Enhanced feature selection technique using slime mould algorithm: a case study on chemical data

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Abstract
Feature selection techniques are considered one of the most important preprocessing steps, which has the most significant influence on the performance of data analysis and decision making. These FS techniques aim to achieve several objectives (such as reducing classification error and minimizing the number of features) at the same time to increase the classification rate. FS based on Metaheuristic (MH) is considered one of the most promising techniques to improve the classification process. This paper presents a modified method of the Slime mould algorithm depending on the Marine Predators Algorithm (MPA) operators as a local search strategy, which leads to increasing the convergence rate of the developed method, named SMAMPA and avoiding the attraction to local optima. The efficiency of SMAMPA is evaluated using twenty datasets and compared its results with the state-of-the-art FS methods. In addition, the applicability of SMAMPA to work with real-world problems is evaluated by using it as a quantitative structure-activity relationship (QSAR) model. The obtained results show the high ability of the developed SMAMPA method to reduce the dimension of the tested datasets by increasing the prediction rate. In addition, it provides results better than other FS techniques in terms of performance metrics.

Keywords Slime mould algorithm · Marine predators algorithm · Optimization feature selection · Quantitative structure-activity relationship (QSAR)

1 Introduction
The rapid growth of computer applications and information technologies produces a tremendous amount of data generated from various devices. The vast amount of data causes a critical problem for data mining which requires implementing practical data pre-processing steps using different techniques. Pre-processing is a necessary step that is employed to prepare and clean the data for the subsequent processing steps of the machine learning [1, 2]. Feature selection (FS) is an essential pre-processing step which is employed to reduce the size of the dataset. It is employed to select a small subset of the relevant features that capture the characteristics of the input data [3, 4]. Generally, FS methods remove noisy, unnecessary, and repeated features. Thus, an effective FS technique can boost the efficiency of data mining applications and various machine learning classification applications [5]. In general, FS methods can be classified into two types, wrapper-based and filter-based [6]. The wrapper-based techniques usually apply a classifier to obtain features, whereas the filter-based methods use data-reliant specifications to evaluate the merits of the features [6, 7]. Therefore, filter-based methods are more effective due to their fast implementation because they do not require classifiers to be involved in the FS process. To obtain a subset of features, we face some challenges. Thus, different search methods are applied to find the best features, including depth search, breadth search, random search, and hybrid search. However, exhaustive search requires a long time for extensive data, which is considered time-consuming.

Recently, with the great developments of the metaheuristics (MH) optimization algorithms, that inspired from nature, various optimization problems, including FS can be solved using these MH algorithms. In the literature, different MH algorithms have been employed for this
to enhance the exploitation ability of SMA during the tors of the MPA. The main aim of using MPA operators is to improve its local search process using the operators of MPA, which motivated us to develop a new version of SMA. The SMA was recently proposed by [33] by simulating the conduct of the marine predators algorithm (MPA). The SMA was developed by [26], as a new MH optimizer that can be utilized to solve various optimization problems. The oscillation mode of slime mould inspires it in nature. More so, it is adopted to solve several optimization problems in literature, such as finding optimal parameters in energy applications [27, 28], air quality forecasting [29], and other engineering applications [30–32]. In addition, MPA is recently proposed by [33] by simulating the conduct of the marine prey and predators. It has received wide attention due to its efficiency and it is adopted in various domains, for example, time series forecasting [34, 35], image segmentation [36], medical image classification [37], parameter estimation [38], and other applications [39, 40].

However, the SMA performance requires more improvements, mainly when applied to real-world applications, which motivated us to develop a new version of SMA to improve its local search process using the operators of the MPA. The main aim of using MPA operators is to enhance the exploitation ability of SMA during the process of finding the optimal solution inside the feasible region. MPA is applied as a local search method since it has been established its performance in several applications, including forecasting cases of COVID-19 [35], and photovoltaic array reconfiguration [41].

The contribution of this study can be summarized as follows:

- Develop a feature selection technique using an enhancement version of the SMA.
- Boost the capability of the local search of the SMA using the operators of MPA.
- Assess the efficiency of the SMAMPA developed method by using a set of twenty UCI datasets and comparing it with other FS methods.
- Verify the applicability of the SMAMPA by implementing it with real-world applications, such as QSAR model.

The structure of this study is as follows. The related works are presented in Sect. 2, where the preliminaries of the applied techniques, SMA, and MPA are described in Sect. 3. In Sect. 4, we describe the proposed SMAMPA approach, and in Sect. 5, the experimental evaluation is presented, including different benchmark datasets and comparisons to existing methods. Finally, the conclusions and future direction are highlighted in Sect. 6.

2 Related works

In this section, we summarize a number of the existing FS methods based on modified and improved optimization algorithms proposed in recent years. In [4], a modified version of the ABC algorithm, called a binary ABC, is proposed for FS. The searchability of the ABC is improved using the evolutionary-based similarity search mechanism, which is integrated into the existing binary ABC variants. It was evaluated using several datasets and compared to the original PSO and ABC besides several modified versions of PSO and ABC. In [42], the authors suggested an FS method based on a hybrid of the Flower Pollination Algorithm (FPA) and Clonal Selection Algorithm (CSA). The proposed BCFA was evaluated using the optimum-path forest classifier, and it showed significant performance with three different datasets. Also, It showed better performance in comparison to several optimization methods.

