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Title: Asynchronous Accelerating Multi-leader Salp Chains for Feature Selection

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Highlights:

- A novel feature selection approach based on binary Salp Swarm Algorithm (SSA) is proposed.
- Asynchronous updating rules and leadership structure were used to adapt the salps' positions.
- The number of leaders in the social organization of the artificial salp chain is well studied.
- The salp chain is divided into several sub-chains.
- The salps in each sub-chain can follow a different strategy to adaptively update their locations.
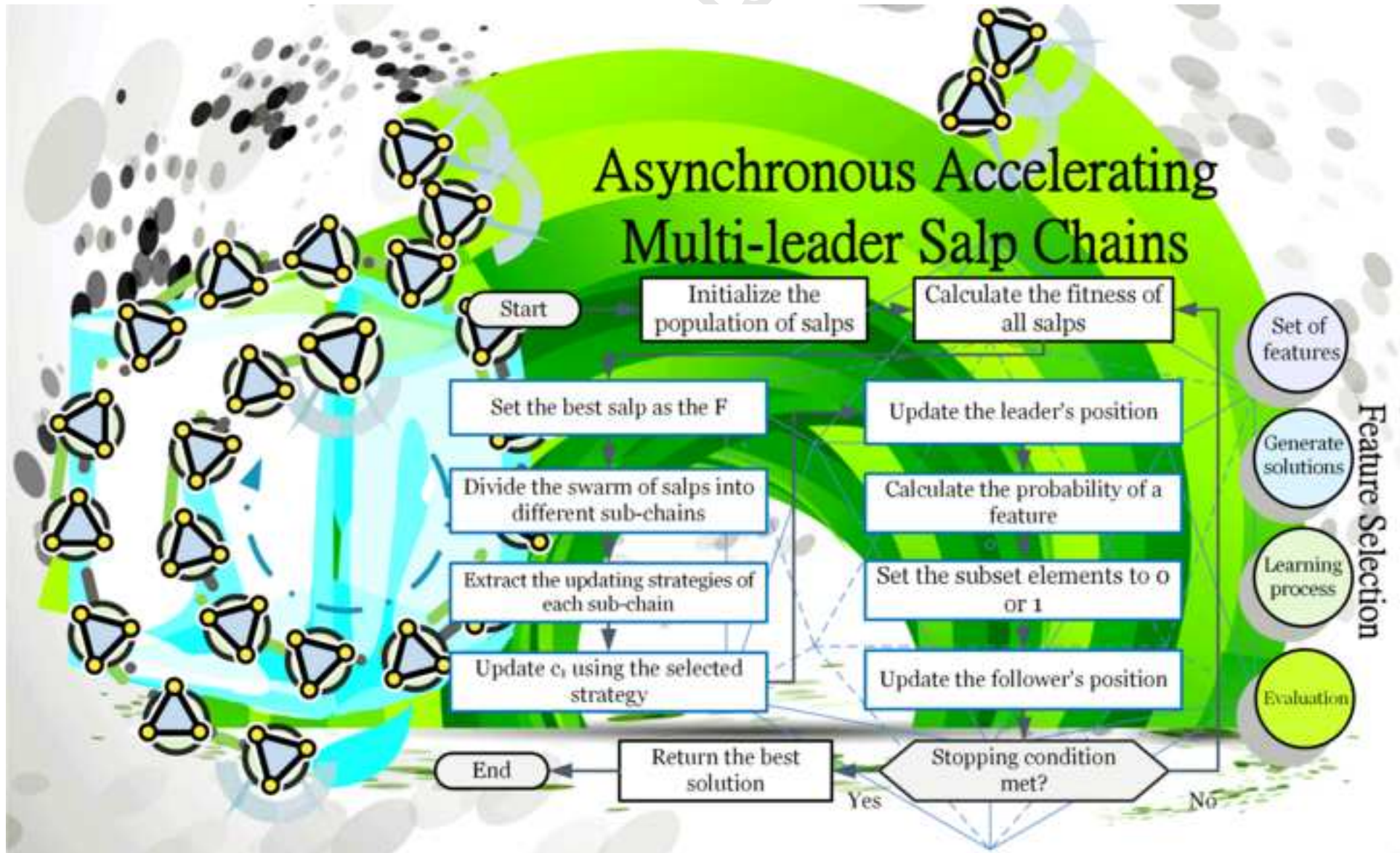
Asynchronous Accelerating Multi-leader Salp Chains for Feature Selection

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Abstract

Feature selection is an imperative preprocessing step that can positively affect the performance of data mining techniques. Searching for the optimal feature subset amongst an unabridged dataset is a challenging problem, especially for large-scale datasets. In this research, a binary Salp Swarm Algorithm (SSA) with asynchronous updating rules and a new leadership structure is proposed. To set the best leadership structure, several extensive experiments are performed to determine the most effective number of leaders in the social organization of the artificial salp chain. Inspired from the behaviour of a termite colony (TC) in dividing the termites into four types, the salp chain is then divided into several sub-chains, where the salps in each sub-chain can follow a different strategy to adaptively update their locations. Three different updating strategies are employed in this paper. The proposed algorithm is tested and validated on 20 well-known datasets from the UCI repository. The results and comparisons verify that utilizing half of the salps as leaders of the chain can significantly improve the performance of SSA in terms of accuracy metric. Furthermore, dynamically tuning the single parameter of algorithm enable it to more effectively explore the search space in dealing with different feature selection datasets.

Keywords: Swarm Intelligence, Salp Swarm Algorithm, SSA, Wrapper Feature Selection, Optimization, Machine Learning, Classification.

