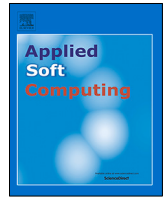




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HSMA_WOA: A hybrid novel Slime mould algorithm with whale optimization algorithm for tackling the image segmentation problem of chest X-ray images



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ABSTRACT

Recently, a novel virus called COVID-19 has pervasive worldwide, starting from China and moving to all the world to eliminate a lot of persons. Many attempts have been experimented to identify the infection with COVID-19. The X-ray images were one of the attempts to detect the influence of COVID-19 on the infected persons from involving those experiments. According to the X-ray analysis, bilateral pulmonary parenchymal ground-glass and consolidative pulmonary opacities can be caused by COVID-19 – sometimes with a rounded morphology and a peripheral lung distribution. But unfortunately, the specification or if the person infected with COVID-19 or not is so hard under the X-ray images. X-ray images could be classified using the machine learning techniques to specify if the person infected severely, mild, or not infected. To improve the classification accuracy of the machine learning, the region of interest within the image that contains the features of COVID-19 must be extracted. This problem is called the image segmentation problem (ISP). Many techniques have been proposed to overcome ISP. The most commonly used technique due to its simplicity, speed, and accuracy are threshold-based segmentation. This paper proposes a new hybrid approach based on the thresholding technique to overcome ISP for COVID-19 chest X-ray images by integrating a novel meta-heuristic algorithm known as a slime mold algorithm (SMA) with the whale optimization algorithm to maximize the Kapur's entropy. The performance of integrated SMA has been evaluated on 12 chest X-ray images with threshold levels up to 30 and compared with five algorithms: Lshade algorithm, whale optimization algorithm (WOA), FireFly algorithm (FFA), Harris-hawks algorithm (HHA), salp swarm algorithms (SSA), and the standard SMA. The experimental results demonstrate that the proposed algorithm outperforms SMA under Kapur's entropy for all the metrics used and the standard SMA could perform better than the other algorithms in the comparison under all the metrics.

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1. Introduction

Starting in China and passing to all the worldwide, a novel virus named COVID-19 outbreaks continuously. This virus infects the victim with fever and respiratory symptoms such as cough and sore throat. However, those symptoms do not confirm the infection with COVID-19 [1], so many attempts have been performed to find a tool that confirms if the person infected with COVID-19. After making chest CT imaging for suspects infected with COVID-19, the bilateral pulmonary parenchymal ground-glass and consolidative pulmonary opacities can be used to determine the infection. A rounded morphology and a peripheral lung distribution could sometimes been spotted [2].

Fortunately, since the CT findings are extracted as a normal image, it could be segmented into similar small regions, some of which may contain the features of COVID-19. The process of segmenting an image is commonly known as an image segmentation problem (ISP) and many algorithms have been applied for overcoming ISP. However, those algorithms still suffer from some problems prevent from reaching better-segmented images. As a result, the need for a new robust algorithm to segment the images has significantly been increased those days, especially with appearing chest CT images.

Recently, a novel algorithm known as the slime mold algorithm (SMA) inspired the slime mold behaviors to obtain the optimal track for gathering food. SMA has already been proposed for tackling the continuous optimization problems and could achieve significant success in comparison with the other algorithms. Accordingly, in this paper, SMA is adopted to tackle the chest X-ray image segmentation problem for the first time,

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as a new addition to separate the similar regions or to extract the region of interest inside an X-ray image. In addition, as an attempt to improve the performance of SMA and proposing a multi-thresholding model has a high ability on tackling ISP, the whale optimization algorithm (WOA) will be integrated with it to borrow its exploration capability within the first half of the iterations and after finishing the predefined first iterations where WOA runs within, the SMA will start to exploit around the best region explored by WOA with disposing of local minima problem under its ability that will re-initialize the solutions within the search space under a certain probability. The proposed model is only observed on X-ray test images infected with COVID-19, so it is proposed for dealing with this type of image. And within our future work, its performance will be validated on a number of test images from The Berkeley Segmentation Dataset and Benchmark to see if its performance is stable on any image or not.

The contribution of this paper is summarized as follows: First, a new integrated approach (HSMA_WOA) is proposed based on the behavior of SMA and WOA for finding the optimal threshold values that overcome the multi-threshold image segmentation problems of chest X-ray images. Second, experiments of HSMA_WOA have been undertaken and outperforming all the compared algorithms in fitness values, PSNR, UQI, SSIM, CPU time, and standard deviation under Kapur's entropy.

The rest of this paper is structured as follows. In Section 2, some proposed works for ISP has been reviewed. Additionally, Kapur's entropy is explained in Section 3. Sections 4 and 5 give a description of the whale optimization algorithm, and the slime mold algorithm, respectively. Section 6 introduces the proposed work for overcoming the image segmentation problem. Section 7 illustrates the results obtained under both Kapur's and entropy functions. Finally, Section 8 concludes the paper.

2. Related work

Nowadays, ISP plays a crucial role in image processing [3] and computer vision [4] to focus on an interesting region rather than the whole image until managing to analyze the image with higher accuracy. 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 methodologies for tackling ISP, such as region-based [13], edge-based [14], feature selection-based clustering [15], and threshold-based [16], has been suggested to help in separating the similar regions into an image. From involving those methodologies, Threshold-based segmentation is deemed the best one for solving the ISP [3,17,18]. Due to its simplicity, speed, and accuracy compared with the others. Thresholding is classified into two types: a bi-level threshold and a multi-level threshold. If the image contains only two similar regions: object and background, then the bi-level threshold is the best candidate for separating those two regions; otherwise, the multi-level threshold is better. Although the multi-level threshold could help in segmenting the image with more than two regions, the time increases exponentially when the number of regions increases.

Some techniques proposed for solving the image segmentation problem are based on an approach that needs to identify some parameters for each class using a probability density function for segmenting the image, those approaches are classified as parametric [19]. Meanwhile, another approach classified as non-parametric [19] maximizes a function (such as Kapur's entropy [20], fuzzy entropy [21], and Otsu function) without needing to calculate parameters at the outset.

Due to the time complexity problem with the increased threshold levels, traditional techniques failed to be the best tool for

solving the ISP. Subsequently, the need for another different technique to overcome the problem of time complexity was significantly increased. Thus, the meta-heuristic algorithms (MHAs) have been more popular among researchers since significant superiorities with less time in several fields were offered by MHAs [22–27] as the most appropriate tool to solve the ISP and overcome the time complexity. Since the w processing time increases exponentially with increasing thresholds, traditional techniques will use the considerable time to search for the optimal threshold.

Recently, many meta-heuristic algorithms have been suggested for overcoming ISP, such as particle swarm optimization (PSO) [28–30], ant-colony optimization algorithm [31], bee colony algorithm (BCA) [32], whale optimization algorithm (WOA) [33], genetic algorithm (GA) [34], multi-verse optimizer [35], cuckoo search (CS) [36], symbiotic organisms search (SOS) [37], Harris hawks optimization algorithm (HHA) [38], and firefly optimization algorithm (FFA) [39], flower pollination algorithm (FPA) [40], crow search algorithm [41], gray wolf optimizer [42], honey bee mating (HBM) optimization [43], locust search algorithm (LSA) [44], moth-flame optimization algorithm (MFA) [33], and firefly optimization algorithm (FFA) [39]. Some of those algorithms are summarized in Table 1.

All the algorithms listed in the literature were proposed for overcoming the ISP of a normal image and medical image of type X-ray images, but no one of which is experimented on the X-ray images that are considered the most important thing to detect the infection with COVID-19. Currently, there are two ways to be blended for much better performance. First, the high ability of WOA can be used to explore a new region to find a better solution within the first half of iterations. Second, the high capacity of SMA can be used to balance between exploitation and exploration. Thus, authors are motivated to make a hybridization between them to propose a new model to combine those two capabilities for overcoming the ISP for COVID-19 X-ray images. Broadly speaking, the SMA is integrated with WOA to finding a better solution, where the WOA will be run within the first CI iteration to explore various regions within the search space. Afterward, the SMA will take the solutions obtained by WOA to exploit them or explore at the expense of the fitness of each solution as an attempt to use up this capability of SMA. Additionally, SMA increases its exploration capability to escape out of the local minima by re-initializing the current solution randomly within the search space of the problem based on a certain probability. This hybrid approach is abbreviated as HSMA_WOA. SMA and HSMA_WOA are compared with several state-of-the-art algorithms under X-ray test images infected with COVID-19. After comparison, we saw that HSMA_WOA could outperform all the algorithms used to compare most of the test images used in our experiment.

3. Kapur's entropy

In this section, the mathematical model of Kapur's entropy method is shown. Kapur's entropy searches for the optimal threshold values by maximizing the variance between the segmented regions [20]. The mathematical model of this method is described as follows:

supposing that $[r_0, r_1, r_2, \dots, r_T]$ refers to the threshold values that subdivide the image into a different similar area, then the Kapur's entropy can be calculated as follows:

$$R(r_0, r_1, r_2, \dots, r_T) = R_0 + R_1 + R_2 + \dots + R_T \quad (1)$$

where:

$$R_0 = - \sum_{i=0}^{r_0-1} \frac{X_i}{W_0} * \ln \frac{X_i}{W_0}, \quad X_i = \frac{N_i}{W}, \quad W_0 = \sum_{i=0}^{r_0-1} X_i \quad (2)$$

Table 1
Some algorithms proposed for solving ISP.