In [43], two binary variants of the whale optimization algorithm (WOA) were proposed for FS. The first variant is implemented by improving the search process using Tournament and Roulette Wheel selection mechanisms. In the second variant, the exploitation of the whale optimization algorithm is improved by using crossover and mutation operators. Sayed et al. [44] proposed a chaotic crow search algorithm (CSA) to overcome the limitations of the original CSA, such as trapping at local optima and low convergence rate. The new modified version, CCSA, was applied as an FS method evaluated using twenty datasets. The CCSA also was compared to different optimization techniques, and it achieved superior performance against several previous FS methods.

The authors in [45] suggested two binary versions of butterfly optimization algorithm (BOA) for FS. They used...
two transfer functions for mapping continuous search spaces to discrete ones. Several UCI benchmark datasets were used to evaluate the proposed method. More so, wide comparisons to some existing FS methods were performed. Evaluation outcomes showed the superior performance of the BOA. Too and Abdullah [46] proposed an FS method using a new variant of the genetic algorithm (GA) and a fast rival GA. They applied a competition strategy to combine crossover schemes and the new selection to boost the global search ability of the GA. Twenty-three UCI benchmark datasets were utilized to test the performance of the modified GA.

Zhang et al. [47] presented an improved variant of the Harris hawks optimization algorithm, called IHHO for FS. The main idea of the IHHO is by applying the salp swarm algorithm to enhance the search ability of the HHO. Several UCI datasets were used to evaluate the IHHO, and it achieved competitive performance compared to several FS methods. Another modified HHO, called Chaotic HHO (CHHO), is proposed for FS by Elgamal et al. [48]. Chaotic maps are applied to improve the population diversity of the HHO in the search space. Moreover, simulated annealing (SA) is applied to the best solution to enhance the exploitation of the HHO. They used Fourteen datasets to evaluate the CHHO compared to several optimization algorithms. Overall results showed that CHHO got the best outcomes.

The authors of [49] proposed a FS method, called ECSA, using a modified version of the crow search algorithm (CSA). The authors proposed three modifications to the traditional CSA to enhance its search capability. Sixteen UCI benchmark datasets were applied to evaluate the ESCA compared to the traditional CSA and several existing FS methods. The ESCA showed competitive performance in all experiments. Too and Mirjalili [6] suggested an FS method called hyper learning binary dragonfly algorithm. They applied a hyper learning strategy to improve the binary dragonfly algorithm, to avoid its limitations, such as trapping at local optima. They evaluated the proposed method using different UCI datasets and a new COVID-19 dataset. Zhong et al. [7] proposed a new FS method based on a modified Tree Growth Algorithm (TGA). A binary TGA is applied for FS applications, and also the evolutionary population dynamic strategy is employed to enhance the search capability of the TGA. Different UCI benchmark datasets were utilized to test the TGA performance.

Several works from the previous review were conducted for addressing FS problems by developing new methods to overcome the drawbacks of the algorithms’ original versions using benchmark and real datasets. The proposed methods showed good abilities to escape getting trapped in local optima, improve the convergence rate, and improve population diversity. However, there is no optimization technique to solve all problems, as stated by the No-Free-Lunch (NFL) theorem. Accordingly, this paper proposes a new optimization method by improving the slime mould algorithm’s local search ability using the MPA operators to solve different feature selection problems using benchmark and real datasets. This improvement can help balance the search methods and avoid local search problems such as trapping in a local optimum and degrading the convergence rate.

3 Background

This section presents the basic definitions of the SMA and MPA, as in what follows.

3.1 Slime mould algorithm

The SMA was firstly introduced by [26] as a novel optimization mechanism for global optimization. The SMA simulates the natural behaviour of the slime mould’s oscillation. The mathematical formulation of SMA is given as:

1. Phase 1 (The food approach): This step models the approach for the slime mould. The following equation describes this phase:

\[
Z = \begin{cases} 
Z_b + v_b \cdot (W \cdot Z_A - Z_B) & r < p \\
Z_c \cdot Z & r \geq p 
\end{cases}
\]  

(1)

where \(v_b\) is defined in the range of \([-a, a]\) and \(v_c\) decreases from 1 to 0. \(Z_b\) corresponds to the best solutions. Additionally, \(Z_A\) and \(Z_B\) are two solutions selected from a randomly, whereas \(W\) represents the mould weight of the slime. While \(p\) is computed as:

\[
p = \tanh[S(i) - DF], \quad i = 1, 2, ..., N
\]  

(2)

From Eq. 2, \(S(i)\) corresponds to the fitness values of the \(Z\) solution. \(DF\) is the best fitness value. The value \(a\) that defines \(v_b\) in Eq. 1 is computed as:

\[
a = \text{arctanh} \left( -\frac{t}{\text{max}_t} + 1 \right)
\]  

(3)

where, \(t\) is the current iteration. \(\text{max}_t\) is the maximum number of iteration. Also, the value of \(W\) is obtained as follows:
1. Phase 1 (High-velocity ratio): here, the prey is extremely fast, then the predator decides to be quiet and not move. This phase occurs at the beginning of the optimization process, and the movement of the prey is modeled as follows:

\[ S_t = R_B \times (\text{Elite}_t - R_B \times Z_t), i = 1, 2, ..., N \]  

\[ Z_t = Z_t + P \times R \times S_t \]  

in which \( R \in [0, 1] \) refers to a vector of random numbers \( P = 0.5 \), and \( R_B \) is Brownian motion vector.

2. Phase 2 (Unit velocity ratio): at this phase, the velocity of the prey and the predator is the same. This case is present in half of the iterative procedure. Here, the predator updates his position using Brownian movements, and the prey uses Levy flights. In this phase, \( Z \) is divided into two parts, and to update the solution in the first part, it applies Eqs. (11)-(12) and the second one uses Eq. (13)-(14).

\[ S_i = R_L \times (\text{Elite}_i - R_L \times Z_i), i = 1, 2, ..., N \]  

\[ Z_i = Z_i + P \times R \times S_i \]  

where \( R_L \) is generated randomly by a Lévy distribution.

