimensions as \( \text{Elite} \) and is used by the predators to update their positions.

\[
\text{Prey} = \begin{bmatrix}
X_{1,1} & X_{1,2} & \ldots & X_{1,d} \\
X_{2,1} & X_{2,2} & \ldots & X_{2,d} \\
\vdots & \vdots & \ddots & \vdots \\
X_{n,1} & X_{n,2} & \ldots & X_{n,d}
\end{bmatrix}
\]

In the main loops of the MPA, the optimization process is divided into three stages based on the velocity ratio, and is modeled as follows:

### A. HIGH VELOCITY RATIO

This is the exploration phase, and is formulated at Eq. 8 and Eq. 9:

\[
\begin{align*}
\text{while } \text{it} < \frac{1}{3} \times \text{max\_iter} & \\
\vec{S}_i & = \vec{R}_B \odot \left( \text{Elite}_i - \vec{R}_L \odot \text{Prey}_i \right) \\
\text{prey}_i & = \text{prey}_i + \vec{R} \odot \vec{S}_i
\end{align*}
\]

where \( \vec{R}_B \) is a vector of random numbers created based on the normal distribution and represents the Brownian motion, \( \odot \) represent the entry-wise multiplication, \( P = 0.5 \), \( 0.5 \) constant is recommended from the original paper, is a constant number, \( R \) is a random numbers vector created uniformly, \( t \) is the current iteration, and \( t_{\text{max}} \) is the maximum number of iterations.

### B. UNIT VELOCITY RATIO

This phase occurs in the intermediate phase of optimization process, where exploration is gradually changed to exploitation. The mathematical model of this phase is represented in Eq. 10, Eq. 11, Eq. 12, and Eq. 13.

\[
\begin{align*}
\text{while } \frac{1}{3} \times \text{max\_iter} < \text{it} < \frac{2}{3} \times \text{max\_iter} & \\
- \text{For the first half of the population} & \\
\vec{S}_i & = \vec{R}_L \odot \left( \text{Elite}_i - \vec{R}_L \odot \text{Prey}_i \right) \\
\text{prey}_i & = \text{prey}_i + \vec{R} \odot \vec{S}_i
\end{align*}
\]

\[
\begin{align*}
- \text{For the second half of the population} & \\
\vec{S}_i & = \vec{R}_B \odot \left( \vec{R}_B \odot \text{Elite}_i - \text{Prey}_i \right) \\
\text{prey}_i & = \text{Elite}_i + P \times \vec{R} \odot \vec{S}_i
\end{align*}
\]

where \( \vec{R}_L \) is the vector created using the Lévy flight strategy.

In this phase, the first half of prey would move with Lévy steps, while the other half uses Brownian steps.

where \( CF \) is an adaptive parameter to control the step size and is generated using Eq. 14.

\[
CF = \left( 1 - \frac{\text{it}}{\text{max\_iter}} \right)^{\frac{2 \times \text{it}}{\text{max\_iter}}} \]

### C. LOW VELOCITY RATIO

This is the exploitation phase and is formulated using Eq. 15 and Eq. 16:

\[
\begin{align*}
\text{while } \text{it} > \frac{2}{3} \times \text{max\_iter} & \\
\vec{S}_i & = \vec{R}_L \odot \left( \vec{R}_L \odot \text{Elite}_i - \text{Prey}_i \right) \\
\text{prey}_i & = \text{Elite}_i + P \times \vec{R} \odot \vec{S}_i
\end{align*}
\]

Some studies confirmed that the surrounding environment such as the eddy formulation, and fish aggregating devices (FADs) affects the behavior of the prey. As a result, the predators spend 80\% of their time searching for their prey in the vicinity, while the remaining time, they search for the prey in another environment. This process is known as FADs and is calculated using Eq. 17.

\[
\text{prey}_i = \begin{cases}
\text{prey}_i + \text{CF} \left( X_{\text{min}} + \vec{R} \times (X_{\text{max}} - X_{\text{min}}) \right) \odot \vec{U} & \text{if } r < \text{FADs} \\
\text{prey}_i + [\text{FADs} \times (1 - r) + r] (\text{prey}_{r1} - \text{prey}_{r2}) & \text{if } r > \text{FADs}
\end{cases}
\]

where \( r \) is a random number in the range of [0, 1]. \( \vec{U} \) is the vector containing the arrays with 0 and 1 values. For each array in \( \vec{U} \), a random number between 0 and 1 is generated and if the generated number is greater than 0.2, then this array is set to 1; otherwise it is set to 0. FADs = 0.2 indicates the influence of the FADs on the searching process.