Reference	Procedure
1 Singla and Patra [45]	The cluster validity measure was used to investigate the boundaries of the threshold levels to find the bounds that may contain the optimal threshold values. Then, it applied GA on the obtained bounds to search for the optimal threshold values within.
2 Manikandan et al. [46]	The real coded GA with the simulated binary crossover has been suggested for tackling the ISP of the medical image by maximizing the Kapur's entropy. This algorithm approved their efficacy compared with the others when solving the ISP of the medical image
3 Maitra, Chatterjee [47]	PSO improved by cooperative and comprehensive learning has been developed for tackling the ISP. Both cooperative and comprehensive learning used with PSO to alleviate the dimensionality curse and prevent the early convergence
4 Liu, Y., et al. [48]	The PSO has been modified using adaptive inertia and the adaptive population for tackling the ISP. Adaptive inertia is used to promote the convergence speed of PSO, while the adaptive population is used to prevent stuck into local optima.
5 Ghamisi et al. [49]	Fractional-order Darwinian PSO has been proposed for overcoming the image segmentation problem based on the Otsu function. The Fractional-derivative was used with PSO to dominate the convergence rate.
6 El Aziz [33]	WOA and MFA were proposed for tackling the ISP by maximizing otsu method, although just for threshold levels reaching 6
7 Chen [50]	In this paper, The Improved FFA (IFFA) has been proposed for solving ISP. IFFA was improved using the Cauchy mutation to avoid local minima and neighborhood strategy to enhance the convergence
8 Agrawal [36]	In this paper, CS has been proposed to extract the optimal threshold values of an image by maximizing the Tsallis entropy.
9 Bhandari [51]	In this paper, the satellite image was segmented using ABC based on maximizing a variety of objective functions. ABC was improved using a chaotic search to initialize the population at the outset and the differential evolution to enhance the exploitation capability.
10 Sanyal [52]	The fuzzy entropy to change between the exploration and exploitation operators was used with The bacterial foraging algorithm (BFA) for getting to the optimal threshold values of an image.
11 Sathya [53]	In this paper, to accelerate the premature convergence of BFA when solving ISP, the best bacteria among all the chemotactic steps is moved to the subsequent generations.
12 Tang [53]	This paper integrated the PSO with BFA to provide the global search capability and promote the premature convergence toward the optimal threshold values
13 Abdel-Basset [54]	A novel equilibrium optimizer (EO) has been proposed for finding the optimal threshold values of an image by maximizing the Kapur's entropy.
14 Abdel-Basset [55]	A novel marine predators algorithm (IMPA) improved using the Ranking-based diversity reduction strategy has been suggested to segment the chest X-ray image
15 Chouksey [56]	In this paper, the antlion optimization (ALO) and the multiverse optimization (MVO) have been developed for tackling the ISP by maximizing the Kapur's entropy and Otsu method. After investigating the performance of ALO, and MVO, the author notified that MVO is better
16 Erik Cuevas [44]	In this paper, the locust search algorithm (LSA) was applied for solving the multi-level thresholding image segmentation under a new objective function in a gaussian mixture model.

$$R_1 = - \sum_{i=r_0}^{r_1-1} \frac{X_i}{W_1} * \ln \frac{X_i}{W_1}, X_i = \frac{N_i}{W}, W_1 = \sum_{i=r_0}^{r_1-1} X_i \quad (3)$$

$$R_2 = - \sum_{i=r_1}^{r_2-1} \frac{X_i}{W_2} * \ln \frac{X_i}{W_2}, X_i = \frac{N_i}{W}, W_2 = \sum_{i=r_1}^{r_2-1} X_i \quad (4)$$

$$R_T = - \sum_{i=r_T}^{L-1} \frac{X_i}{W_T} * \ln \frac{X_i}{W_T}, X_i = \frac{N_i}{W}, W_T = \sum_{i=r_T}^{L-1} X_i \quad (5)$$

$R_0, R_1, R_2, \dots, R_T$ refer to the entropies obtained by each threshold value, and N_i indicates the count of the pixels having a value I , the gray level. And $W_0, W_1, W_2, \dots, W_T$ refers to the percent of the pixels in each region to the pixels in the whole image. And T indicates the threshold levels.

In order to extract the optimal threshold values, the following equation is maximized:

$$F(r_0, r_1, r_2, \dots, r_T) = \max\{R(r_0, r_1, r_2, \dots, r_T)\} \quad (6)$$

The proposed algorithm will use Eq. (6) as an objective function to get the optimal threshold values.

4. Standard whale optimization algorithm (WOA)

In WOA [57], the behaviors of the humpback whales are simulated to proposed new optimization algorithms for tackling the

continuous optimization problems. These whales move surround the prey in a spiral shape and then move toward prey in a shrinking circle when attacking. This behavior is called bubble-net foraging. This hunting mechanism is mimicked within the WOA by a trade-off between a spiral model and a shrinking encircling prey with a probability of 50%, generating the new solution within the optimization process. The encircling mechanism is athletes described as follows:

$$\vec{S}(t + 1) = \vec{S}^*(t) - \vec{A} \cdot \vec{D} \quad (7)$$

$$\vec{A} = 2\vec{a} \cdot \vec{rand} - \vec{a} \quad (8)$$

$$\vec{a} = 2 - 2 \frac{t}{t_{max}} \quad (9)$$

$$\vec{D} = \left| \vec{C} \cdot \vec{S}^*(t) - \vec{S}(t) \right| \quad (10)$$

$$\vec{C} = 2 \cdot \vec{rand} \quad (11)$$

where \vec{S} is a vector that expresses the current whale, t is the current generation, \vec{S}^* refers to the values of the best whale in the population, \vec{r} is a numerical vector generated randomly between 0 and 1. t_{max} refers to the maximum generations, and a is a parameter linearly decreased from 2 to 0 and is the distance control factor. The distance between the position of the victim and the whale is used where the helix-shaped movements simulated by a spiral model are done. The spiral model is mathematically

modeled as:

$$\vec{S}(t+1) = \vec{S}^*(t) + \vec{D}' \cdot e^{lb} \cdot \cos(2\pi l) \quad (12)$$

$$\vec{D}' = \left| \vec{S}^*(t) - \vec{S}(t) \right| \quad (13)$$

where \vec{D}' is the difference between the best-so-far solution and i th solution, l is a number created randomly between $[-1, 1]$, the logarithmic spiral shape is described by b as a constant. The best-so-far solution may be a local minima problem, so focusing completely on it within the optimization process may waste the search process within any beneficial mentioned. Therefore, the whale search for another position may contain the prey within the search area by picking a random whale from the population to move the current whale toward finding a better solution. Specifically, if $A < 1$, then the current whale is directed based on a whale picked randomly from the population. The mathematical model of this exploration phase is:

$$\vec{S}(t+1) = \vec{S}^*(t) - \vec{A} \cdot \vec{D} \quad (14)$$

$$\vec{D} = \left| \vec{C} \cdot \vec{S}_{rand}(t) - \vec{S}(t) \right| \quad (15)$$

where \vec{S}_{rand} is a position vector picked randomly from the population. Finally, the steps of the standard WOA are listed in Algorithm 1.

Algorithm 1 The standard WOA

1. Initialization $S_i (i = 1, 2, 3, \dots, N)$
 2. Evaluate each S_i using the fitness function
 3. Find the best s^*
 4. $t = 1$ // current iteration
 5. **while** ($t < t_{max}$)
 6. **for** each S_i
 7. Update a, A, p, C , and l
 8. **if** ($p < 0.5$)
 9. **if** ($|A| < 1$)
 10. Update $\vec{S}_i(t+1)$ based on Eq. (7)
 11. **else**
 12. Update $\vec{S}_i(t+1)$ based on Eq. (14)
 13. **end if**
 14. **else**
 15. Update $\vec{S}_i(t+1)$ based on Eq. (12)
 16. **end if**
 17. **end for**
 18. Check the fitness value of each updated S_i
 19. Update the best S^* with S_i if better.
 20. $t++$
 21. **end while**
-

5. Slime mold algorithm (SMA)

Chen [56] has recently been proposed a new optimization algorithm inspired by the behaviors of the slime mold in obtaining the optimal path for connecting food. This algorithm was known as the slime mold algorithm (SMA). The mathematical model of the SMA based on Chen proposition [56] is described in the following.

In the first stage, when SMA searches for the food, it uses its odor in the air as a means of reaching the food. Based on the behavior of the slime mold, it is formulated as follows to simulate

the contraction mode [58] :

$$\vec{S}(t+1) = \begin{cases} \vec{S}_b(t) + \vec{vb} * (\vec{W} * \vec{S}_A(t) - \vec{S}_B(t)), & r < p \\ \vec{vc} * \vec{S}(t), & r \geq p \end{cases} \quad (16)$$

\vec{vb} is randomly generated within $[a, -a]$ as:

$$\vec{vb} = [-a, a] \quad (17)$$

$$a = \operatorname{arctanh}\left(-\left(\frac{t}{t_{max}}\right) + 1\right) \quad (18)$$

And \vec{vc} linearly decreases from 1 to 0, t indicates the iteration current, t_{max} indicates the maximum of iteration, \vec{S}_b is a vector that contains the location with the highest odor concentration found so far. $\vec{S}(t+1)$ indicates the next position taken by the current slime mold (SM). $\vec{S}(t)$ is the current position of the SM, and \vec{S}_A and \vec{S}_B are two vectors containing the location of two randomly selected individuals from the population. The variable r is a random number between 0 and 1. \vec{W} describes the slime mold weight and calculated as follows:

$$\vec{W}(\operatorname{smellindex}(l)) = \begin{cases} 1 + r * \log\left(\frac{bF - S(i)}{bF - wF} + 1\right), & \text{condition} \\ 1 - r * \log\left(\frac{bF - S(i)}{bF - wF} + 1\right), & \text{other} \end{cases} \quad (19)$$

$$\operatorname{smellindex} = \operatorname{sort}(S) \quad (20)$$

where r is a random number created within the range of 0 and 1, bF is the best fitness value within the current iteration, while wF stands for the worst one, $\operatorname{smellindex}$ refers to the indices of the sorted fitness values, $\operatorname{condition}$ indicates $S(i)$ ranks of the first half of the population. In relative to parameter p in Eq. (21) is modeled as follows:

$$p = \tanh(|f(i) - DF|) \quad (21)$$

where $i \in 1, 2, 3, \dots, n$, $f(i)$ is the fitness of the current \vec{X} , DF is the best fitness obtained so far.