3. Phase 3 (Low-velocity ratio): Within this phase, the predator has velocity faster than the prey, which occurred in the last third of the updating process using Eq. (15)

\[ S_i = R_L \times (R_L \times \text{Elite}_i - Z_i), i = 1, 2, ..., N \]  

\[ Z_i = \text{Elite}_i + P \times CF \times S_i \]  

where \( CF = \left(1 - \frac{t}{max_t}\right)^{\frac{2}{\max_t}} \) 

From Eqs. 13 and 14 the values of \( t \) and \( max_t \) are the current and total number of iterations, respectively.

According to [33] the MPA has another two key points.

- The first one is related to the Eddy formation and the effect of fish aggregating devices (FADS) that can modify the behavior of the predators. The MPA employs the following equation to handle these situations:

\[ Z_t = \begin{cases} 
Z_t + CF[Z_{min} + R \times (Z_{max} - Z_{min})] 	imes U & r_5 < \text{FAD} \\
Z_t + [\text{FAD}(1 - r) + r][Z_{r_1} - Z_{r_2}] & r_5 > \text{FAD} 
\end{cases} \]  

From Eq. 17 \( U \) refers to a binary vector. \( \text{FAD} = 0.2 \). \( r \in [0, 1] \). \( r_1 \) and \( r_2 \) denote random prey.

- The second one is the marine memory, here \( Z \) remembers its position, so, this behavior gives MPA
ability to save the previous $Z_b$. This solution is used and compared with the new $Z_b$.

4 The SMAMPA method

The SMAMPA is described in this section. It applies both SMA and MPA algorithms to improve its performance. In this context, the MPA applies as a local search of the original version of SMA to improve its ability to solve optimization problems. This improvement adds more flexibility to the method to explore the search space and improve diversity.

The basic structure of the SMAMPA is shown in Fig. 1. It starts by defining the parameters and creating the search space by initializing the problem population. After this step, the best solution is determined and saved by evaluating the fitness function. Furthermore, each solution is updated by either the SMA or MPA algorithms; this switching is based on the quality of the fitness function value; the quality is calculated as in Equation 19. Therefore, if the probability of the solution is more significant than $\alpha$, the solution will be updated by SMA, else it will be updated by MPA. In this paper, the probability value ($\alpha$) is set to 0.5. These steps are iterated for all solutions; then, the best solution, among all solutions, is selected. This sequence loops till reaching the stop condition, then the final results are presented. In detail, the SMAMPA begins by initializing the parameters of both SMA and MPA. Then the SMA generates a $Z \{x_i, i = 1, 2, ..., X_N\}$ random binary population with $N$ and $D$ size and dimension. Then, the first fitness values are computed by the operators of the SMA. The following equation is used to calculate the fitness function value Eq. (18):

$$f(x_i(t)) = \xi E_{x_i(t)} + (1 - \xi)\left(\frac{|x_i(t)|}{|C|}\right)$$

where $E_{x_i(t)}$ defines the classification error (in this study we use kNN as a classifier). $\xi \in [0, 1]$ balances between the classification error and the number of the selected features. The proposed method calculates the probability ($Pr_{oi}$) by Eq. 19 to update the solution by the operators of MPA or SMA (i.e., if $Pr_{oi} > 0.5$ the SMA will be used else, MPA will be used)

$$Pr_{oi} = \frac{F_i}{\sum_{i=1}^{N} F_i}$$

where, $f$ is the values of the fitness function. These sequences are iterated until meeting the stop condition. In the final step, the best solution is presented as the output of the proposed method.

5 Experiment results and discussion

5.1 Performance metrics

Minimum (Min) result and maximum (Max) result of the fitness value are applied using Eqs. 20 and 21, respectively.

$$\text{Min} = \min_{1 \leq k \leq N} F_i$$

$$\text{Max} = \max_{1 \leq k \leq N} F_i$$

where $F$ is the fitness function values
Accuracy: It is used to compute the classification accuracy in the experiments. It is calculated using Eq. 22.

\[
\text{Accuracy} = \frac{TP + TN}{TP + FP + FN + TN} \tag{22}
\]

where \(TP\) and \(TN\) define true positive and true negative. \(FP\) and \(FN\) define false positive and false negative.

Standard deviation (Std): It is computed using Eq. 23. It evaluates the stability of the algorithms. The results of the fitness function are used to compute this measure (\(\mathcal{F}\) is the mean of \(F\)).

\[
\text{Std} = \sqrt{\frac{1}{N} \sum_{k=1}^{N} (F_k - \mathcal{F})^2} \tag{23}
\]

### 5.2 Compared techniques and parameter settings

The SMAMPA is evaluated and compared to nine recently published metaheuristic algorithms (i.e., MPA, GA, SMA, PSO, HHO, SSA, MFO, WOA, and GOA) in the fitness values (i.e., minimum and maximum), standard deviation, accuracy, classification accuracy, and computational time. The SMAMPA method is also compared with eight advanced metaheuristic algorithms (i.e., BDA [50], BSSAS3 [14], bGWO2 [12], GLR [51], SbBOA [45], BGOAM [52], Das [53], and S-bBOA [45]).

The parameters setting of these algorithms is identical to that declared in their original studies. Table 1 presents the settings of the parameters of all applied methods. The MATLAB 2015a executes all the algorithms. All methods run on a 16GB RAM Intel Core i7 1.8 GHz 2.3 GHz processor. The solution numbers applied in this paper are set to 30. The maximum iteration number is set to 500. Each competitor algorithm is applied 30 independent runs and the average of its results are presented in the tables.