1. Introduction

Curse of dimensionality is a challenging problem that impacts the performance of data mining techniques (e.g., classification). A classifier's accuracy and efficiency have an inverse relation with data dimensionality. Feature Selection (FS) is one of the most important preprocessing steps that aim to improve the whole data mining process by reducing the size

of the dataset through removing the irrelevant and redundant features [41]. The feature selection has a significant impact on the whole data mining process since it affects the memory size required for the task completion, execution time and the model performance [11]

In general, feature selection methods differ from each other with respect to two key aspects: how they evaluate the feature subset (filter and wrapper methods) and how they search for the optimal feature subset in the feature space (complete/exhaustive search, random search and heuristic search) [41, 24]. From the evaluation perspective, filter methods (e.g., Chi-Square, Information Gain, Gain Ratio, and Relief) select the set of features independently from the learning algorithm (e.g., classification), and they use a number of known metrics to decide which features should be eliminated [35]. In wrapper methods, however, the features are selected to learn the model (e.g. classifier), so a feature is to be removed from or added to the feature subset based on the resulting performance of the learning algorithm (e.g., classification accuracy for a specific classifier) [39]. Filters are faster than wrappers because the evaluation measures they use are computationally cheaper than those the wrappers use (e.g., classifier's accuracy) [41]. However, wrappers have been widely investigated for classification accuracy since they have been proven to be beneficial in finding feature subsets that suite a predetermined classifier [42].

Searching for the best feature subset is another stepping stone in FS. Finding the best set of features cannot be achieved or guaranteed unless we use an exhaustive search by trying all subset combinations from N total number of features, which leads to 2^N tries [28]. The heuristic search can find the (near) optimal solution without the need to explore or discover the whole dimension (search) space [39] as opposed to an exhaustive search. This is the reason behind the utilization of various metaheuristic algorithms to solve FS problems such as Record-to-Record Travel Algorithm (RRTA) [46, 45], Genetic Algorithm (GA) [44], Particle Swarm Optimization (PSO) [8], and Ant Colony Optimization (ACO) [37], and Grasshopper Optimization Algorithm (GOA) [48].

Swarm Intelligence (SI) algorithms are mostly nature-inspired and mimic the philosophy of intelligent swarming behavior of fish, birds, ants, bees, etc [17, 31, 30, 32]. In recent years, many researchers applied SI techniques to different problems such as neural network optimization [5, 22, 18, 21, 4], clustering analysis [6, 61], feature selection [64, 23, 3], and email spam filtering [20, 19]. Examples of SI algorithms are: Krill Herd (KH) [26], Grey Wolf Optimizer [56, 34], and Firefly Algorithm (FA) [65]. A key significant strength of the SI algorithms is their global search capability as they can produce multiple solutions in each run. A common challenge for all metaheuristics is the parameter settings since they usually have a set of initial parameters to be tuned [33]. The process of tuning parameter has significant impacts on the performance of the searching process, but it is very time-consuming. According to [63], there are no universally optimal parameter values to be used for all metaheuristic algorithms, so it highly depends on the problem. In other words, the parameters should be tuned or at least tested when solving a new problem.

Another key challenge for SI algorithms is the process of balancing the conflicting phases of exploration (diversification) and exploitation (intensification) during the searching process. Having a good balance during the search process will prevent an algorithm from a premature convergence and enables the individuals in the swarm to accurately approximate the global optimum. In some SI algorithms, there is one parameter that plays a significant role in

2

balancing exploration and exploitation as in GWO [56] and Particle Swarm Optimization [38].

To tune exploration and exploitation, dynamic, adaptive, and time-varying parameter tuning can be used during the search process instead of having one fixed value from the beginning of the search process (e.g. inertia weight in PSO), or changing the parameter gradually over to the course of iterations by following the same strategy for all individuals in the population (e.g. GWO).

The SSA [52] algorithm is a recent SI technique that mimics the swarming behavior of salps in the ocean to build an engine for exploration and exploitation of problem landscape. This algorithm can produce a superior, excellent performance when applied to global optimization and challenging engineering problems. However, our initial investigation showed that this algorithm requires modifications and adaptations when applying the FS problems due to high-dimensionality of such problems. This motivated our attempts to propose several modifications and new operators for the SSA algorithm to solve FS problems. A new approach for dynamically updating the main SSA's parameter (c_1) is proposed based on four different strategies. The population will be divided into many sub-populations (sub-chains) to be updated asynchronously, where an independent strategy will be utilized to update each sub-chain asynchronously to deepen the efficacy of the SSA in terms of exploratory and exploitative tendencies.

In the proposed FS approach, each salp represents a feature subset (solution) where a specific classifier is used to evaluate its fitness. Subsequently, each salp updates its location in the search space based on whether it is the first salp (leader) or a follower. The leader moves towards the food source (F), while each follower moves towards the salp preceded it. One of the main advantages of SSA is that it has only one parameter (c_1) responsible for balancing between exploration and exploitation. In the basic SSA, c_1 parameter is gradually decreased over the course of iterations. This mechanism is used to update the position of all salps in the population. In this paper, we applied the basic SSA algorithm (BSSA) to FS problems and found that it shows promising and competitive results as compared to those obtained from the previously proposed approaches. This was the motivation of the first improvement, in which multi leaders are used instead of using one leader as in the basic SSA. To further improve SSA, we divide the salp chain into many asynchronous sub-chains. In fact, a new binary SSA with asynchronous updating rules for c_1 parameter and leadership structure is proposed in this work based on two stages to mitigate the premature convergence and stagnation of salps in local solutions when solving feature selection problems.

The rest of this paper is organized as follows: In Section 2, the related works to FS problem and parameter tuning are discussed. A general overview of SSA is given in Section 3. A detailed description of the proposed approach is presented in Section 4. The effectiveness of proposed SSA-based approach is investigated and validated through a set of extensive experiments and results analysis in Section 5. Finally, conclusions and future work are given in Section 6.

2. Related Works

There are many works focused on both applications of SI algorithms and applying or developing other mechanisms for these algorithms to improve their performance when solving

3

challenging problems including FS. Hence, in this section, the related works are reviewed.

During the last decade, many SI algorithms have been employed to solve FS problems. As one of the seminal SI algorithms, PSO has been widely applied to FS problems. Moradi *et al.* [57] proposed a hybrid PSO with a local search to select the salient features to be included in the feature subset. Moreover, two different FS PSO-based approaches were proposed in [27]. In these two approaches, a new variable (V_{min}) was added to the PSO algorithm.