In the second phase, the wrapped phase simulates the contraction mode in the venous structure of slime mold, which tunes their positions according to the quality of the food, when the food concentration is high, the weight of this region is bigger. Otherwise, the region's weight is turned to explore other regions, as shown in Eq. (15). The SM needs to decide when to leave the current area to another one until finding a variety of food sources at the same time rather than the current better one. Generally, the mathematical model of updating the SM position could be re-modeled, as shown in Eq. (18) to simulate the methodology of the SM to find various food sources at the same time when foraging another area.

$$\vec{S}^*(t+1) = \begin{cases} \operatorname{rand} * (UB - LB) + LB, & \operatorname{rand} < z \\ \vec{S}_b(t) + \vec{vb} * (\vec{W} * \vec{S}_A(t) - \vec{S}_B(t)), & r < p \\ \vec{vc} * \vec{S}(t), & r \geq p \end{cases} \quad (22)$$

where rand and r are two numbers generated randomly between 0 and 1, and UB and LB are the upper and lower bounds of the problem's search space. z is a probability used to determine if the SMA will search for another food source or search around the best current one. In relative to \vec{W} , \vec{vb} , and \vec{vc} , they are used to mimic the venous width variation. Finally, the steps of SMA are presented by Algorithm 2.

Algorithm 2 The Slime mould algorithm (SMA)

```

1. Initializations step
2. While ( $t < t_{max}$ )
3. Evaluate each  $S_i$ 
4. Update the global best fitness  $GF$ , and global best position  $GP$ 
5. Compute  $W$  using Eq.19
6. for each  $S_i$ 
7. Update  $p$ ,  $vb$ , and  $vc$ 
8. Update  $S_i$  based on Eq.22
9. end for
10.  $t++$ 
11. end while
12. Output: return  $GF$ ,  $GP$ 

```

6. The proposed work

Within this part, our methodology for overcoming ISP for COVID-19 X-ray images will be illustrated in detail to show our plan for finding the threshold values that will help in extracting the region of interest within the infected images. Specifically, within this section, the following steps that contract the main structure of our proposition will be discussed: Initialization, SMA for ISP, hybrid SMA with WOA.

6.1. Initialization

As an inhabit of all the meta-heuristic algorithms, a set consists of N solutions has been proposed at the start. Each one has a number of dimensions distributed within 0 and 255 randomly using Eq. (23).

$$\vec{S}_i = \vec{L}_{min} + \vec{r} * (\vec{L}_{max} - \vec{L}_{min}) \quad (23)$$

Where \vec{L}_{min} , and \vec{L}_{max} indicate the boundaries of the gray levels, \vec{r} is a random numerical vector in the range of [0,1], and S_i indicates the i th solution.

6.2. SMA for ISP

Last but not least, SMA is adapted for overcoming the ISP of the COVID-19 X-ray images by maximizing Kapur's entropy. This adaptation will help in extracting similar regions within images that may contain similar features of COVID-19. The main advantages of SMA include a high ability to balance between exploration and exploitation. When the distance between the fitness of the current individual is high, it will try to move toward it in an attempt to exploit it. Meanwhile, if the distance is small, then it will explore another food source to find a better solution. Finally, the steps of SMA for overcoming ISP are listed in Algorithm 3.

Algorithm 3 adapting SMA for ISP

```

1. Initializations step,  $S_i, i = 0, 1, 2, 3, 4, \dots, N$ 
2. While ( $t < t_{max}$ )
3. Compute the fitness of each  $S_i$  using Eq.6.
4. Update the global best fitness  $GF$ , and global best position  $GP$ 
5. Compute  $W$  using Eq.19
6. for each  $S_i$  mould
7. Update  $p$ ,  $vb$ , and  $vc$ 
8. Update  $S_i$  using Eq.22
9. end for
10.  $t++$ 
11. end while
12. Output: return  $GF$ ,  $GP$ 

```

6.3. Hybrid SMA_WOA (HSMA_WOA)

In this version, the SMA will be used with the WOA for tackling the ISP, where the SMA is used to pay attention to the best so-far regions obtained by the WOA. At the same time, the WOA is applied at the start of the optimization process until a predefined iteration CI is reached. CI is the end iteration where the WOA will stop and SMA starts. Specifically, WOA is applied at the outset to use up its exploration capability within the first half of the iteration for exploring the search space. After reaching the CI, the WOA will be stopped. SMA then starts to pay attention to searching for a better solution using the high-ability of SMA that will exploit around the best-so-far if the distance between the fitness value of the current solution and the best-so-far solution is higher than a specific value generated randomly. Otherwise, it will work on exploring another region searching for a better food source. In addition to disposing of the local minima using the SMA's exploration capability that re-initialized the solutions that were within a predefined probability randomly within the search space. This hybridization is aimed to exploit the exploration capability of the WOA at the start. The next step is to enhance the significant balancing capability of SMA and increase their ability to get out of local minima. Therefore, this can achieve full exploration capability when a number generated random SMA is less dependent on the z factor.

The main advantages of this model are as follows:

1. By using the high-ability of the WOA at the start of the optimization process, it can explore most of the regions within the search space to find a better solution.
2. After exploring the search space using the exploration capability of WOA, the SMA is used to exploit around the best-so-far solution if the distance between the fitness of the current one and the best-so-far fitness is higher than a threshold value generated randomly between 0 and 1. Otherwise, the current SM will try to explore another region for another best-so-far solution. Additionally, SMA used another capability to explore another region for a better solution. This capability is based on re-initializing randomly the current mold within the search space of the problem according to a certain probability.
3. This high-ability on exploring at the first half of the optimization process and adjusting that determines if the exploration or exploitation capability will be used within the second half of the optimization process help in proposing a model with high-ability on exploration, exploitation and avoiding dropping into local minima.
4. Having only two parameters, r and CI need to be updated accordingly.

The main drawbacks of this model are as follows:

1. Difficulties in picking the relevant value for CI can lead to using up the ability of this hybridization.
2. It still suffers from the probability of falling into local minima problem if the best-so-far solution obtained by WOA is local minima. The value of z of the SMA used to escape local minima is small, and increasing this value will enhance the probability of randomly re-initializing the current solution within the search space and, subsequently, the convergence toward the best solution significantly reduce.

At the final, the final brief steps for the hybridization of both WOA and SMA are presented by Algorithm 4.

Algorithm 4 HSMA_WOA

```

1. Initializations step,  $S_i, i = 0, 1, 2, 3, 4, \dots, N$ 
2. While ( $t < t_{max}$ )
3.   If ( $t < CI$ )
4.     Apply the WOA shown in Algorithm 1
5.     Continue;
6.   end if
7.   Compute the fitness of each  $S_i$  using Eq.6
8.   Update the global best fitness  $GF$ , and global best position  $GP$ 
9.   Compute  $W$  using Eq.19
10.  for each  $S_i$  mould
11.    Update  $p, vb$ , and  $vc$ 
12.    Update  $S_i$  using Eq.22
13.  end for
14.   $t++$ 
15. end while
16. Output: return  $GF, GP$ 

```

7. Results and discussion

In this section, extensive experiments have been conducted to validate the proposed algorithms' performance and compare their performance with some of the state-of-the-art algorithms when tackling the ISP. Those experiments were performed on a set of chest X-ray COVID-19 images, namely X1, X2, X3, X4, X5, X6, X7, X8, X9, X10, X11, and X12 (see Fig. 1).

Additionally, a device equipped with 32-bit windows seven ultimate has been prepared for conducting our experiments. This device has the following capabilities:

- Core i3 processor with speed 2.20 GHz
- 1 GB of RAM

In order to check the efficacy of the proposed algorithm, it is compared with several well-known algorithms, such as Lshade [59], FFA [39], WOA [33], SSA [60], and HHA [38]. All those algorithms are further implemented using Java programming language. For the compared algorithms, the parameter values are the same as found in the original paper rather than the maximum iteration and population size that are set to 150, and 30 respectively, for a fair comparison. Additionally, all algorithms run 20 independently times to check the stability and consistency of the results obtained by each one.

Regarding our proposition, the CI parameter needs to be carefully picked for reaching the best performance for this approach, so several values for it, such as 0, 30, 50, 70, 90, 100, 120, and 150, are checked under test images X1, X2 and X3 to see the best value. And after running the algorithm under each CI value 20 independent runs and drawing the convergence curve of the best run for X1, X2 and X3 in Fig. 2(a), (b), and (c), respectively, we witness that the value 100 is the best for it on X1, and X3. While CI=90 is the best on X2 and its performance is converged with CI=100 on X3. So, the best two candidate values for CI under our experiments are 90 and 100.

Regarding the r parameter, five values, such as 0.01, 0.02, 0.03, 0.04, and 0.04, are selected to test the performance of the proposed algorithm under them. After running the algorithm under each r value 20 independent runs, the best run for each value is pictured in Fig. 2(d) and (e) for X1 and X2, respectively. According to those figures, $r=0.02$ is the best among the others, so it will be used for r within the next extensive experiments. Finally, Table 2 gives the parameter values of the proposed algorithm.

The remainder of this section is listed as follows:

1. Section 7.1: Analyzes the Stability and CPU time.
2. Section 7.2: Discusses the quality of images using Fitness values.

Table 2

Parameter setting for the proposed.

Parameter	Value
Number of runs	20
Population size	30
The maximum number of iteration	150
Z	0.02
CI	100

3. Section 7.3: Discusses the quality of images using peak signal to noise ratio.
4. Section 7.4: Discusses the quality of images using a structured similarity index metric.
5. Section 7.5: exposes the outcomes of the universal quality image metric.
6. Section 7.6: Convergence rate among SMA, HSMA_WOA, and WOA.