### 5.3 Experiment series 1: UCI datasets

In this section, twenty benchmark datasets are tested to demonstrate the SMAMPA optimizer’s efficiency. These datasets were taken from the Machine Learning Repository (UCI) [61]. Table 2 shows the tested datasets that contain different numbers of features, number of instances, and number of classes. The applied datasets are collected from different areas, including biology, games, physics, and biomedical.

The results obtained by the given SMAMPA method in the average measure of the fitness function, as stated in
are recorded in Table 3. SMAMPA is observed to beat the other comparative well-known methods in 85% of the tested datasets. PSO algorithm is the second-best method. SMAMPA got better performance than other comparative methods for all tested datasets except Sonar, ExactlyD, and krvskpD datasets. According to the average fitness values measure, the results demonstrated that the given SMAMPA has a promising ability in addressing this kind of problem.

The results are given by the introduced SMAMPA in terms of minimum fitness values, as stated in Eq. (20), are recorded in Table 4. SMAMPA is observed to defeat the other comparative well-known methods in 75% of the tested datasets. PSO algorithm is the second-best method. Based on minimum fitness values, SMAMPA has achieved the minimum fitness values with promising results for most datasets compared to other rival algorithms. It got better results in almost all the tested datasets except glassD, WaveformD, SpectD, Exactly2D, and krvskpD datasets. The results confirmed that the proposed SMAMPA could solve different feature selection challenges according to the minimum fitness values.

The results achieved by the SMAMPA for the maximum fitness values, as declared in Eq. (21), are shown in Table 5. SMAMPA is recognized to overcome the other

### Table 2 The details descriptions of the used UCI datasets

| Name          | Features | Instances | Classes | Type  |
|---------------|----------|-----------|---------|-------|
| breastWDBCD   | 30       | 569       | 2       | Biology |
| ionosphereD   | 34       | 351       | 2       | Physical |
| wineD         | 13       | 178       | 3       | Chemistry |
| breastcancerD | 9        | 699       | 2       | Biology |
| sonarD        | 60       | 208       | 2       | Biology |
| glassD        | 9        | 214       | 7       | Physics |
| tic-tac-toeD  | 9        | 958       | 2       | Game |
| LymphographyD | 18       | 148       | 2       | Biology |
| waveformD     | 40       | 5000      | 3       | Physics |
| clean1dataD  | 166      | 476       | 2       | Artificial |
| ZooD          | 16       | 101       | 6       | Artificial |
| SPECTD        | 22       | 267       | 2       | Biology |
| ecoliD        | 7        | 336       | 8       | Biology |
| CongressEWD   | 16       | 435       | 2       | Politics |
| M-of-nD       | 13       | 1000      | 2       | Biology |
| ExactlyD      | 13       | 1000      | 2       | Biology |
| Exactly2D     | 13       | 1000      | 2       | Biology |
| VoteD         | 16       | 300       | 2       | Politics |
| heartD        | 13       | 270       | 2       | Biology |
| krvskpD       | 36       | 3196      | 2       | Game |

### Table 3 Results of the fitness values measure

| Name          | SMAMPA   | MPA   | SMA   | GA    | HHO    | PSO   | SSA   | WOA   | MFO   | GOA   |
|---------------|----------|-------|-------|-------|--------|-------|-------|-------|-------|-------|
| breastWDBCD   | 0.0925   | 0.181 | 0.3409| 0.1250| 0.1194 | 0.1049| 0.1118| 0.1404| 0.1733| 0.2134|
| ionosphereD   | 0.1537   | 0.279 | 0.4061| 0.2340| 0.2144 | 0.1885| 0.2276| 0.2442| 0.2750| 0.3253|
| wineD         | 0.0000   | 0.015 | 0.1715| 0.0151| 0.0058 | 0.0038| 0.0566| 0.0207| 0.1259| 0.1514|
| breastcancerD | 0.1543   | 0.26  | 0.4009| 0.2153| 0.1924 | 0.1669| 0.2093| 0.2193| 0.2604| 0.3268|
| glassD        | 0.1347   | 0.146 | 0.2226| 0.1521| 0.1428 | 0.1409| 0.1508| 0.1501| 0.1854| 0.2197|
| sonarD        | 0.1196   | 0.275 | 0.4116| 0.2075| 0.1951 | **0.1133**| 0.1839| 0.2409| 0.2717| 0.3255|
| LymphographyD | 0.2576   | 0.41  | 0.5342| 0.3557| 0.3015 | 0.2767| 0.3168| 0.3590| 0.4508| 0.5160|
| tic-tac-toeD  | 0.0000   | 0.094 | 0.5068| 0.1666| 0.0018 | 0.0079| 0.0223| 0.0237| 0.4428| 0.5172|
| waveformD     | 0.6337   | 0.681 | 0.9037| 0.6513| 0.6568 | 0.6346| 0.6499| 0.6598| 0.6736| 0.7360|
| clean1dataD  | 0.1920   | 0.285 | 0.4374| 0.2569| 0.2627 | 0.2242| 0.2677| 0.2962| 0.2716| 0.3439|
| SPECTD        | 0.3078   | 0.406 | 0.4791| 0.3695| 0.3528 | 0.3355| 0.3571| 0.3814| 0.4045| 0.4789|
| ZooD          | 0.0000   | 0.004 | 0.1878| 0.0150| 0.0033 | 0.0042| 0.0483| 0.0078| 0.0901| 0.1220|
| ecoliD        | 0.1998   | 0.21  | 0.3398| 0.2235| 0.2171 | 0.2169| 0.2252| 0.2208| 0.2764| 0.3337|
| CongressEWD   | 0.1132   | 0.274 | 0.4035| 0.1842| 0.1645 | 0.1363| 0.1812| 0.1775| 0.2308| 0.3025|
| ExactlyD      | 0.0050   | 0.292 | 0.5858| 0.1897| 0.0539 | **0.0000**| 0.0576| 0.2399| 0.4333| 0.5944|
| Exactly2D     | 0.4801   | 0.504 | 0.5699| 0.5048| 0.4929 | 0.4884| 0.5081| 0.4956| 0.5447| 0.5816|
| M-of-nD       | 0.0000   | 0.335 | 0.4790| 0.1419| 0.0383 | **0.0000**| 0.0388| 0.1382| 0.3096| 0.4955|
| VoteD         | 0.1250   | 0.196 | 0.4115| 0.2015| 0.1727 | 0.1626| 0.1871| 0.1973| 0.2595| 0.3431|
| krvskpD       | 0.1193   | 0.258 | 0.5281| 0.1954| 0.1752 | **0.1192**| 0.1718| 0.2022| 0.1578| 0.3534|
| heartD        | **0.3408**| 0.368 | 0.5425| 0.3794| 0.3575 | 0.3471| 0.3617| 0.3804| 0.4255| 0.4969|