Ant Lion Optimizer (ALO) [51] was used as the searching engine in a wrapper FS method in [68]. In addition, a crossover operator was employed to enhance the exploratory behaviour of ALO in [15]. A set of chaotic maps was used to control the main controlling parameter of ALO in [67]. Recently, a new hybrid algorithm that optimizes based on The Whale Optimization Algorithm (WOA) [54] and Simulated algorithm (SA) was designed as an FS method in [50]. In [14], GWO [56] with an adaptive parameter control was proposed [14]. More works about the GWO for FS can be found in [15]. A set of FS approaches were proposed in [49]. The authors proposed a binary ALO algorithm equipped with eight transfer functions to convert the continuous version of ALO to a binary one were investigated.

In the previous approaches, different parameter settings have been used for different optimizers. Every time the parameters change, an algorithm delivers a different performance. This indicates that the parameter values are problem dependent. Many researchers tried to use some adaptive mechanisms to control the parameters in different optimizers [10, 1, 69].

2.1. Related works to parameter tuning

In [1], a new Self-Adaptive Cohort Intelligence (SACI) was proposed to tackle the FS problem. Another FS approach that employed an adaptive searching algorithm was proposed in [59]. Moreover, Young *et.al* proposed a novel FS approach that incorporates an adaptive parameter tuning mechanism for Support Vector Machine (SVM) [66]. In general, adaptive metaheuristics have been widely proposed in other applications. The PSO has been enhanced by incorporating an adaptive mechanisms in many works in the literature to control the inertia weight parameter, which plays an important role in preventing the premature convergence by balancing the exploration and exploitation stages [55]. In 2009, a modified PSO inspired from the foraging behavior of black storks was proposed [9]. Two types of particles with two different groups of acceleration mechanisms were defined in their approach. Moreover, Ziyu and Dingxue [69] designed a modified PSO that uses time-varying values for adjusting the most important parameters (i.e., c_1 and c_2). In addition, some linear [7] and non-linear [12] time-varying acceleration functions were used to adjust the values of c_1 and c_2 parameters in PSO. In all previous modified PSO approaches, the results showed that PSO with the dynamic parameter settings is superior to the classical PSO.

Recently, a Self-adaptive Fruit Fly Optimization (SFFO) was proposed, and it was shown to be efficient in solving high-dimensional global optimization problems [60]. A self-adaptive GA was proposed in [62] to solve some constrained problems. In [58], a modified Harmony Search (HS) with an on-line parameter tuning mechanism was proposed. In 2015, Mafarja and Abdullah [46] proposed a novel FS approach that employed an intelligent fuzzy logic operator to control the main parameter in Record-to-Record algorithm dynamically through the search process. A multi-level Great Deluge (GD) algorithm was proposed by Mafarja and Abdullah [43]. In this approach, a dynamic updating mechanism was used to set the level parameter in GD algorithm. Moreover, two adaptive memetic algorithms with adaptive

4

updating strategies were proposed by Mafarja et al. [47]. For more approaches that use adaptive mechanisms to control some parameters in metaheuristics, readers can refer to the following surveys [13], [13] and [2].

2.2. Related works on termite colonies

Despite the fact that all individuals in animal flocks do their duties as a group member, they are not all similar in their intelligence and ability to collect food. Each individual has a specific task to do in a specific situation. For example, in ABC algorithm [36], the bees are divided into three groups depending on their role in the swarm. Employed bees are responsible for exploiting the food sources and share the quality of those food sources with onlooker bees via a waggle dance. Onlooker bees help the employed bees to exploit the food sources depending on the information they received via the waggle dance. Scout bees are the individuals who are responsible for exploring the search space searching for new food sources. Moreover, in GWO [56], four different groups of wolves (α, β, δ, and γ) are defined in the algorithm. The α group leads the flock, the adult wolves in the β group usually help α group and follow them, while δ wolves come at the third level and ω wolves come in the lowest level.

A similar behavior can be seen in a termite colony (TC) [29], where the termites are divided into four types; soldier, worker, babysitter, and queen. Soldiers protect the colony from enemies, the workers provide food for the colony, while the queen and babysitters reproduce and raise children. From the previous examples of swarm-based algorithms, it is clear that all groups of individuals have a common goal of promoting the swarm's survival, while each group has its own role and accordingly its own behavior. Thus, each type can be considered as a group and all groups are targeting promoting the swarḿs survival.

3. Overview of the SSA

Mirjalili *et al.* [52] proposed the SSA to simulate the swarming behavior of salps for optimization purposes. The efficacy of the conventional SSA on FS datasets has not been evaluated so far. This algorithm shows satisfactory exploratory and exploitive behaviors that make it potentially suitable for FS problems, which cannot be experienced when using some traditional and successful optimizers such as GA, and PSO. The SSA is a competent, flexible, simple, and easy to be coded and implemented in parallel and serial modes. In addition, the only parameter of SSA in balancing the exploration at first stages and exploitation at advanced phases can be adaptively decreased during the process. To avoid being trapped in local solutions, the locations of search agents can be updated progressively with regard to other salps in the dynamic swarm. The dynamic activities of salps can escape the SSA algorithm from local solutions. It also saves the best agent obtained so far to guide the agents towards more rich regions in the exploration space.

The SSA is a nature-inspired algorithm that iteratively attracts a number of individuals (i.e., salps) inside the search space of a given problem. Subsequently, each salp updates its location in the search space whether it is the first salp in the chain (leader) or a follower. The leader moves towards a target food source (F), while each follower can move towards other salps (and leader directly or indirectly) [52].