7.1. Stability and CPU time analysis

In this section, the time taken by each algorithm until finding the threshold levels is observed to see any algorithm could achieve the minimum of time. In addition, some algorithms produce spaced-out results in the different runs, so the stability of the obtained has to be calculated to see which algorithm could achieve converged results in all. This is known using the standard deviation (Std) calculated based on the following formula:

$$Std = \sqrt{\frac{1}{n-1} \sum_{i=1}^n (f_i - \bar{f})^2} \quad (24)$$

Where n indicates the number of times, each algorithm tried. f_i is the fitness value of the i th run, and \bar{f} is the average of all the fitness values gotten. SD must be minimized to get to a better result.

Under Kapur's function, respectively, Figs. 3 and 4 show the average of SD and CPU time values obtained by each algorithm within 20 independent runs. As a result of inspecting those figures, HSMA_WOA could reach less SD and CPU time values, while Lshade, and HHA achieve the worst value for both Std and CPU time.

7.2. Fitness values under Kapur

Regarding the fitness values of Kapur's method, Table 3 shows the fitness values obtained by the compared algorithm and the proposed under this function. After calculating the average of the fitness values within 20 runs on each threshold level for each image, those values are recorded in Table 3 and displayed graphically in Fig. 5. Based on this table, the proposed could outperform the others in most cases. This is confirmed based on Fig. 5 that shows the superiority of the proposed algorithm with a value of 29.29 compared with the others with a difference of at least 0.0418.

7.3. Peak signal to noise ratio (PSNR)

In this section, another metric called PSNR has been used to measure the segmented image's quality compared with the original image. PSNR determines the ratio between the square of the maximum gray level, 255^2 , and the mean square error (MSE) between the original and separated one and it is calculated using as follows:

$$PSNR = 10 \log_{10} \left(\frac{255^2}{MSE} \right) \quad (25)$$

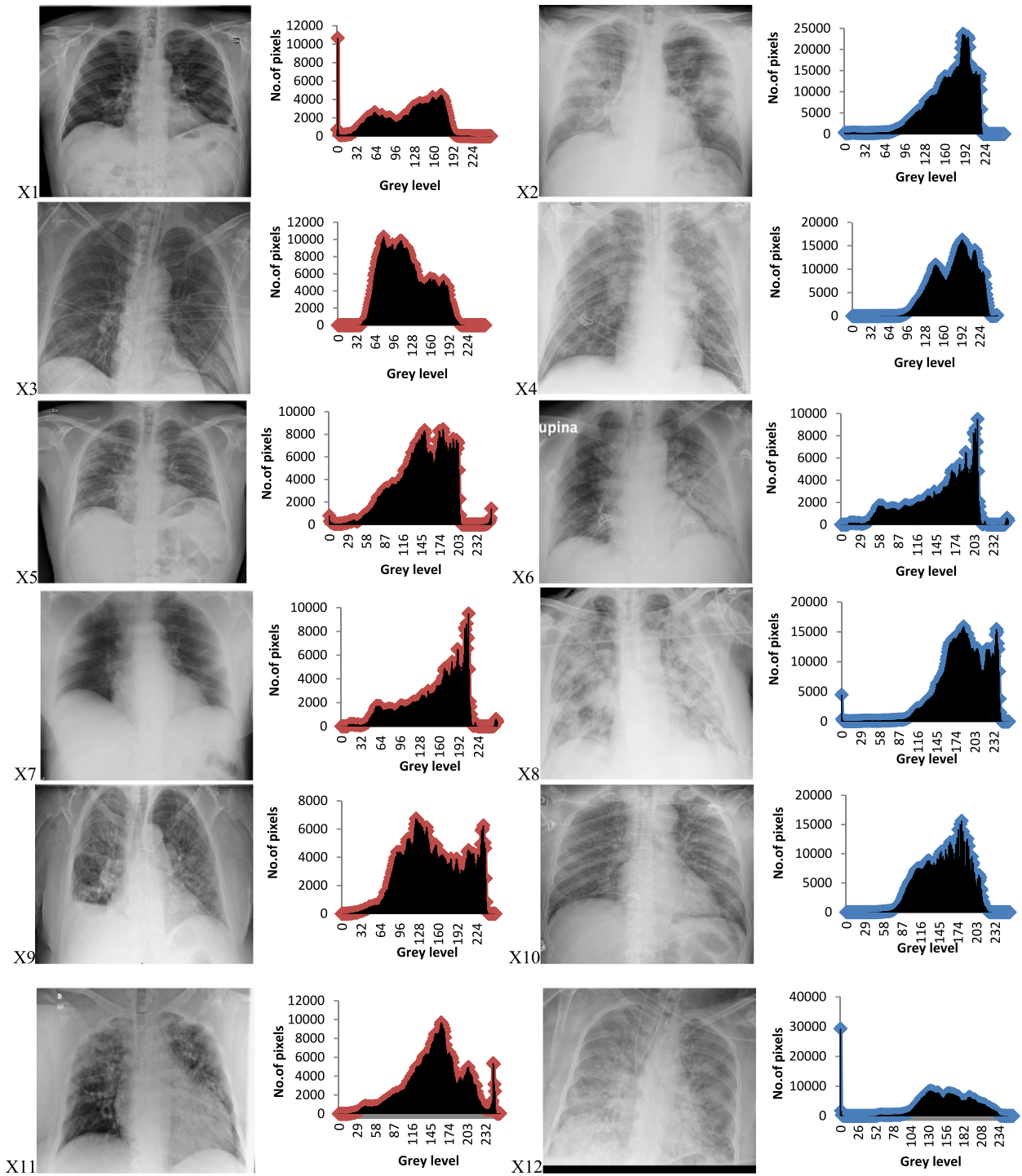


Fig. 1. The original COVID-19 images and their histograms.

And MSE is calculated as shown in the following equation:

$$MSE = \frac{\sum_{i=1}^M \sum_{j=1}^N |A(i, j) - S(i, j)|}{M * N} \quad (26)$$

Where $A(i, j)$ is the gray level of the segmented image and $S(i, j)$ is the gray level of the row i th and column j th in the original image matrix. M , and N are the number of columns and rows within the image. PSNR must be maximized to get to better quality.

Based on the segmented images under Kapure’s function, the average PSNR value within 20 runs is calculated and introduced

in Table 4. By observing this table, it is obvious that HSMA_WOA could be superior in 59 cases and equal in 14 out of 144, while SMA could be the best for 26 cases and equal in 14 out of 144. Generally, the proposed algorithms could be superior and equal in 104 out of 144. As a result, both SMA and HSMA_WOA could reach better-segmented images in all the superior cases compared with the other algorithms. In order to illustrate the results in Table 4 graphically, Fig. 6 is given to show the average of the PSNR values obtained by each algorithm. Based on this figure, the proposed algorithms: SMA, HSMA_WOA is considered superior compared with the others and HSMA_WOA is superior in comparison with SMA.

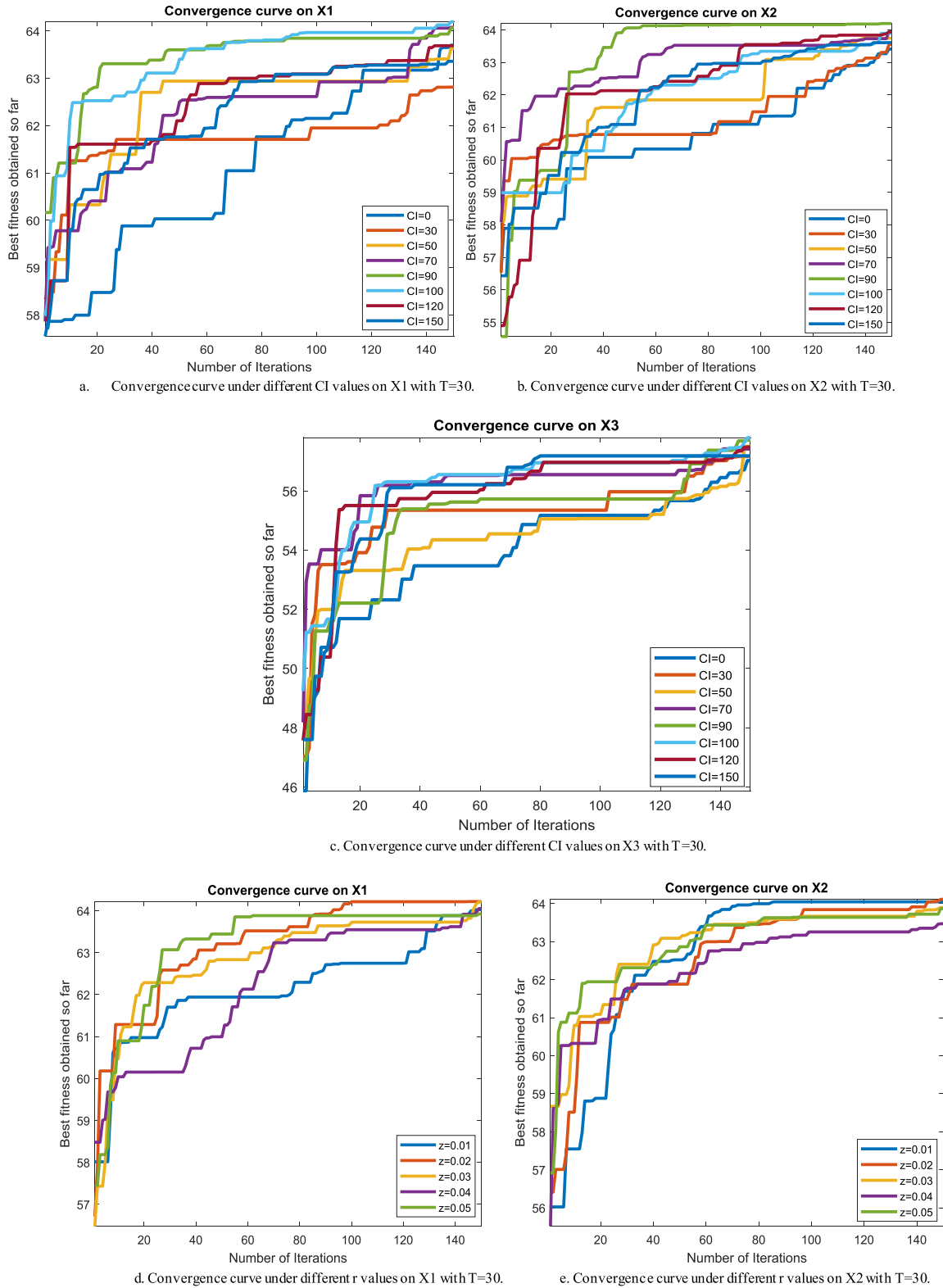


Fig. 2. Adjustment of CI and z parameters.