Bold values indicate the best result
comparative methods in 95% of the tested datasets. PSO method is also the second-best method. Except for the ExactlyD dataset, the proposed SMAMPA improved performance in all tested datasets than other comparative methods.
approaches. The outcomes demonstrated that the proposed integration method between the SMA and MPA search processes has a powerful ability to trade with complicated feature selection problems.

Figure 2 displays the average, minimum, and maximum fitness values for the comparative methods overall used datasets. It can be seen that the developed SMAMPA reached the best results in terms of the three measures (i.e., average, minimum, and maximum fitness values). SMAMPA got the smallest values using all measures in the tested datasets, which is strong evidence regarding the ability of SMAMPA in solving the FS problems. The modification of the proposed method proved its searchability in finding better solutions than the original SMA and MPA, as well as, this modification got all the best outcomes compared to the comparative algorithms.

Table 6 displays each algorithm’s accuracy measure values overall the used datasets. The proposed SMAMPA gathered the best high accuracy values in 95% of the tested datasets, pursued by PSO. However, the PSO obtained the best values in three datasets (i.e., ExactlyD, Exactly2, and M-of-n). In general, the SMAMPA exhibited an excellent ability to select the most vital features in the selection stage and produce the highest accuracy values in the classification stage. Figure 3 illustrates the average of the accuracy values for the all methods. We can recognise that the proposed method got the highest accuracy values compared to all comparative techniques; this supports our claim regarding the proposed SMAMPA; it works more efficiently than traditional methods and is also more efficient than other comparative algorithms. The second best method is the PSO algorithm; it got more reliable results than the rest of the comparison techniques in solving these widespread problems.

Table 7 displays each algorithm’s Std measure of the fitness function assessments using all the given datasets. The proposed SMAMPA obtained stable results according to Std values in 50% of the tested datasets, pursued by PSO, WOA, HHO, GA, and finally, the MPA. This result declares that the SMAMPA’s stability is better than other comparative methods according to its performance. The obtained results’ distribution is excellent and smaller than other comparative methods overall, the tested datasets. Figure 4 illustrates the average of the Std of the fitness function values for all compared methods. We can see obviously that the suggested SMAMPA got the smallest Std values compared to all comparative techniques; this supports our claim regarding the performance of the proposed SMAMPA again; it achieves promising results compared to other methods by giving low distribution and similar outcomes across a wide range of executions. The following best method is the PSO algorithm, pursued by HHO.

Table 8 lists the numbers of the selected features for all the tested methods. Table 8 shows the shorter length of the obtained optimal subset of features acquired by the comparative techniques. Investigating the results, SMA produced the nominal feature size in ten datasets, pursued by SMAMPA (six datasets). Compared with MPA, SMA, GA, HHO, PSO, SSA, WOA, MFO, and GOA, the SMAMPA can typically find the nominal subset of selected features that can adequately represent the main idea, as shown in Fig. 5. Owing to the MPA method, SMAMPA can override the local optima problem and thoroughly recognize the most helpful feature selection solution.

According to the computational time given in Table 9 and Fig. 6, the proposed SMAMPA got comparable computational time to solve the given problems. The main important thing in these experiments to tackle the FS problem is the evaluation measures, like the accuracy, because the given problem needs to be solved one time and not more.
5.4 Comparison with the state-of-the-art

This part evaluates the SMAMPA and compares further with different advanced and well-known published methods in the literature. These methods are BDA [50], BSSAS3 [14], bGWO2 [12], GLR [51], SbBOA [45], BGOAM [52], Das [53], and S-bBOA [45].

Table 10 shows all the tested methods using versions benchmark datasets. The given values of the comparative methods in this table are taken from their original papers. The “**” sign denotes no given results for this case. The proposed SMAMPA obtained better results in 70% of the tested datasets according to given values. It got the most high-grade results in almost all the tested datasets except ionosphereD, BreastcancerD, LymphographyD, ExactlyD, Exactly2D, and VoteD. The following best method is BDA, which got the most beneficial results in 53%, as this method has results for 15 datasets, followed by BSSAS3.