5

The population X that contains n salps with d-dimensions can be shown by a $n \times d$-dimensional matrix, as given in Eq. 1:

$$X_i = \begin{bmatrix} x_1^1 & x_2^1 & \dots & x_d^1 \\ x_1^2 & x_2^2 & \dots & x_d^2 \\ \vdots & \vdots & \dots & \vdots \\ x_1^n & x_2^n & \dots & x_d^n \end{bmatrix} \tag{1}$$

In the mathematical model of the SSA algorithm, the location of the leading salp should be updated by Eq. 2

$$x_j^1 = \begin{cases} F_j + c_1 \left((ub_j - lb_j) c_2 + lb_j \right) & c_3 \geq 0.5 \\ F_j - c_1 \left((ub_j - lb_j) c_2 + lb_j \right) & c_3 < 0.5 \end{cases} \tag{2}$$

where x_j^1 is the leaderś position and F_j is the food source position in the jth dimension, ub_j is the upper bound of jth dimension and lb_j is the lower bound of jth dimension, c_2 and c_3 are two random numbers in the interval $[0, 1]$, that direct the next position in j^{th} dimension towards $+\infty$ or $-\infty$ as well as dictating the step size, c_1 is the core variable of the SSA for controlling the fine balance between exploration and exploitation propensities, which is defined as in Eq. 3:

$$c_1 = 2e^{-\left(\frac{4l}{L}\right)^2} \tag{3}$$

where l indicates the current iteration, while L indicates the maximum number of iterations. The c_1 variable is gradually decreased over the course of iterations to allow more exploration at the beginning steps of the searching process, then more exploitation in last steps.

The followers' positions are updated using Eq. 4.

$$x_j^i = \frac{1}{2} \left(x_j^i + x_j^{i-1} \right) \tag{4}$$

where $i \geq 2$ and x_j^i represents the position of the ith follower at the jth dimension.

The search process of SSA is shown in Algorithm 1. Inspecting the pseudo-code, it can be seen that SSA starts the optimization process by initializing a population of random solutions (salps). It then evaluates each salp and the best salp in the population is denoted as F to be chased by the salp chain as demonstrated in Fig. 1. In the meantime, the variable c_1 is updated using Eq. 3. Equation 2 is used to update the leader's position, while Eq. 4 is utilized to update the location of the followers. Until the satisfaction of the stopping criterion, all the above steps except initialization are repeated.

3.1. Binary SSA (BSSA)

The SSA algorithm was originally designed to solve problems with continuous variables. Due to the nature of FS problems, the salps in SSA are supposed to move in restricted directions in the binary space (0 and 1 values). One of the popular methods to convert a continuous optimizer to suit binary problems is to use transfer functions (TF) [53]. The purpose of TF is to define a probability of updating an element in the feature subset (solution)

6

Algorithm 1 Pseudo-code of the SSA algorithm

Initialize the salp population $x_i(i = 1, 2, \ldots, n)$
while (end condition is not satisfied) **do**
    Calculate the fitness of each salp
    Set **F** as the best search agent
    Update c_1 by Eq. 3
    for (each salp (x_i)) **do**
        if $(i == 1)$ **then**
            Update the leader's position by Eq. 2
        else
            Update the follower's position by Eq. 4
    Update the salps based on the upper and lower bounds of variables
Return **F**
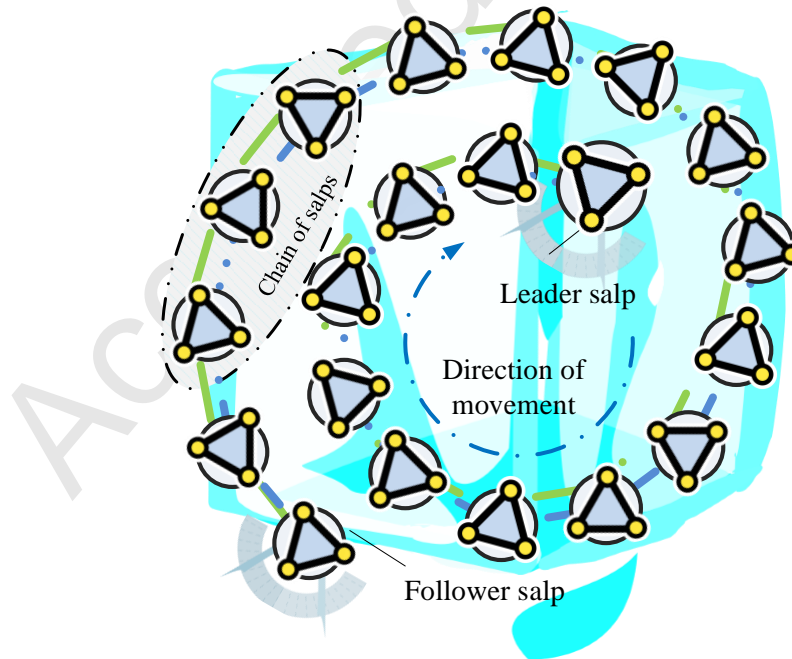
Figure 1: A depiction of the salp chain

7

to be 1 (selected) or 0 (not selected). Kennedy and Eberhart [38] proposed a TF to convert the continuous version of PSO to a discrete version as in Eq. 5.

$$T(x_j^i(t)) = \frac{1}{1 + \exp^{-x_j^i(t)}} \tag{5}$$

where x_j^i is the jth element in solution x in the jth dimension, and t is the current iteration

Depending on the produced probability from Eq. 5 a solution's element in the next iteration can be updated using Eq. 6

$$x_i^k(t+1) = \begin{cases} 0 & \text{If } rand < T(x_i^k(t+1)) \\ 1 & \text{If } rand \geq T(x_i^k(t+1)) \end{cases} \tag{6}$$

where $x_i^d(t+1)$ is the $i-th$ element at d^{th} dimension in x solution. This function is depicted in Fig. 2.
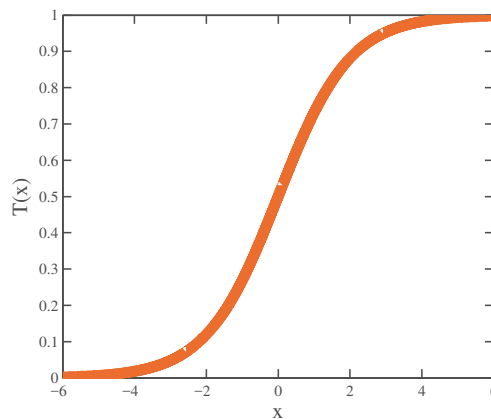
Figure 2: Transfer Function.