7.4. Structured similarity index metric (SSIM)

Unfortunately, PSNR calculates only the ratio of the error between the segmented and the source image without taking into consideration the structure of the image. Therefore, SSIM [61] is proposed to measure the similarity, contrast distortion and brightness between the original and the segmented one using the

following formula:

$$SSIM(O, S) = \frac{(2\mu_o\mu_s + a)(2\sigma_{os} + b)}{(\mu_o^2 + \mu_s^2 + a)(\sigma_o^2 + \sigma_s^2 + b)} \tag{27}$$

Where μ_o is the average intensities of the original image, while μ_s indicates the average intensities of the segmented image. σ_o ,

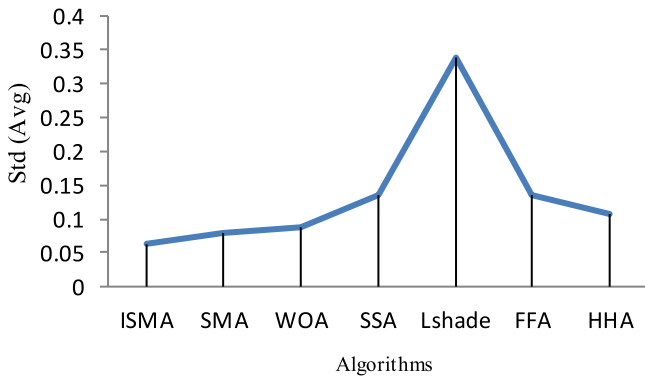


Fig. 3. The Std values obtained under Kapure's function.

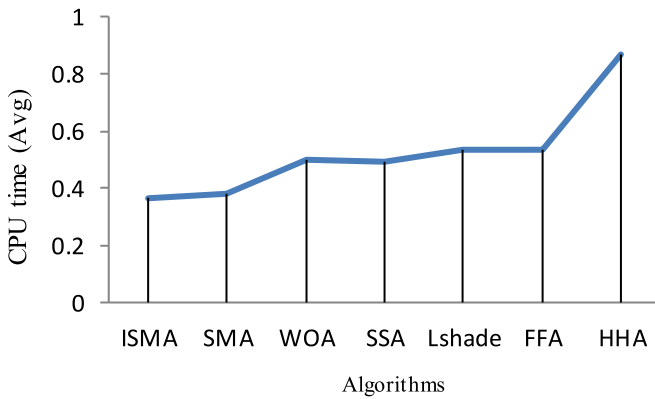


Fig. 4. Comparison of the CPU time values obtained under Kapur.

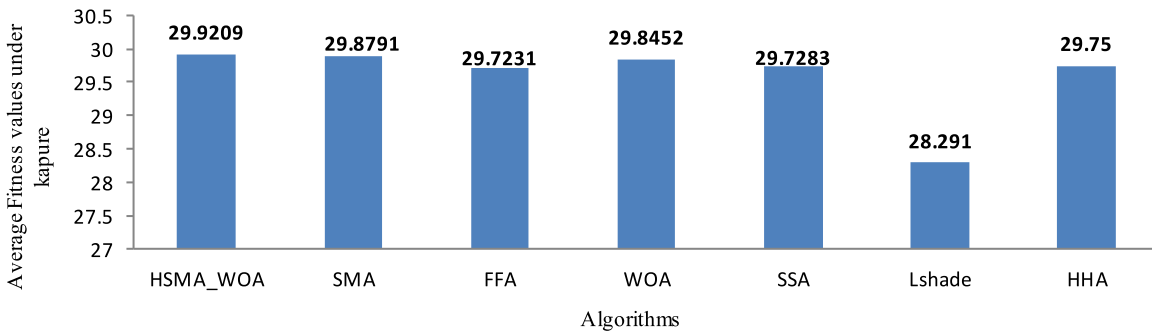


Fig. 5. Average fitness values obtained under Kapure's method.

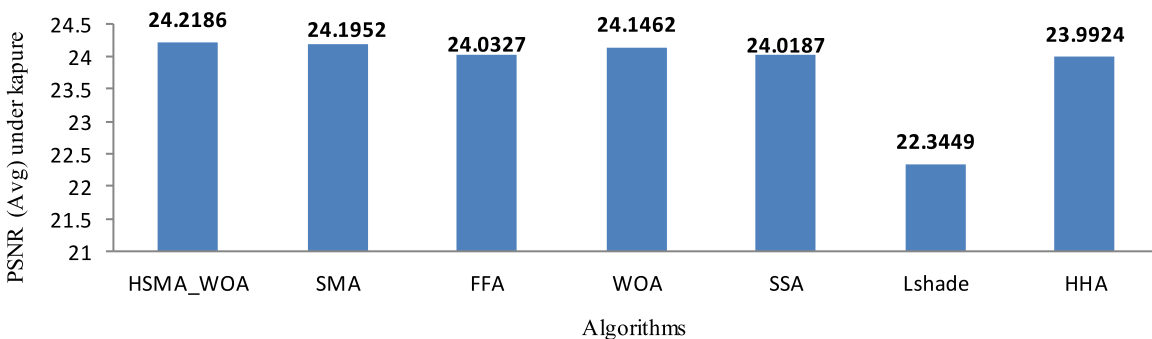


Fig. 6. Average PSNR values under Kapure's entropy.

σ_s are the SD of the original and segmented images, respectively. σ_{os} are the covariance between the two images. And a, b is equal to 0.001 and 0.003, respectively. SSIM must also be maximized to get better results.

In order to inspect the results under using Kapur's entropy as a fitness function, the average SSIM values obtained within 20 runs under Kapur's are calculated and given in Table 5. This table shows that HSMA_WOA could get to the best in 57 cases and equal in 24 while its performance on the other cases is converged with the other algorithms. Meanwhile, SMA could outperform in 24 and equal in 22. Fig. 7 shows the superiority of HSMA_WOA in comparison with SMA that is superior to the others.

7.5. Universal quality index (UQI)

UQI [62] is an indicator similar to SSIM in measuring the quality of the segmented image based on the similarity structure between the two images rather than the error rate and mathematically formulated as in Eq. (24).

$$UQI(O, S) = \frac{(4\sigma_{os}\mu_o\mu_s)}{(\mu_o^2 + \mu_s^2)(\sigma_o^2 + \sigma_s^2)} \quad (28)$$

where O refers to the original image, S is the segmented image, μ_o are the mean intensities of the original image, μ_s are the mean intensities of the and segmented image. σ_o and σ_s are the standard deviations for both the source and predicted image; σ_{os} is the covariance between the separated and source image. A higher value of UQI indicates better results.

After executing each algorithm, 20 runs and calculated the average UQI within them obtained by each one under Kapur's entropy, it is introduced in Table 5. By observing outcomes in this table, we notify that HSMA_WOA could overcome the others in 58 cases and equal in 20 others. In the same context, SMA could achieve the best in 18 and equal in 19. Specifically, the proposed algorithms could be superior and equal in 101 out of 144 test cases. Based on that, the proposed algorithms are competitive

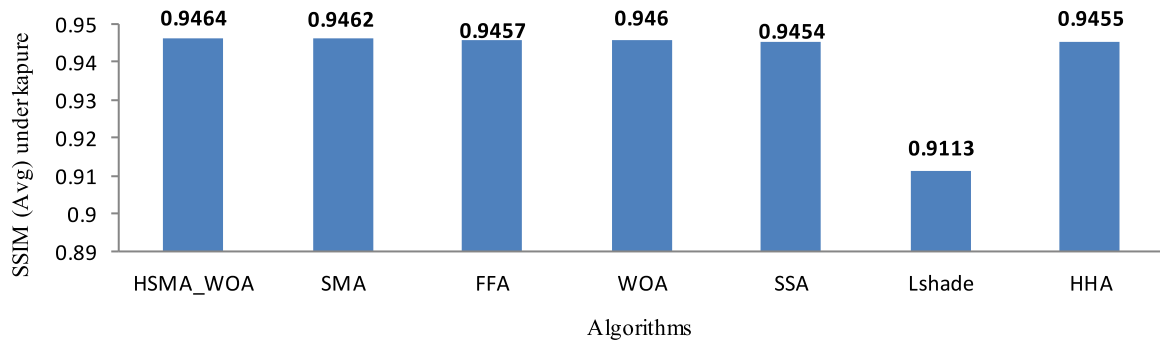


Fig. 7. Average SSIM values obtained under Kapur's entropy.

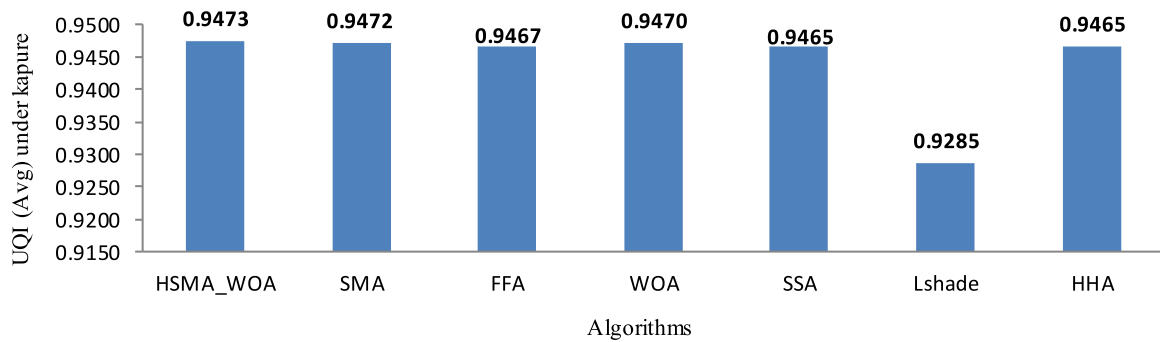


Fig. 8. Average UQI values obtained under Kapur's entropy.

with others for generating a better-segmented image. In order to illustrate the data in Table 6, Fig. 8 is taken to show the average UQI obtained by the algorithms within 20 runs and all the test images and threshold levels. This figure shows the superiority of the comparison of the proposed algorithms with the others under Kapur's method.