Recap, SMAMPA has a more trustworthy exploration experience than other comparative optimization techniques. This result is confirmed because the other tested algorithms did not allow SMAMPA to investigate other search areas in the search regions. Moreover, this proved the proposed SMAMPA to sustain solutions heterogeneity remarkably better than other feature selection methods. Besides, SMAMPA always got superior fitness values than other algorithms, proving its ability to evade restricted optima. In comparison, the other methods may quickly fall...
into the local optima problem. Investigating the selected number of optimal features by SMAMPA has sufficient exploration energy than other comparative algorithms, proved by selecting fewer features over the tested benchmark datasets.

5.5 Experiment series 2: real—world quantitative structure-activity relationship application

In this section, we evaluate ability of the proposed method in selecting the most relevant features using real—world problems. Quantitative structure-activity relationship (QSAR) models is a mathematical framework in chemometrics to explain the structural relationship between chemical compounds and biological activity [62–65]. The QSAR modelling has been conducted to study the proposed algorithm and verify its effectiveness. Six high-dimensional datasets are adopted. The first dataset is the inhibitors of influenza A viruses (H1N1). An RNA virus called influenza causes a respiratory infection. It is a highly dangerous illness that is associated with high rates of mortality and morbidity. The influenza virus has two main glycoproteins on its surface: neuraminidase and haemagglutinin. Thus, utilizing compounds that block neuraminidase can prevent host cells from becoming infected with viruses and prevent the virus from spreading across cells. According to IC50, this dataset contained two

| Table 7 | Results of the Std measure |
|---------|-----------------------------|
|         | STD | SMAMPA | MPA | SMA | GA | HHO | PSO | SSA | WOA | MFO | GOA |
| breastWDBC | 0.036 | 0.136 | 0.166 | 0.045 | 0.037 | 0.038 | 0.055 | 0.040 | 0.041 | 0.045 |
| ionosphereD | 0.050 | 0.115 | 0.094 | 0.048 | 0.048 | **0.047** | 0.052 | 0.048 | 0.065 | 0.066 |
| wineD | **0.000** | 0.038 | 0.111 | 0.030 | 0.020 | 0.016 | 0.082 | 0.034 | 0.053 | 0.065 |
| breastcancerD | 0.047 | 0.098 | 0.103 | **0.044** | 0.047 | 0.045 | 0.047 | 0.050 | 0.066 | 0.056 |
| glassD | **0.017** | 0.022 | 0.049 | 0.025 | 0.021 | 0.023 | 0.033 | 0.025 | 0.041 | 0.046 |
| sonarD | 0.070 | 0.132 | 0.077 | **0.064** | 0.082 | 0.094 | 0.084 | 0.086 | 0.083 | 0.068 |
| LymphographyD | 0.087 | 0.178 | 0.084 | 0.062 | 0.055 | 0.062 | 0.076 | **0.053** | 0.105 | 0.116 |
| tic-tac-toeD | **0.000** | 0.224 | 0.248 | 0.183 | 0.011 | 0.040 | 0.098 | 0.087 | 0.098 | 0.190 |
| waveformD | 0.016 | 0.106 | 0.140 | 0.017 | **0.013** | 0.014 | 0.019 | 0.019 | 0.036 | 0.055 |
| clean1dataD | 0.051 | 0.047 | 0.093 | 0.038 | 0.042 | **0.037** | 0.045 | 0.042 | 0.046 | 0.054 |
| SPECTD | **0.042** | 0.065 | 0.096 | 0.055 | 0.060 | 0.048 | 0.052 | 0.048 | 0.065 | 0.065 |
| ZooD | **0.000** | 0.012 | 0.157 | 0.019 | 0.010 | 0.011 | 0.069 | 0.015 | 0.061 | 0.092 |
| ecoliD | 0.032 | 0.046 | 0.109 | 0.028 | 0.025 | 0.025 | 0.038 | **0.024** | 0.047 | 0.104 |
| CongressEWD | **0.035** | 0.169 | 0.155 | 0.043 | 0.043 | 0.061 | 0.069 | 0.046 | 0.070 | 0.109 |
| ExactlyD | 0.020 | 0.274 | 0.134 | 0.224 | 0.083 | **0.000** | 0.118 | 0.181 | 0.207 | 0.116 |
| Exactly2D | **0.018** | 0.048 | 0.069 | 0.024 | 0.025 | 0.026 | 0.041 | 0.026 | 0.031 | 0.041 |
| M-of-nD | **0.000** | 0.314 | 0.201 | 0.151 | 0.068 | **0.000** | 0.110 | 0.125 | 0.184 | 0.127 |
| VoteD | 0.052 | 0.083 | 0.150 | 0.058 | **0.038** | 0.065 | 0.067 | 0.044 | 0.078 | 0.087 |
| krvskpD | **0.016** | 0.144 | 0.121 | 0.029 | 0.021 | 0.018 | 0.027 | 0.028 | 0.031 | 0.116 |
| heartD | 0.031 | **0.027** | 0.093 | 0.043 | 0.039 | 0.038 | 0.039 | 0.045 | 0.063 | 0.079 |

Bold values indicate the best result.
classes of active compound (IC50 < 20 \mu M) and weakly active compound (IC50 > 20 \mu M). This data consists of 2644 features and 479 instances [66].

The second dataset represents the anti-hepatitis C virus (hepatitis). Hepatitis C virus (HCV)-related liver conditions are among the most prevalent medical issues in the world today. The compounds employed have anti-hepatitis C virus action and were thiourea derivatives. This dataset containing 2952 features and 121 instances. According to EC50, the compounds were split into two sets: active and inactive compounds when EC50 < 0.1 \mu M and EC50 ≥ 0.1 \mu M, respectively [67].