4. The Proposed Approach

Population-based metaheuristics divide the search for the global optima into two phases, exploration (diversification) and exploitation (intensification). In exploration phase, the optimizer tries to explore the search space as much as possible in the hope to find more promising regions, while in the exploitation it tries to dig the neighborhood area of a specific solution in the hope of finding the global minimum. To avoid stagnation at the local minimum, the optimizer allows more exploration in the first stages of the optimization process, while in the later stages, more exploitation is allowed.

In the basic SSA, there is only one leader, who is responsible for exploiting the neighborhood of the best solution (F), while the other $N-1$ individuals in the population (followers) are used to explore the search space. This mechanism might drive other salps toward locally optimal solutions when solving high-dimensional problems with a large number of local optima. This drawback motivated our attempt to divide the population into multiple sub-swarms with different leading salps to achieve more balance between exploration and

8

Table 1: Updating strategies

Algorithm	Chain	Updating formula for c_1
TCSSA1	Sub-chain1	$(-2.05t/T) + 2.55$
	Sub-chain2	$(-2.05t/T) + 2.55$
	Sub-chain3	$(-2t^3/T^3) + 2.5$
	Sub-chain4	$(-2t^3/T^3) + 2.5$
TCSSA2	Sub-chain1	$2.5 + 2(t/T)^2 - 2(2t/T)$
	Sub-chain2	$0.5 + 2\exp[-(4t/T)^2]$
	Sub-chain3	$(-2t^3/T^3) + 2.5$
	Sub-chain4	$2.5 - (2\log(t)/\log(T))$
TCSSA3	Sub-chain1	$1.95 - 2t^{1/3}/T^{1/3}$
	Sub-chain2	$1.95 - 2t^{1/3}/T^{1/3}$
	Sub-chain3	$(-2t^3/T^3) + 2.5$
	Sub-chain4	$(-2t^3/T^3) + 2.5$

exploitation. In this work, extensive experiments are conducted to set the best number of leaders that may lead to better performance than the basic SSA.

In the basic SSA, all salps behave the same and considered as one group, and one strategy is employed to update their positions. Theoretically, dividing the salps in SSA into many subgroups (sub-chains) with the same target (finding the best solution) could result in enhancing the efficiency of the SSA in exploration and exploitation phases, simultaneously. In this paper, different strategies are utilized for updating the c_1 parameter to make a more stable balance between the global and local search.

4.1. Updating strategies

In this paper, several strategies with different behaviors are utilized for updating the c_1 parameter in SSA. In each strategy, different functions with different properties (i.e., slopes, curvatures, and interception points) are employed to investigate their influence on the performance of SSA. Those functions are reported in Table 1, where T represents the max number of iterations and t shows the current iteration. These functions consist of descending linear and polynomial, as well as exponential and logarithmic functions and their mathematical behaviors can be seen in Fig. 3. As may be observed in Fig. 3, c_1 is decreased over the iterations. It is clear that salps tend to have higher global search capability at the beginning of the optimization when c_1 values are close to the upper limit (2), while more local search capability is allowed at the final stages. The basic idea of dividing the salp chain into four sub-chains is inspired from the behavior of termite colonies in exploring/exploiting the search space. Thus, three different versions of the SSA are proposed in this paper, which were named as TCSSA1, TCSSA2, and TCSSA3.

As it can be seen, in the TCSSA1 algorithm, two linear relations are utilized for group 1, in addition to linear and cubic rules for the next strategies, and 2 cubic rules for the third strategy. The TCSSA2 variant employs logarithmic, cubic, exponential, and quadratic rules for its strategies. These rules can generate different exploratory and exploitative temporal patterns that can be changed during the searching period. For example, salps that use rule

9
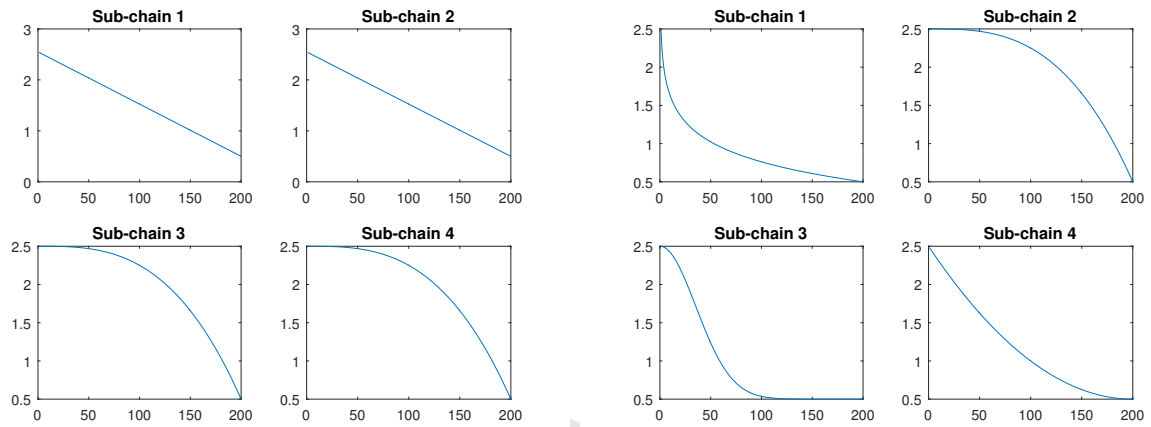
(a) TCSSA1 chains

(b) TCSSA2 chains
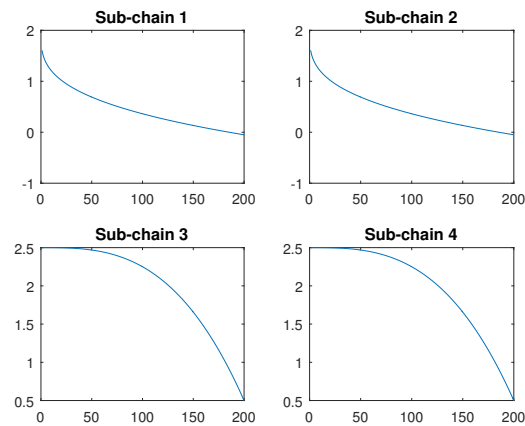
(c) TCSSA3 chains

Figure 3: Mathematical equations of the employed autonomous chains for updating c_1 coefficient