Fig. 9 shows the segmented images obtained by the proposed algorithm on X1, X2, X3, and X3 under both Kapur's for the threshold levels 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, and 30.

7.6. Comparison of convergence curve among SMA, HSMA_WOA, and WOA

In this part, the convergence rate by SMA, HSMA_WOA, and WOA will be observed to illustrate the effectiveness of our approach. Generally speaking, X1, X2, X3, X4, X5, and X6 test images with 30 threshold levels are used to check the convergence rate of each algorithm. After running each algorithm, the output in each iteration on each test image from X1 to X6 is plotted in Figs. 10–15, respectively. Inspecting these figures show that within the first CI=100 iteration, the convergence is accelerated as possible, but at the end of CI, the outcomes have no change and the possibility of reaching a better solution is so hard because the algorithm may be gotten stuck into local minima. As a result, it is time to integrate SMA with WOA to refresh its performance to get out of local optima, find better solutions and use the significant exploitation capability of SMA.

8. Conclusion and future work

According to the ongoing outbreaks of COVID-19 worldwide since December 2019, the entire world has moved to rely on technology to find tools and techniques to help identify the infected persons out of the normal ones. After many attempts

and confirmed by the medical scientists, chest CT images could significantly identify whether the suspected patients have been infected. COVID-19 infection could be identified by the bilateral pulmonary parenchymal ground-glass and consolidative pulmonary opacities. Sometimes a rounded morphology and a peripheral lung distribution could be spotted. However, CT scan is so expensive compared to X-ray, and unfortunately, the specification of the infection under X-ray is so hard. The reason was that the X-ray images were considered normal images, so it could be processed using a machine learning technique to specify if this person infected or not. But when machine learning focused on the whole image, their accuracy reduced significantly. Therefore, it was necessary to find a tool to extract similar regions within the image until managing to improve the accuracy of the machine learning technique when classifying the CT images.

The process of separating or extracting the similar regions into an image was called image segmentation problem. According to that, in this paper, our techniques were based on extracting the similar small regions into chest images as an attempt to extract the regions that may contain COVID-19, and this process was known as image segmentation problem (ISP). Several techniques were proposed for tackling ISP. A technique called threshold-based segmentation was distinguished from involving those techniques with its simplicity, speed, and accuracy when segmenting an image. Hence, a new hybrid multi-thresholding approach based on the SMA behavior with WOA for overcoming ISP was proposed in this paper. Its effectiveness was observed with five state-of-art algorithms such as WOA, SSA, Lshade, HHA, and FFA. The comparison was performed by applying the algorithms on a set of chest X-ray images with threshold levels between 2 and 30. Based on the results obtained by each algorithm, the performance of the proposed algorithm was verified to outperform all other algorithms in the fitness values, SSIM, PSNR, UQI, CPU time and (Std).

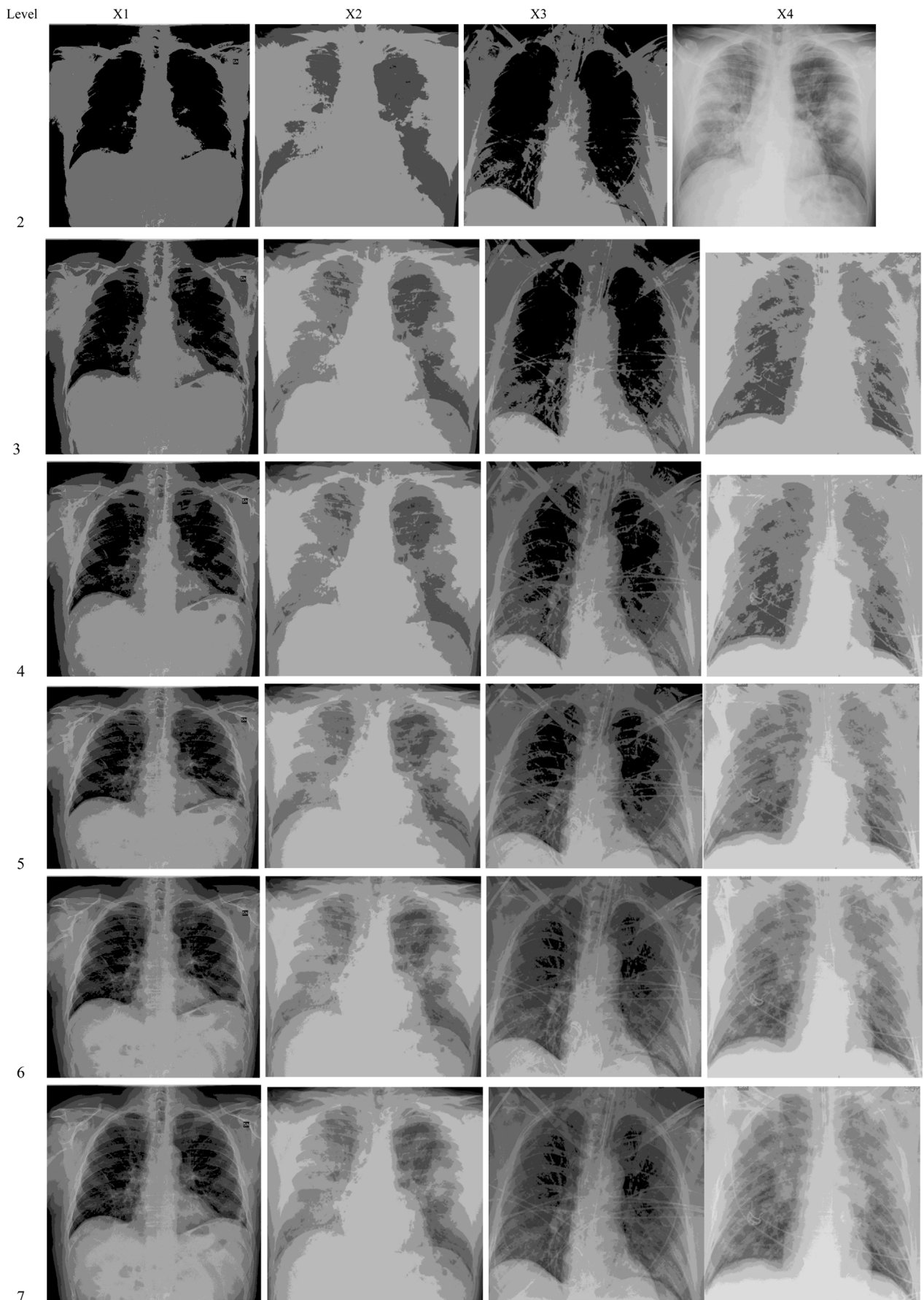


Fig. 9. Segmented images by proposed algorithm under Kapure's entropy.

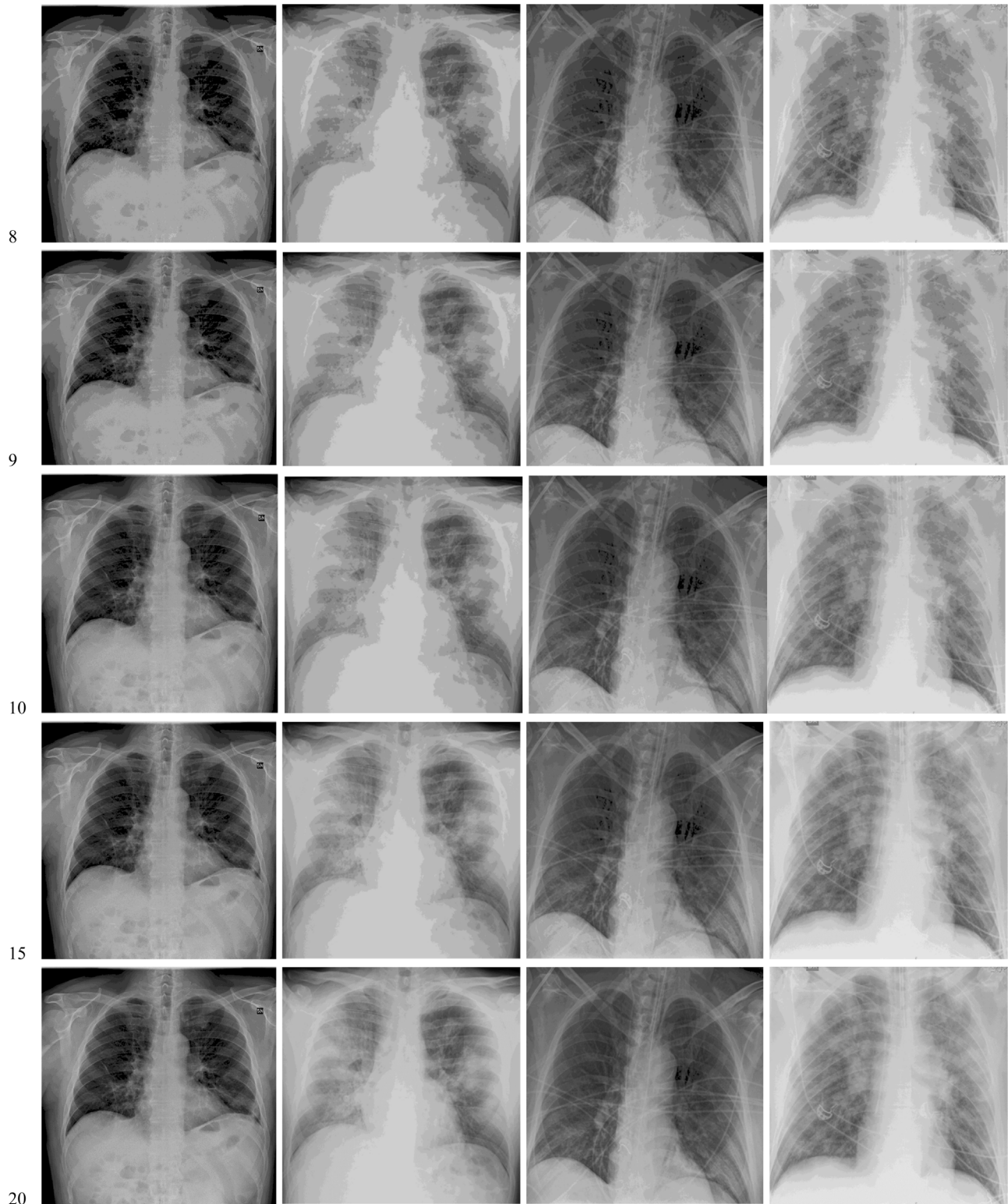


Fig. 9. (continued).