The third dataset, called Chalcone, relates to a wide range of antibiotics with unique bioactivities against Candida albicans. The minimum inhibitory concentration (MIC) against C. albicans in mM/L was used to measure the antibacterial activities, which were expressed as pMIC, or the logarithm of the reciprocal of MIC. The median, or 1.30, of all 212 pMICs was taken into consideration as the cut-off to categorize these antimicrobial drugs into two groups based on the bioactivity distribution over the entire datasets. The first group consisted of 108 active compounds with pMIC values more than 1.30, and the remaining 104 inactive compounds made up the second group. The fourth, fifth, and the sixth datasets were publicly available in the UCI repository [61].

The proposed algorithm results, SMAMPA, are evaluated in terms of classification accuracy, selected features,
and standard deviation (Std). All results are summarized in Tables 13, 14 and 15.

From the Table 12, we assess the superiority of proposed algorithms, compared to others well-known algorithms. However, SMAMPA can be described as stable methods in most of all datasets except Biodeg dataset in which GA algorithm is better.

As can be seen from Table 13, the proposed algorithm, SMAMPA, has a significantly larger accuracy. These results demonstrated that the reduction in features contributes to the improvement of the accuracy resulting from the other algorithms. In terms of the selected features (Table 14), it can see that the SMAMPA obtained better values than the compared methods. It selected fewer features with high classification accuracy. Related to Std in Table 15, the SMAMPA algorithm achieved the low Std results in the H1N1, OralToxicity, and AndrogenReceptor datasets and was considered the most stable algorithm than the other algorithms. Furthermore, the hepatitis and Chalcone datasets presented competitive results for the SMAMPA with other algorithms. In general, SMAMPA algorithm can be considered as stable algorithm. From the above analysis, the SMAMPA method showed a high selecting ability for the essential features with high accuracy and good stability.

### Table 9: Results of the computational time

| Dataset          | Time | SMAMPA | MPA | SMA | GA | HHO | PSO | SSA | WOA | MFO | GOA |
|------------------|------|--------|-----|-----|----|-----|-----|-----|-----|-----|-----|
| breastWDBC       | 15.31| 16.93  | 6.60| 7.06| 15.64| 6.30 | 6.34| 6.34| 6.29| 6.95 |
| ionosphereD      | 14.92| 16.63  | 6.40| 6.89| 15.40| 6.17 | 6.17| 6.29| 6.13| 6.80 |
| wineD            | 14.68| 16.42  | 6.23| 7.17| 15.41| 6.44 | 6.41| 6.39| 6.43| 6.72 |
| breastcancerD    | 13.75| 15.30  | 6.26| 6.75| 15.05| 6.03 | 6.04| 6.15| 6.04| 6.69 |
| glassD           | 14.74| 15.52  | 5.18| 7.36| 12.11| 6.56 | 6.64| 6.18| 6.57| 6.76 |
| sonarD           | 13.38| 14.74  | 6.29| 6.71| 14.59| 6.05 | 6.04| 6.03| 6.03| 7.14 |
| LymphographyD    | 9.48 | 11.68  | 5.27| 6.61| 13.16| 5.67 | 5.87| 5.63| 5.82| 6.11 |
| tic-tac-toeD     | 15.83| 16.50  | 6.99| 8.16| 15.92| 7.27 | 7.37| 7.39| 7.38| 7.36 |
| waveformD        | 41.40| 61.29  | 12.34| 20.30| 40.94| 18.07| 18.09| 19.70| 18.56| 18.41 |
| clean1dataD      | 16.31| 17.89  | 6.68| 7.83| 16.75| 7.01 | 7.04| 6.96| 7.07| 10.07 |
| SPECTD           | 13.58| 13.76  | 5.88| 6.71| 14.61| 6.06 | 6.09| 5.87| 6.03| 6.48 |
| ZooD             | 10.76| 12.97  | 4.93| 7.29| 14.70| 6.17 | 6.38| 6.31| 6.44| 6.52 |
| ecoliD           | 10.22| 10.51  | 4.62| 5.79| 11.67| 5.18 | 5.19| 5.12| 5.24| 5.23 |
| CongressEWD      | 14.20| 15.61  | 6.45| 7.25| 15.53| 6.49 | 6.47| 6.37| 6.45| 6.83 |
| ExactlyD         | 15.28| 16.51  | 6.69| 7.89| 16.48| 7.11 | 7.06| 6.96| 7.03| 7.35 |
| Exactly2D        | 13.33| 14.54  | 6.94| 7.77| 16.19| 7.03| 6.89| 6.30| 6.99| 7.58 |
| M-of-nD          | 15.44| 16.55  | 6.89| 8.05| 16.76| 7.20| 7.23| 7.13| 7.23| 7.55 |
| VoteD            | 13.74| 15.14  | 6.44| 7.25| 15.56| 6.56| 6.47| 6.43| 6.54| 6.73 |
| krvskpD          | 16.11| 43.54  | 10.45| 14.12| 29.58| 12.57| 12.55| 13.85| 12.70| 13.12 |
| heartD           | 15.23| 21.67  | 10.30| 11.53| 24.90| 10.28| 10.32| 10.35| 10.32| 11.04 |