10

1 in the TCSSA2 version tend to switch the exploration and exploitation tendencies earlier than salps use rule 2. The TCSSA3 also utilizes a series of principal third root and cubic rules for updating its behaviors. In SSA with dynamic updating strategies (TCSSA) (see Fig. 4), first, a set of salps is randomly generated in the problem search space to initialize the population. After that, the particles are randomly divided into some predefined autonomous groups. At each iteration, the fitness value of each salp is calculated and the minimum value is denoted as F. For each salp, the parameter c_1 is updated using one of the four updating strategies. After calculating the c_1 value, the positions of salps will be updated using Eqs. 2 and 4. Then, the leader's location (produced from 2) is converted to binary using Eqs. 5 and 6. Algorithm 2 shows the pseudo-code of the proposed TCSSA.
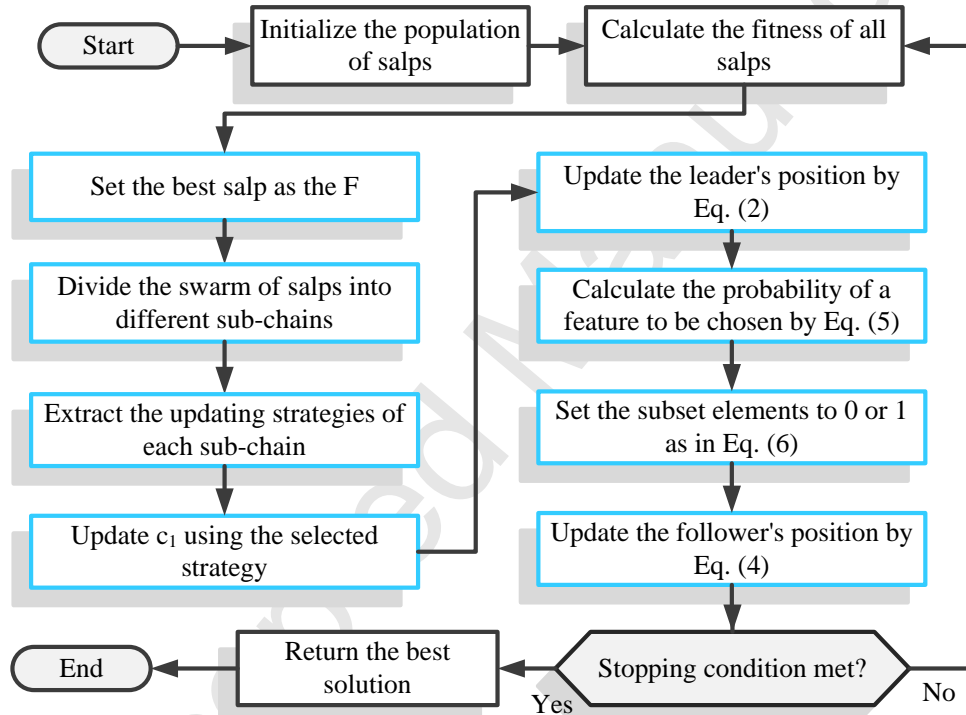
Figure 4: Flowchart of the proposed TCSSA algorithm

4.2. The proposed SSA for FS problems

The proposed wrapper-based FS technique utilizes the SSA-based algorithm as the searching process and k-NN classifier as an evaluator. We first investigated the best number of leaders, and we found that using half of the population ($N/2$) as leaders and the remaining salps as followers leads to the best performance of the algorithm, thus BSSA uses $N/2$ salps as leaders in all experiments. Then, three different updating strategies were used to adaptively update the c_1 parameter in BSSA, namely TCSSA1, TCSSA2, TCSSA3. To design the objective function of the FS task, two main points should be addressed initially: how to model the solutions and how to assess them.

In this paper, a feature subset is modeled as a binary vector. The length of this vector is equal to the number of features in the problem. When the feature is selected, the value is

11

Algorithm 2 Pseudo-code of the modified SSA algorithm

Initialize the salp population $x_i(i = 1, 2, \ldots, n)$ considering ub and lb

while (stopping condition is not met) **do**

    Calculate the fitness of each salp

    Set **F** as the best search agent

    Divide the population of salps into different sub-chains

    for (each salp (x_i)) **do**

        if $(i \leq N/2)$ **then**

            Extract the updating strategies of salps

            Update c_1 using the selected strategy

            Update the leader's position by Eq. 2

            Calculate the probability of a feature to be

            selected using Eq. 5

            Set the subset elements to 0 or 1 as in Eq. 6

        else

            Update the follower's position by Eq. 4

Return **F**

1; otherwise, it is assigned by 0. Two criteria are utilized to judge the excellence of a feature subset: the minimum inaccuracy rate (maximum classification accuracy) and the minimum number of selected features. These oppose objectives are assembled in the form of a fitness function. This function is demonstrated in Eq. 7:

$$\downarrow Fitness = \alpha \gamma_R(D) + \beta \frac{|R|}{|C|} \tag{7}$$

where $\gamma_R(D)$ shows the classification error value of the classifier, $|R|$ is the number of selected features in a reduct, and $|C|$ is the number of conditional features in the dataset, and $\alpha \in [1, 0]$, $\beta = (1 - \alpha)$ are factors to show the prominence of quality and subset length based on the observation and recommendations in [16].