MPA accomplishes memory saving by saving the old position of the prey. And, after updating the current solutions, the fitness values of each current solution and each old solution are compared, and if the fitness of the old one is better than the current one, they are swapped. The steps of MPA are listed in Algorithm 1.

### IV. THE HYBRID PROPOSED MODEL

In this section, standard MPA and improved MPA (IMPA) have been developed for overcoming the multi-thresholding image segmentation problems. The steps of adaptation are shown in the next sections.

### A. INITIALIZATION

In this phase, the number of prey \( N \) and the number threshold are predefined. Then each threshold is initialized randomly within 0 and 255 (the gray levels of the 8-bit image) using Eq. 18.

\[
P_{i,j} = L_{\min} + r \times (L_{\max} - L_{\min})
\]

where \( L_{\min} \) and \( L_{\max} \) indicate the upper and lower bounds of the gray level values in the image histogram, and \( r \) is a random number generated randomly in the range of [0, 1].
### Algorithm 1 The Marine Predators Algorithm (MPA)

1. Initialize the population of prey $p_i$ ($i = 1, 2, 3, \ldots, n$)
2. Set parameter’s value
3. $P = 0.5$; Top_Predator_fit = MAX_VALUE
4. Top_Predator_Position = NULL
5. **while** (it $<$ $t_{\text{maxIter}}$)
   6. **for** each $i$ prey
      7. Calculate the fitness value of prey $f(P_i)$
      8. if ($f(P_i) < \text{Top_Predator_Best}$)
         9. Top_Predator_Best = $f(P_i)$
         10. Top_Predator_Position = $P_i$
      **End if**
   **End for**
7. **if** ($it < \frac{1}{2} * t_{\text{max}}$)
   8. Update the current $P_i$ using Eq. (9)
   **Else**
   9. if ($\frac{1}{2} * t_{\text{max}} < it < \frac{3}{2} * t_{\text{max}}$)
      10. Update the current $P_i$ using Eq. (11)
   **Else**
   11. Update the current $P_i$ using Eq. (13)
   **End if**
   **End if**
12. **end for**
13. Construct The Elitement
14. Accomplish the memory saving
15. Assign $CF$ using Eq. (14)
16. for each $i$ prey
17. if ($it < \frac{1}{2} * t_{\text{max}}$)
   18. Update the current $P_i$ using Eq. (9)
   **Else**
   19. Update the current $P_i$ using Eq. (16)
   **End if**
   **End for**
20. Calculate the fitness value of prey $f(P_i)$
21. if ($f(P_i) < \text{Top_Predator_Best}$)
   22. Top_Predator_Best = $f(P_i)$
   23. Top_Predator_Position = $P_i$
   **End if**
24. **end for**
25. Accomplish the memory saving
26. Accomplish the FADs for each predator $P_i$ using Eq. (17)
27. $it ++$
28. **end while**

### Algorithm 2 RDR

1. $P$ : the number of prey
2. $CR$ : a vector of size N and contain 0’s value in the start
3. $i = 0$
4. perIter = 3
5. **while** ($i < N$)
6. **if** ($\text{fit}(P_i) > \text{fitLocal}(P_i)$)
   7. $CR_i = +$
   **else**
   8. $CR_i = 0$
   **end if**
   9. $i ++$
   **end while**
   **for** each $i$ particle
10. **if** ($CR_i > \text{perIter}$)
   11. Update $P_i$ toward the best one using Eq.19
   **end if**
   **end for**

```
\[
\vec{P}_b = \vec{P}_b + r \ast (\vec{P}_b - \vec{P}_i)
\]
```

where $\vec{P}_i$ refers to a worst particle that fails in finding a better solution within a consecutive number of iteration, $\vec{P}_b$ refers to a vector of the best solution, and $r$ is a number generated randomly in the range of [0, 1]. This technique that reduces the distance between the optimal solution and the particles that couldn’t find a better solution within a consecutive number of iterations is called RDR. Algorithm 2 illustrates the steps of the RDR technique.