With rapidly-increased reported cases worldwide and the need to verify our algorithm with new images, the future work will involve validating the performance of the proposed algorithm on a set of the test images taken from The Berkeley Segmentation

Dataset and Benchmark. The aim will be focused on checking whether its performance is stable on the other images. Furthermore, the improved Slime mold algorithm will be applied to



Fig. 9. (continued).

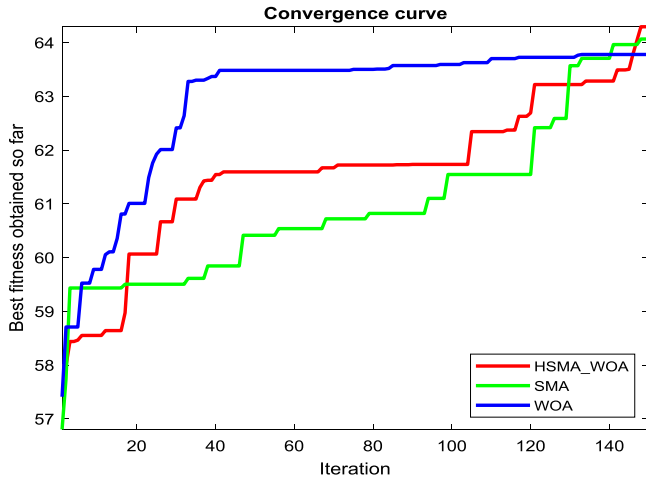


Fig. 10. Convergence curve on X1.

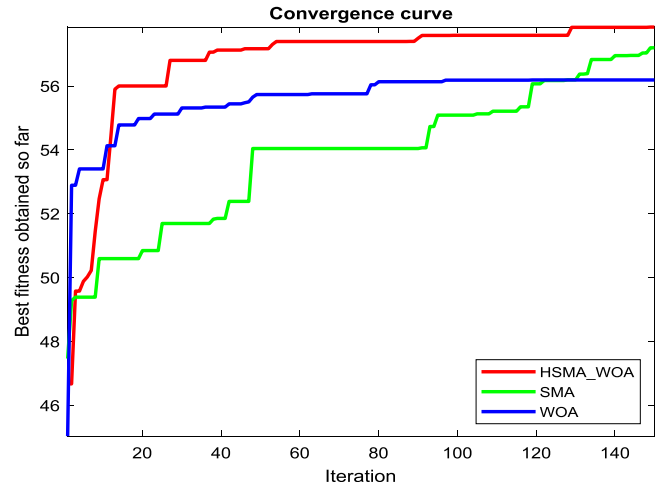


Fig. 12. Convergence curve on X3.

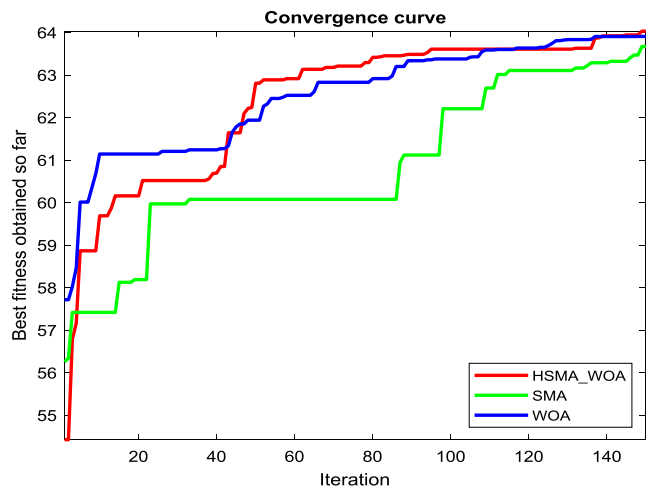


Fig. 11. Convergence curve on X2.

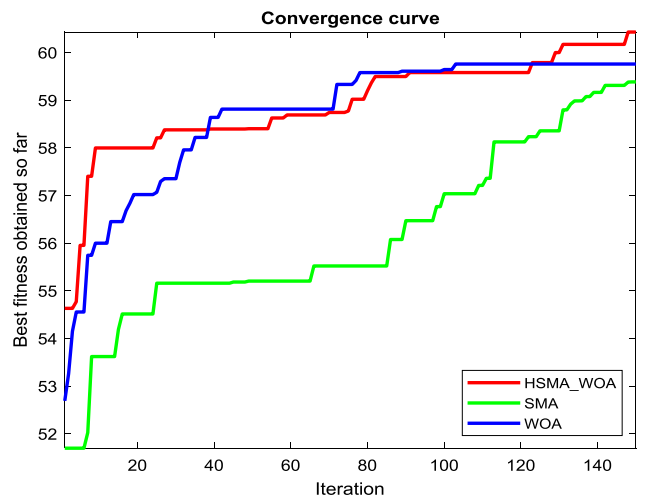


Fig. 13. Convergence curve on X4.

solve flow shop scheduling problems, DNA fragment assembly problems, and parameter estimation of the photovoltaic solar cell.

CRedit authorship contribution statement

Mohamed Abdel-Basset: Investigation, Methodology, Resources, Supervision, Visualization, Writing - original draft, Writing - review & editing. **Victor Chang:** Formal analysis, Investigation, Project administration, Validation, Writing - review & editing. **Reda Mohamed:** Conceptualization, Formal analysis, Methodology, Writing review & editing.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Table 6
UQI values under Kapur’s entropy.