**Bold values indicate the best result**
### Table 10: Accuracy compression between SMAMPA and the other methods in the literature

| Name               | SMAMPA | BDA   | BSSAS3 | bGWO2 | GLR   | ShBOA  | BGOAM  | Das   | S-bBOA |
|--------------------|--------|-------|--------|-------|-------|--------|--------|-------|--------|
| breastWBCD        | 0.990  | 0.979 | 0.948  | 0.935 | –     | 0.971  | 0.970  | –     | 0.971  |
| ionosphereD       | 0.974  | 0.991 | 0.918  | 0.834 | 0.000 | 0.907  | 0.946  | 0.865 | 0.907  |
| wineD             | 1.000  | 1.000 | 0.993  | 0.920 | 0.978 | 0.984  | 0.989  | 0.961 | 0.984  |
| breastcancerD     | 0.974  | –     | 0.976  | 0.975 | –     | 0.969  | 0.974  | 0.971 | 0.969  |
| glassD            | 0.798  | –     | –      | –     | 0.730 | –      | –      | 0.692 | –      |
| sonarD            | 0.989  | 0.980 | 0.937  | 0.729 | 0.829 | 0.936  | 0.915  | 0.793 | 0.936  |
| LymphographyD     | 0.932  | 0.992 | 0.890  | 0.700 | –     | 0.868  | 0.912  | –     | 0.868  |
| tic–tac–toeD      | 1.000  | –     | 0.821  | –     | –     | 0.798  | 0.791  | –     | 0.798  |
| waveformD         | 0.794  | 0.758 | 0.733  | 0.789 | –     | 0.743  | 0.751  | –     | 0.743  |
| clean1dataD       | 0.961  | –     | 0.880  | 0.727 | –     | 0.883  | –      | –     | 0.883  |
| SPECTD            | 0.903  | 0.850 | 0.836  | 0.822 | –     | 0.846  | 0.826  | –     | 0.846  |
| ZooD              | 1.000  | 1.000 | 1.000  | 0.879 | –     | 0.978  | 0.958  | 0.960 | 0.978  |
| ecoliD            | 0.862  | –     | –      | –     | 0.852 | –      | –      | 0.789 | –      |
| CongressEWd       | 0.987  | 0.987 | 0.963  | 0.938 | –     | 0.959  | 0.976  | 0.526 | 0.959  |
| ExactlyD          | 1.000  | 1.000 | 0.980  | 0.776 | –     | 0.972  | 1.000  | –     | 0.972  |
| Exactly2D         | 0.465  | 0.773 | 0.758  | 0.750 | –     | 0.760  | 0.736  | –     | 0.760  |
| M–of–nD           | 1.000  | 1.000 | 0.991  | 0.963 | –     | 0.972  | 1.000  | –     | 0.972  |
| VoteD             | 0.982  | 0.989 | 0.951  | 0.920 | –     | 0.965  | 0.963  | –     | 0.965  |
| krVSkgD           | 0.986  | 0.979 | 0.964  | 0.956 | –     | 0.966  | 0.974  | –     | 0.966  |
| heartD            | 0.883  | 0.876 | 0.860  | 0.776 | –     | 0.824  | 0.836  | 0.784 | 0.824  |

Bold values indicate the best result.

### Table 11: Description of the real-world datasets

| Dataset      | Features | Instances | Classes |
|--------------|----------|-----------|---------|
| H1N1         | 2644     | 479       | 2       |
| hepatitis    | 2952     | 121       | 2       |
| Chalcone     | 2821     | 100       | 2       |
| biodeg       | 41       | 1055      | 2       |
| OralToxicity | 1024     | 8992      | 2       |
| AndrogenReceptor | 1024 | 1687      | 2       |

### Table 12: Real application: Average of the fitness functions values

| Name             | SMAMPA | MPA   | SMA   | GA    | HHO   | PSO   | SSA   | WOA   | MFO   | GOA   |
|------------------|--------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| H1N1             | 0.3714 | 0.3724| 0.4898| 0.4160| 0.3897| 0.4011| 0.4110| 0.3973| 0.4363| 0.5443|
| hepatitis        | 0.1235 | 0.2023| 0.3982| 0.3818| 0.2719| 0.3679| 0.3919| 0.2400| 0.4362| 0.4514|
| Chalcone         | 0.2906 | 0.3166| 0.5244| 0.4837| 0.3823| 0.4820| 0.5135| 0.3636| 0.5472| 0.5352|
| Biodeg           | 0.3310 | 0.3229| 0.4204| 0.3168| 0.3482| 0.3312| 0.3427| 0.3614| 0.3711| 0.3561|
| OralToxicity     | 0.2504 | 0.2530| 0.2645| 0.2559| 0.2576| 0.2581| 0.2593| 0.2572| 0.2639| 0.2624|
| AndrogenReceptor | 0.2758 | 0.2819| 0.3194| 0.2860| 0.2858| 0.2870| 0.2877| 0.2923| 0.3087| 0.3107|

Bold values indicate the best result.
6 Conclusion and future work

This study developed a new feature selection (FS) method by enhancing the original style of the slime mould algorithm (SMA). We leverage the exploration ability of the marine predators algorithm (MPA) to work as a local search method for the proposed method. The modified version, namely, SMAMPA, was evaluated on twenty well-known UCI benchmark datasets, using different evaluation metrics. Moreover, it was compared to the traditional SMA, MPA, and several state-of-art optimization methods. The developed SMAMPA showed superior performance over several optimization algorithms and several modified optimization algorithms. Furthermore, to verify the efficiency of the SMAMPA on more complicated and high-dimensional real-world problems, six datasets related to chemometrics, were used. Evaluation outcomes also showed the high performance of the SMAMPA, and it
obtained the best results compared to other optimization algorithms. According to the superior results of the developed SMAMPA, in future work, it could be further investigated in more complicated problems, such as multi-optimization problems, big data mining, and medical image processing.

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**Data Availability** The datasets generated during and/or analysed during the current study are available in the UCI repository [61].

**Declarations**

**Conflict of interest** The authors declare that there is no conflict of interest.

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