In Algorithm 2, a vector of size equal to the number of prey is created and initialized in 0’s value. Then the old fitness is compared with the current fitness, and if the old fitness is still better, the rank $CR_i$ of the $i$th particle is increased by 1. Otherwise, it is reset to 0 again. This will help to identify the number of particles that couldn’t reach better solutions within a consecutive number of iterations. After that, each particle couldn’t find a better solution within the consecutive number of iterations CN, predefined, will be updated towards the best solution using Eq.19.

### B. RANKING-BASED DIVERSITY REDUCTION TECHNIQUE (RDR)

Some particles may be far away from an optimal solution which will require a long time to find and the number of iterations may terminate before a better solution is reached. Therefore, we propose an algorithm to calculate the consecutive number of iterations in which each particle was not able to identify a better solution. After identifying the worst particles that fail to find a better solution within a consecutive number of iterations, in Algorithm 2 those particles will be updated towards the best solution found so far to reduce the distance from the optimal solution using the Eq.19.

### C. THE PROPOSED IMPA

The steps of adapting the IMPA using the RDR for overcoming multi-thresholding problems are illustrated in Fig 1. The initialization step is considered the first step for all meta-heuristic algorithms, so it is firstly used for initializing the prey randomly, as shown in Fig 1. Within the initialization step, the fitness of each prey would be calculated, and the one with the highest fitness value is defined as the Top_Predator_Best, and its position as the Top_Predator_Position. After that, the first stage of the primary optimization process will start to update the current positions using one of the updating equations illustrated in Section 2 at the expense of the current iteration and prey.
After finishing the first stage of the optimization process, the fitness value of each prey is calculated, and memory saving is accomplished. Last but not least, the second stage of the optimization process implements the FADs methodology. FADs helps MPA dispose of local optima, subsequently finding better solutions. Finally, after the selected number of iterations, the RDR strategy is called to reduce diversity through the population, as elaborated in Section 4.2. The first and second stages of the optimization process, in addition to the RDR strategy, will be repeated until the termination criterion is satisfied.

Note that \( i \) in Fig. 1 indicates the current particle number, and \( N \) refers to the maximum number of particles.

Memory saving in MPA replaces the old solution with the current one if the current is better; otherwise the old one is used in the population to be updated toward another direction for finding better solutions. But what happen if the old one is always better? This means that the predator would stay in its position, motionless, and the distance with the best solution would not change. As long as the particles are far away of the best solution, the probability of finding a better solution reduces. Subsequently, a significant number of
FIGURE 2. Illustration the original images and their histograms used in our experiment.
iterations would be neglected. To solve this problem, the RDR strategy is used to move the particle that failed to find a better solution within a consecutive number of iterations, gradually toward the best solution even if the updated position isn't better than the old one. This will help the particle in exploring whether other regions may contain a better solution. Because the best solution is unified for all the members, the diversity between the members of the population will reduce when the particles move toward it. Accordingly, many better solutions may be generated, due to the exploration of more regions by the particles that couldn't find better solution within a consecutive number of iterations.

V. RESULTS AND DISCUSSION
In this section, the conducted experiments are offered and discussed to show the superiority of our proposed algorithm for solving ISP. This section is organized as follows:

- Section A. Describes Test Images
Section B. discusses Stability Analysis of all the compared algorithms.

Section C. discusses the results of The Peak Signal to Noise Ratio (PSNR) metric.

Section D. discusses the results of the Signal to Noise Ratio (PSNR) metric.

Section E. demonstrates the outcomes of the Structures similarity index metric (SSIM).

Section F. elaborates the results of the universal quality index (UQI).