img	T	HSMA_WOA	SMA	FFA [39]	WOA [33]	SSA [60]	HHA [38]	LShade [59]	Img	HSMA_WOA	SMA	FFA [39]	WOA [33]	SSA [60]	HHA [38]	LShade [59]
X1	2	0.7479	0.7479	0.7478	0.7477	0.7479	0.7479	0.7262	X7	0.8641	0.8729	0.8729	0.8641	0.8729	0.8729	0.8647
	3	0.8760	0.8760	0.8761	0.8760	0.8760	0.8764	0.8590		0.9042	0.9042	0.9042	0.9042	0.9042	0.9042	0.8844
	4	0.9260	0.9259	0.9263	0.9258	0.9264	0.9255	0.9004		0.9380	0.9383	0.9379	0.9380	0.9379	0.9383	0.9126
	5	0.9538	0.9537	0.9553	0.9539	0.9550	0.9536	0.9285		0.9590	0.9593	0.9582	0.9590	0.9583	0.9590	0.9438
	6	0.9671	0.9668	0.9681	0.9669	0.9661	0.9666	0.9378		0.9673	0.9672	0.9662	0.9675	0.9665	0.9671	0.9398
	7	0.9752	0.9727	0.9742	0.9755	0.9755	0.9738	0.9512		0.9700	0.9718	0.9698	0.9697	0.9692	0.9701	0.9571
	8	0.9758	0.9777	0.9796	0.9765	0.9794	0.9760	0.9583		0.9734	0.9732	0.9713	0.9734	0.9721	0.9722	0.9583
	9	0.9804	0.9796	0.9831	0.9800	0.9827	0.9792	0.9670		0.9757	0.9745	0.9727	0.9756	0.9734	0.9752	0.9610
	10	0.9830	0.9836	0.9862	0.9832	0.9853	0.9821	0.9734		0.9776	0.9771	0.9745	0.9769	0.9745	0.9767	0.9619
	15	0.9925	0.9926	0.9931	0.9926	0.9933	0.9918	0.9838		0.9825	0.9824	0.9797	0.9824	0.9793	0.9798	0.9723
20	0.9954	0.9952	0.9955	0.9953	0.9958	0.9941	0.9908		0.9845	0.9845	0.9832	0.9842	0.9818	0.9827	0.9788	
30	0.9971	0.9974	0.9972	0.9971	0.9975	0.9964	0.9944		0.9867	0.9861	0.9854	0.9861	0.9850	0.9858	0.9841	
X2	2	0.8263	0.8263	0.8263	0.8263	0.8263	0.8263	0.7989	X8	0.7406	0.7406	0.7406	0.7406	0.7406	0.7406	0.7506
	3	0.9181	0.9181	0.9180	0.9181	0.9180	0.9180	0.8696		0.9064	0.9063	0.9065	0.9064	0.9063	0.9066	0.8912
	4	0.9248	0.9248	0.9244	0.9251	0.9244	0.9250	0.8966		0.9338	0.9337	0.9312	0.9329	0.9361	0.9372	0.9108
	5	0.9532	0.9533	0.9524	0.9534	0.9527	0.9531	0.9137		0.9541	0.9537	0.9491	0.9529	0.9478	0.9543	0.9308
	6	0.9639	0.9631	0.9627	0.9639	0.9627	0.9640	0.9243		0.9666	0.9650	0.9622	0.9662	0.9614	0.9659	0.9375
	7	0.9653	0.9666	0.9640	0.9654	0.9643	0.9656	0.9438		0.9713	0.9704	0.9695	0.9714	0.9699	0.9714	0.9457
	8	0.9781	0.9779	0.9737	0.9782	0.9746	0.9778	0.9427		0.9783	0.9779	0.9730	0.9771	0.9735	0.9767	0.9588
	9	0.9819	0.9815	0.9798	0.9822	0.9792	0.9812	0.9618		0.9820	0.9811	0.9772	0.9815	0.9770	0.9815	0.9643
	10	0.9845	0.9842	0.9817	0.9840	0.9818	0.9831	0.9647		0.9854	0.9838	0.9797	0.9848	0.9786	0.9841	0.9572
	15	0.9924	0.9923	0.9887	0.9922	0.9884	0.9913	0.9732		0.9893	0.9893	0.9844	0.9885	0.9865	0.9884	0.9796
20	0.9952	0.9947	0.9924	0.9954	0.9912	0.9936	0.9861		0.9935	0.9918	0.9890	0.9932	0.9880	0.9910	0.9834	
30	0.9975	0.9973	0.9945	0.9976	0.9946	0.9958	0.9916		0.9966	0.9959	0.9943	0.9965	0.9935	0.9949	0.9907	
X3	2	0.7345	0.7345	0.7345	0.7345	0.7345	0.7345	0.7353	X9	0.8269	0.8269	0.8269	0.8269	0.8269	0.8269	0.8227
	3	0.8029	0.8027	0.8032	0.8029	0.8029	0.8029	0.8111		0.9160	0.9160	0.9160	0.9160	0.9160	0.9160	0.9103
	4	0.8801	0.8790	0.8806	0.8790	0.8806	0.8804	0.8546		0.9528	0.9527	0.9525	0.9527	0.9525	0.9527	0.9358
	5	0.9125	0.9130	0.9202	0.9106	0.9193	0.9093	0.8676		0.9608	0.9607	0.9593	0.9605	0.9598	0.9604	0.9503
	6	0.9605	0.9576	0.9604	0.9605	0.9600	0.9603	0.9105		0.9732	0.9733	0.9730	0.9733	0.9729	0.9731	0.9569
	7	0.9653	0.9649	0.9706	0.9654	0.9695	0.9646	0.9153		0.9795	0.9794	0.9783	0.9794	0.9781	0.9794	0.9679
	8	0.9783	0.9747	0.9809	0.9775	0.9806	0.9765	0.9354		0.9833	0.9836	0.9821	0.9835	0.9815	0.9835	0.9706
	9	0.9849	0.9816	0.9849	0.9844	0.9851	0.9843	0.9404		0.9864	0.9861	0.9848	0.9864	0.9841	0.9857	0.9739
	10	0.9867	0.9860	0.9874	0.9863	0.9877	0.9861	0.9579		0.9888	0.9890	0.9871	0.9889	0.9871	0.9887	0.9738
	15	0.9916	0.9921	0.9935	0.9907	0.9936	0.9912	0.9760		0.9939	0.9941	0.9934	0.9929	0.9929	0.9921	0.9844
20	0.9940	0.9950	0.9964	0.9936	0.9963	0.9934	0.9819		0.9963	0.9962	0.9952	0.9955	0.9949	0.9942	0.9909	
30	0.9971	0.9978	0.9983	0.9967	0.9983	0.9968	0.9912		0.9981	0.9979	0.9970	0.9977	0.9973	0.9971	0.9949	
X4	2	0.7793	0.7793	0.7793	0.7793	0.7793	0.7793	0.7374	X10	0.8214	0.8214	0.8214	0.8216	0.8214	0.8217	0.7919
	3	0.8818	0.8818	0.8818	0.8818	0.8818	0.8819	0.8067		0.9120	0.9120	0.9120	0.9121	0.9120	0.9120	0.8731
	4	0.9376	0.9377	0.9376	0.9377	0.9367	0.9369	0.8665		0.9419	0.9422	0.9422	0.9425	0.9426	0.9421	0.9078
	5	0.9552	0.9548	0.9527	0.9551	0.9531	0.9551	0.9100		0.9610	0.9610	0.9602	0.9611	0.9602	0.9610	0.9137
	6	0.9670	0.9670	0.9643	0.9668	0.9646	0.9665	0.9163		0.9714	0.9715	0.9701	0.9719	0.9699	0.9714	0.9298
	7	0.9733	0.9735	0.9714	0.9734	0.9700	0.9712	0.9284		0.9766	0.9769	0.9748	0.9763	0.9741	0.9762	0.9352
	8	0.9764	0.9767	0.9740	0.9764	0.9729	0.9757	0.9377		0.9805	0.9812	0.9794	0.9808	0.9797	0.9798	0.9533
	9	0.9789	0.9782	0.9756	0.9762	0.9767	0.9780	0.9477		0.9849	0.9852	0.9836	0.9849	0.9829	0.9837	0.9552
	10	0.9813	0.9808	0.9780	0.9809	0.9782	0.9797	0.9532		0.9886	0.9879	0.9852	0.9884	0.9854	0.9873	0.9629
	15	0.9883	0.9873	0.9845	0.9881	0.9824	0.9874	0.9684		0.9935	0.9932	0.9920	0.9933	0.9923	0.9913	0.9694
20	0.9912	0.9901	0.9884	0.9905	0.9854	0.9894	0.9744		0.9963	0.9954	0.9945	0.9960	0.9949	0.9945	0.9838	
30	0.9931	0.9918	0.9908	0.9926	0.9907	0.9921	0.9857		0.9972	0.9972	0.9967	0.9971	0.9953	0.9964	0.9919	
X5	2	0.8640	0.8640	0.8640	0.8640	0.8640	0.8640	0.8496	X11	0.8261	0.8261	0.8261	0.8261	0.8261	0.8261	0.8213
	3	0.9314	0.9314	0.9314	0.9314	0.9314	0.9314	0.8955		0.9010	0.9010	0.9010	0.9010	0.9010	0.9010	0.8939
	4	0.9371	0.9369	0.9366	0.9374	0.9368	0.9378	0.9051		0.9392	0.9391	0.9388	0.9392	0.9386	0.9391	0.9246
	5	0.9410	0.9407	0.9409	0.9416	0.9424	0.9374	0.9225		0.9550	0.9548	0.9545	0.9549	0.9543	0.9547	0.9370
	6	0.9595	0.9570	0.9584	0.9587	0.9556	0.9576	0.9335		0.9649	0.9646	0.9641	0.9647	0.9637	0.9647	0.9453
	7	0.9659	0.9644	0.9618	0.9642	0.9608	0.9625	0.9426		0.9717	0.9715	0.9703	0.9716	0.9705	0.9716	0.9582
	8	0.9731	0.9721	0.9664	0.9727	0.9687	0.9698	0.9489		0.9775	0.9774	0.9757	0.9772	0.9760	0.9773	0.9623
	9	0.9745	0.9748	0.9695	0.9746	0.9690	0.9722	0.9539		0.9819	0.9817	0.9790	0.9818	0.9787	0.9807	0.9679
	10	0.9746	0.9741	0.9706	0.9720	0.9692	0.9721	0.9622		0.9843	0.9843	0.9828	0.9841	0.9821	0.9838	0.9709
	15	0.9824	0.9831	0.9806	0.9805	0.9797	0.9794	0.9716		0.9913	0.9907	0.9884	0.9915	0.9887	0.9903	0.9811
20	0.9858	0.9859	0.9856	0.9844	0.9854	0.9837	0.9780		0.9940	0.9945	0.9930	0.9933	0.9926	0.9925	0.9870	
30	0.9881	0.9877	0.9875	0.9872	0.9879	0.9865	0.9850</									

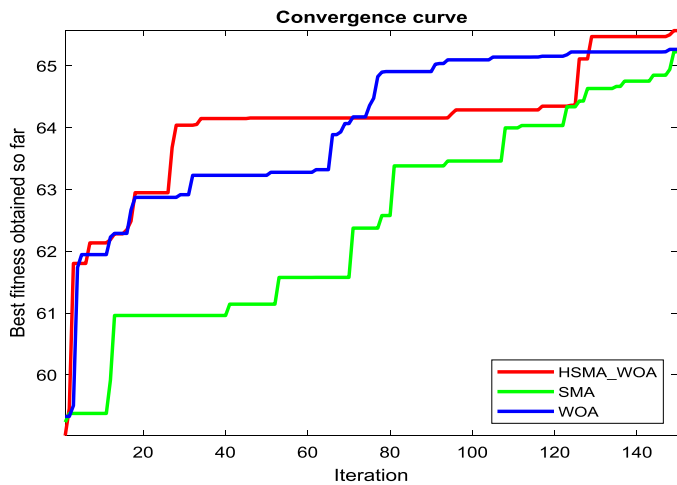


Fig. 14. Convergence curve on X5.

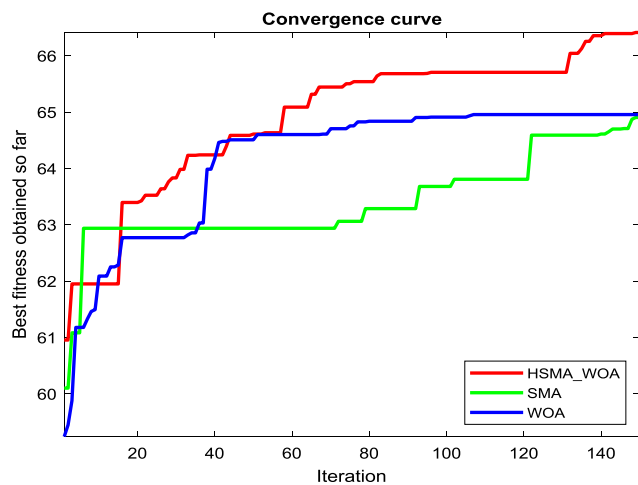


Fig. 15. Convergence curve on X6.

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