5. Experimental Results and Discussion

This section summarizes the results of the proposed SSA with dynamic updating strategies for different feature selection datasets.

Data Sets: Table 3 shows the details of 20 well-regarded data sets that have been utilized in this work to evaluate the efficiencies of algorithms. This set of problems from UCI repository [40] covers a large variety of characteristics with different features and instances.

Experiment settings: An initial empirical study is presented to assess the influence of both α and β on the performance of the proposed approach. Different values for α and β were used to measure the fitness, accuracy, and reduction rates to locate the best combination. Colon dataset sample was used in all experiments. Table 2 shows the accuracy, fitness, and reduction rates with different combinations of α and β values.

Inspecting the results in Table 2, it can be seen that accuracy rate and fitness, and reduction rates are changing with the different values of α and β, and the best results are

12

obtained when $\alpha = 0.99$ and $\beta = 0.01$. The study's summary is compatible with the values that are commonly used in literature as well [67].

Table 2: Impact of α and β on the fitness, accuracy and Red. rate results based on Colon dataset.

α	β	Fitness	Accuracy	Red. rate
0.80	0.20	0.22583	0.83077	43.08961
0.60	0.40	0.29625	0.76154	45.76281
0.40	0.60	0.26798	0.80000	44.14000
0.20	0.80	0.28612	0.80000	44.26250
0.99	0.01	**0.15633**	**0.84615**	**46.04657**
0.96	0.04	0.16108	0.84615	44.77375
0.93	0.07	0.24922	0.76923	43.22441

For comparisons, we used three different optimizers: Binary Gravitational Search Algorithm (BGSA), Binary Bat Algorithm (BBA), and binary Grey Wolf Optimizer (bGWO). The details of parameters of these optimizers are outlined in Table 4. The values have been selected based on both some initial simulations and previous researches. The proposed algorithms are evaluated to determine the superior reduct according to the error values of KNN classifier having a Euclidean distance measure ($K = 5$ [16]). To study the optimality of the solutions and validate the exploration and exploitation tendencies of optimizers, 80% of instances in every case were employed for training and the rest of them was used for testing stage [25].

System details: All results are computed in a same condition using MATLAB 2013 and a system with Intel Core(TM) i5-5200U 2.2GHz CPU and 4.0GB RAM.

Table 3: List of used datasets

No.	Dataset	No. of Features	No. of instances
1.	Exactly	13	1000
2.	Exactly2	13	1000
3.	HeartEW	13	270
4.	Lymphography	18	148
5.	M-of-n	13	1000
6.	PenglungEW	325	73
7.	SonarEW	60	208
8.	SpectEW	22	267
9.	CongressEW	16	435
10.	IonosphereEW	34	351
11.	KrvskpEW	36	3196
12.	Tic-tac-toe	9	958
13.	Vote	16	300
14.	WaveformEW	40	5000
15.	WineEW	13	178
16.	Zoo	16	101
17.	Clean1	166	476
18.	Semeion	265	1593
19.	Colon	2000	62
20.	Leukemia	7129	72

13

Table 4: Parameter settings

Parameter	Value
Population size	10
Number of iteration	100
Dimension	Number of features
Number of runs for each technique	30
α in fitness function	0.99
β in fitness function	0.01
a in GWO	[2 0]
Q_{min} Frequency minimum in BBA	0
Q_{max} Frequency maximum in BBA	2
A Loudness in BBA	0.5
r Pulse rate in BBA	0.5
G_0 in GSA	100
α in GSA	20

Results and discussion: Table 5 compares the average fitness results of BSSA with different number of leaders from $N/2$ to $N/10$. Based on the Friedman non-parametric statistical test (F-test) results, we found that using $N/2$ salps as the leaders of other individuals results in obtaining more promising solutions for BSSA compared to other alternatives. The average accuracy and feature reduction rates of the BSSA with different number of leaders when $N=10$ are demonstrated and compared graphically in Fig. 5. Figure 5 displays a color representation (Heatmap) of the values of accuracy, reduction rate, and number of leaders, and F-test ranking over all datasets. Using these abstract graphical representations, several algorithms can be simultaneously judged in terms of different metrics.

As per accuracy results in Fig. 5a and in accordance with the reflected results in Table 5, for majority of datasets such as M-of-n, Exactly, and Semeion, the version with $N/2$ leaders has been colored by lighter degrees, which reveals the superiority of the BSSA with $N/2$ salps compared to other versions. According to the ranking results (F-test) reported in the top of Fig. 5a, the BSSA with $N/2$ salps has attained higher accuracies and as a result, it has obtained the best place among other versions. The reason of these observations is that the multi-leader structure with $N/2$ salps has effectively extended the exploitative searching patterns of the BSSA; hence, it can show a successful performance in balancing the exploration and exploitation tendencies and jumping out of LO, whereas the other variants with different number of leaders still were susceptible to LO stagnation.

According to the reduction rates exposed in Fig. 5b, it is observed that they are scattered between 30% to 50% for the majority of datasets, and those values have been colored by lighter degrees. The F-test ranking of the reduction rate results of the BSSA with $N/6$ salps, $N/3$ salps, and $N/2$ salps are close to each other. It is detected that different variants reveal a competitive efficacy and the distribution of colors cannot indicate a great gap between the rates of different alternatives. As a summary, the proposed approach considers both objectives (accuracy and feature reduction rate), to compromise between those two objectives, each objective has an impact level by setting α and β coefficients. Since we are interested in the accuracy objective ($\alpha=0.99$) much higher than the reduction rates ($\beta=0.01$), we chose the appropriate number of leaders ($N/2$) based on the F-test ranking of the accuracy results.

The average convergence performances of different BSSA versions with different number

14

of leaders are demonstrated in Fig. 6. From Fig. 6, it can be observed that the convergence behaviors of BSSA with $N/2$ salps are more accelerated than other variants for Exactly, Lymphography, M-of-n, SpectEW, CongressEW, KrvskpEW, and WaveformEW, which is consistent with the results in Table 5. The dissimilarities of the acceleration values in the experimented curves also reveal the substantial impact the number of leading salps on the quality of the selected features.