Section G. demonstrate the obtained Kapure’s entropy values

Section H. shows some segmented images using IMPA, and MPA

A. DESCRIPTION OF TEST IMAGES

In our experiment, eight COVID-19 Chest images taken from https://github.com/ieee8023/covid-chestxray-dataset are used to validate the performance of our proposed algorithm and other algorithms in extracting the similar regions.

These images are labelled X1, X2, X3, X4, X5, X6, X7, X8, and X9. The original images and the histogram of each are shown in Fig.2. We compared our proposed model and selected state-of-art algorithms: SCA [56], WOA [31], EO [57], HHA [36] and SSA [58] using the same parameters and running environment. The population size \( N \) was set to 20, and the maximum iterations \( t_{\text{max}} \) set to 150 for a fair comparison. The experiments are performed on a desktop computer equipped with Windows 7 ultimate platform and 1 GB memory space. The RDR strategy is implemented on each particle that exceeds 3 iterations (CN = 3) without a better solution.

B. STABILITY ANALYSIS

To measure the dispersion of the results obtained by each algorithm, the standard deviation (Std) is calculated using Eq. 20.

\[
\text{Std} = \sqrt{\frac{1}{n-1} \sum_{i=1}^{n} (f_i - \bar{f})^2}
\]  

\[(20)\]
where \( n \) is the number of runs, \( f_i \) indicates the fitness value of the \( i \)-th run, and \( \bar{f} \) is the mean of the fitness value obtained within all the runs. Note that the lower value of Std metric refers to better stability.
To check the stability of our proposed model, the average of Std values was calculated for each algorithm using 20 independent runs on all test images and all the threshold levels and introduced in Fig. 3, which shows that IMPA and MPA have lower Std values compared with the other algorithms investigated. As a result, both IMPA and MPA provide results with better consistency and stability.

C. PEAK SIGNAL TO NOISE RATIO (PSNR)

PSNR is an indicator used to evaluate the similarity of the predicted image with the original by calculating the ratio between the square of 255 and the mean square error between the original image and the predicted one. This metric can be calculated using Eq. 21 and Eq. 22.

$$\text{PSNR} = 10 \log_{10} \left( \frac{255^2}{\text{MSE}} \right)$$  \hspace{1cm} (21)

where $\text{MSE}$ is the mean squared error which is calculated as follows:

$$\text{MSE} = \frac{\sum_{i=1}^{M} \sum_{j=1}^{N} |A(i, j) - S(i, j)|}{M \times N} \hspace{1cm} (22)$$

where $A(i, j)$, $S(i, j)$ represent the gray level of the predicted and original images, respectively. $M$, and $N$ are the number of columns and rows of the image matrix. The greater value of the PSNR refers to a better quality of the predicted image. The average PSNR values obtained over 20 runs by each algorithm using Kapur’s entropy are listed in Table 1, which shows that both IMPA and MPA have the best performance in 40 cases out of 72, while IMPA alone has the best performance in 31 cases. With small threshold levels, proposed IMPA algorithm is competitive with the EO algorithm. In contrast, the proposed algorithm presents the best PSNR values with an increase in the number of thresholds level. Based on this analysis, the proposed algorithm can determine the relevant threshold values for each image, especially for
FIGURE 6. Average SSIM values obtained by each algorithm for selected threshold levels between 10 and 100.

The images with high threshold levels, and subsequently, the segmented image generated by IMPA is very close to the original. Fig. 4 shows the average of the PSNR values across 20 runs, from which it can be seen that the proposed IMPA algorithm has the best performance for high threshold levels, and its performance is competitive of EO and MPA for small threshold levels.

D. SIGNAL TO NOISE RATIO (SNR)

SNR [59] is the error summation method that is used to measure the quality of the predicted images by calculating the ratio of the error between the original and the segmented images, and is computed using the Eq. 23.

\[
\text{SNR} = 10 \log_{10} \left( \frac{I^2}{SE^2} \right) \tag{23}
\]

where \( I \) is the average of the intensities of the original image and is calculated using Eq. 24.

\[
I = \frac{\sum_{i=1}^{M} \sum_{j=1}^{N} X(i,j)}{M \times N} \tag{24}
\]

and SE is the squared error and is calculated using Eq. 25.

\[
SE = \sum_{i=1}^{M} \sum_{j=1}^{N} |X(i,j) - Y(i,j)| \tag{25}
\]

where \( X(i,j) \) and \( Y(i,j) \) represent the original and the segmented images, respectively. Note that the higher value of SNR refers to better performance.

The average of SNR values obtained over 20 runs by each algorithm using Kapur’s entropy are listed in Table 2, which shows that IMPA is competitive with EO for small threshold levels and is superior for high threshold levels, as shown in Fig. 5.

E. STRUCTURED SIMILARITY INDEX METRIC (SSIM)

The SSIM [60] metric is used to calculate the difference between the structure of the segmented and original image, which takes into consideration the structure similarity, brightness, and contrast distortion between the original and segmented images. The mathematical model of SSIM is
formulated as in Eq. 26.

\[
\text{SSIM}(O,S) = \frac{(2\mu_o\mu_s + a)(2\sigma_{os} + b)}{\mu_o^2 + \mu_s^2 + \sigma_{oo} + \sigma_{ss} + a + b}
\]

where \(\mu_o, \mu_s\) are the mean intensities of the original and segmented image; \(\sigma_o, \sigma_s\) are the standard deviation of the original and segmented image; \(\sigma_{os}\) is the co-variance between the predicted and original image; and \(a, b\) are constant.
values equal to 0.001 and 0.003 respectively. A higher value of SSIM indicates better results.

The average SSIM values obtained over 20 runs by each compared algorithm using Kapur’s entropy are listed in Table 3, from which it can be identified that both IMPA and MPA are competitive with EO for both small and high thresholds levels. Fig. 6 shows the average of the SSIM values over 20 runs.

**F. UNIVERSAL QUALITY INDEX (UQI)**

UQI [61] is an indicator used to measure the quality of the segmented image based on three factors: loss of correlation, brightness, and contrast distortion instead of the error summation between the original and segmented. The mathematical model of UQI is formulated as in Eq. 27.

\[
UQI(O, S) = \frac{4\sigma_{os}(\mu_o\mu_s)}{\mu_o^2 + \mu_s^2} \frac{(\sigma_o^2 + \sigma_s^2)}{\sigma_o^2 + \sigma_s^2} \tag{27}
\]

O, and S refer to the original and segmented images, \(\mu_o\), \(\mu_s\) are the mean intensities of the original and segmented image; \(\sigma_o\) and \(\sigma_s\) are the standard deviation of the original and segmented image; \(\sigma_{os}\) is the co-variance between the predicted and original image. A higher value of UQI indicates better results.

The average UQI values obtained over 20 runs by each algorithm using Kapur’s entropy are listed in Table 4, which shows that both IMPA outperforms all the other algorithms in 26 of 72 cases, while achieves the same values as EO in 15 cases. Meanwhile, MPA outperforms both EO and IMPA in 2 cases of 72. Further, EO outperforms our proposed IMPA in 19 cases of 72. The proposed IMPA therefore achieves high quality for the segmented images especially for the images with the upper threshold levels. Fig. 7 introduces the average of the UQI values obtained over 20 run at each threshold level.

**G. FITNESS VALUES USING KAPUR’S ENTROPY**

Table 5 shows the average of the fitness values across 20 runs obtained by each algorithm using Kapur’s entropy. It can be seen that both IMPA and MPA outperform the other algorithms in 55 cases of 72, while IMPA alone could outperform in 50 cases of the 72, presenting the best fitness
values with all threshold levels in most cases. Fig. 8 shows the average of the fitness values within 20 times obtained by each algorithm using Kapur’s entropy for selected threshold levels from 10 to 100. Fig. 9 presents the average across 20 runs of Kapur’s entropy for all threshold levels, from which it can be seen that the proposed IMPA algorithm outperforms all other algorithms investigated.

**H. CONVERGENCE RATE**
The convergence toward the best solution is illustrated in Fig. 10; at the outset of iterations, MPA has high exploration capabilities, so the convergence rate toward the best solution is low compared with the other algorithms, as shown in Fig. 10. After that, at the intermediate phase of the optimization process specifically between maximum iterations
FIGURE 10. Convergence rate towards the best value obtained by each algorithm using Kapur’s entropy.
and maximum iterations, MPA is between the exploration and exploitation operators, where it divides the population into two parts: the first part will move using the exploration operator and while the second will be moved using the exploitation operator. So in this case, MPA moves faster toward the best solution, and the convergence rate increases, this is illustrated in Fig.10 at the half of the iterations. In the final stage, all the prey would be moved with the exploitation step, so the convergence rate increases significantly towards the best solution.

However, MPA still suffers from low convergence due to spending many iterations in exploration, so RDR is used to help IMPA to achieve a high convergence rate toward the optimal solution as shown in Fig.10. Further, IMPA can outperform all the other algorithms in convergence rate for all threshold levels, especially for high threshold levels. In Figure 10, the convergence rate is shown for all algorithms for the threshold levels 20, 30, 40, 80, and 100. For threshold level 20, WOA has a higher convergence rate, but after 100 iterations, the performance of WOA drops, while IMPA increases significantly. For threshold level 20, MPA couldn’t outperform WOA. For threshold levels 30, 40, 80, and 100, IMPA, and MPA could outperform all the other algorithms in convergence rate during the second half of iterations.

I. SEGMENTED IMAGES OF THE PROPOSED MODEL

This section shows a graphical comparison between MPA and IMPA to illustrate better the performance improvement. Table 6 shows the segmented images obtained by the proposed IMPA algorithm and MPA. All the results of the performance metrics discussed before confirm that IMPA could produce higher quality segmented images than MPA. As a result, the segmented images produced by IMPA, and introduced in Table 6 is better than the images produced by MPA, and introduced also in Table 6. It is noticeable in Table 6 that IMPA outperforms MPA for all threshold levels.

VI. CONCLUSION AND FUTURE WORK

In this paper, we proposed a new hybrid model to detect the COVID-19 using an improved marine predators algorithm (IMPA) and a ranking-based diversity reduction (RDR) strategy to obtain the number of particles that can’t find a
TABLE 6. The segmented images obtained by the proposed IMPA algorithm.

| Threshold level | IMPA | MPA |
|-----------------|------|-----|
| 10              | ![Image X1](#) ![Image X6](#) | ![Image X1](#) ![Image X6](#) |
| 20              | ![Image X1](#) ![Image X6](#) | ![Image X1](#) ![Image X6](#) |
| 30              | ![Image X1](#) ![Image X6](#) | ![Image X1](#) ![Image X6](#) |
| 40              | ![Image X1](#) ![Image X7](#) | ![Image X1](#) ![Image X7](#) |
| 50              | ![Image X1](#) ![Image X7](#) | ![Image X1](#) ![Image X7](#) |
| 60              | ![Image X1](#) ![Image X7](#) | ![Image X1](#) ![Image X7](#) |
| 80              | ![Image X1](#) ![Image X7](#) | ![Image X1](#) ![Image X7](#) |
| 100             | ![Image X1](#) ![Image X7](#) | ![Image X1](#) ![Image X7](#) |
better solution within a consecutive number of iterations. Our model works on the x-ray images to extract similar small regions, in an attempt to obtain the regions that may contain COVID-19. Extracting these regions can be treated as an image segmentation problem. The performance of our proposed IMPA algorithm was compared with five state-of-art algorithms—whale optimization algorithm (WOA), sine-cosine algorithm (SCA), salp swarm algorithm (SSA), Harris hawks algorithm (HHA), and Equilibrium optimizer (EO)—using a set of chest X-Ray images with threshold levels between 10 and 100. The performance of our proposed IMPA algorithm is shown to outperform all other investigated algorithms in the fitness values, Std, and a range of threshold metrics. In addition, the performance of our proposed model and EO was shown to be convergent on all the thresholds level in SSIM and UQI metrics.

In the future work, the proposed algorithm can be applied to color image segmentation and different medical applications.

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