In this regard, and according to the main metrics such as classification accuracy and fitness results, the version with $N/2$ salps as the leaders of swarm is adopted as the basic SSA approach (called BSSA), and considered as the base of the new improvements (using different updating strategies). Thus, the performance of BSSA is compared in terms of classification accuracy, fitness, and reduction rate (Red. Rate) to the binary algorithms with varied updating strategies in Table 6. From Table 6, it can be realized that the best optimizer in terms of accuracy and fitness measures is the TCSSA3. Based on the observed reduction rates, the best variants are the TCSSA1, TCSSA2, TCSSA3, and BSSA, respectively. Based on accuracy, the TCSSA3 can dominate other versions in dealing with 60% of datasets. It returns superior costs with acceptable STD values in the majority of cases. With regard to fitness values, it is superior to other techniques on the majority of problems. For Leukemia dataset, which has the highest number of features compared to other cases, the TCSSA3 algorithm has revealed the maximum accuracy 95.09 % and lowest fitness results indicating the advanced explorative and exploitative capacities of this version. According to the overall ranks, the TCSSA3 can be chosen as the peak method in terms of the main metrics. In addition, Table 7, Table 8, and Table 9 show a sample of the actual selected features with their frequency of ten runs for Exactly, SpectEW, and Zoo datasets.

The comparison of convergence rates is also provided in Fig. 7. From Fig. 7, it can be seen that for 55% of datasets, the TCSSA3 algorithm outperforms other versions in terms of fitness and accuracy, the convergence rate is also superior, and for the rest of cases, it has a competitive speed compared to the TCSSA1, which was also observed in Table 6. The results evidently show that the characteristics of the updating strategies can affect the exploratory and exploitative patterns SSA. The combination of exploratory and exploitative behaviors in the TCSSA3 can prevent salps from stagnation in locally optimal solutions. Hence, we can recognize a better efficacy of the TCSSA3 with the third group. Individual salps in the TCSSA3 can still strengthen the exploratory propensities even in the latter steps; enable it in avoiding the local optima (LO) and immature convergence drawbacks.

Table 10 compares the efficacy of TCSSA1 and TCSSA3 in terms of average and STD of measured metrics (i.e., fitness, accuracy and reduction rate) to those of other state-of-the-art techniques (i.e., bGWO, BGSA, and BBA). It is worth mentioning that those methods were implemented with the same parameter settings of BSSA based approaches (see Table 4), and used for comparison purposes. From Table 10, we can see that the performance of the proposed approaches in terms of average accuracy and fitness values are better than all other algorithms in 95% of datasets, where TCSSA1 obtained the best results in six datasets and TCSSA3 outperformed others in 14 datasets. Based on reduction rates, we observed that the BBA can slightly outperform other competitors.

Regarding the average accuracies, it can be observed that the TCSSA3 has reached to higher levels than 95% on Exactly, M-of-n, CongressEW, KrvskpEW, Vote, WineEW, Zoo, semeion, and Leukemia problems, while the second-best optimizer, bGWO, goes higher than

15

Table 5: The obtained results of the BSSA with different number of leaders based on average fitness results

Benchmark	Metric	N/2	N/3	N/4	N/5	N/6	N/7	N/8	N/9	N/10
Exactly	AVG	**0.02278**	0.02605	0.04884	0.04999	0.09631	0.06280	0.08858	0.11940	0.06850
	STD	0.02347	0.02262	0.04951	0.04625	0.07236	0.05025	0.06541	0.06821	0.04865
Exactly2	AVG	0.26964	0.29285	**0.24746**	0.28074	0.26787	0.27260	0.28357	0.26553	0.28382
	STD	0.00656	0.01704	0.01723	0.00777	0.02501	0.01097	0.00984	0.01658	0.00453
HeartEW	AVG	0.19466	0.19021	0.18614	0.16391	0.18094	0.20737	0.19184	**0.16268**	0.19888
	STD	0.00726	0.01057	0.00482	0.00618	0.00826	0.01117	0.01393	0.00747	0.01305
Lymphography	AVG	**0.13389**	0.16853	0.14983	0.15280	0.18755	0.19333	0.18821	0.14600	0.13912
	STD	0.00830	0.01068	0.01371	0.01918	0.01654	0.02064	0.01672	0.02378	0.02176
M-of-n	AVG	**0.00899**	0.02217	0.02558	0.04083	0.03812	0.04283	0.04581	0.04551	0.04857
	STD	0.00830	0.01511	0.02208	0.02878	0.03396	0.03067	0.02859	0.03267	0.02848
penglungEW	AVG	0.11125	0.19665	**0.06036**	0.22641	0.07693	0.10046	0.14550	0.27286	0.11881
	STD	0.00523	0.00761	0.00490	0.01115	0.01219	0.01682	0.01108	0.01211	0.01467
SonarEW	AVG	0.11559	0.10579	0.11965	0.11157	0.17110	**0.10019**	0.13206	0.13779	0.14074
	STD	0.01041	0.01085	0.00975	0.01060	0.01285	0.01301	0.01340	0.01104	0.00742
SpectEW	AVG	**0.13271**	0.19108	0.19959	0.18274	0.18294	0.19102	0.17342	0.18982	0.17172
	STD	0.00884	0.00763	0.00823	0.01166	0.01024	0.00885	0.00953	0.01203	0.01502
CongressEW	AVG	**0.03243**	0.05330	0.06819	0.04078	0.06177	0.04553	0.04607	0.03459	0.05146
	STD	0.00473	0.00475	0.00601	0.00566	0.00612	0.00823	0.00589	0.00540	0.00847
IonosphereEW	AVG	0.09549	0.12779	0.11092	0.10051	0.08622	0.11842	**0.07252**	0.08248	0.12242
	STD	0.00775	0.01014	0.00741	0.00484	0.00627	0.00601	0.00655	0.00948	0.00813
KrvskpEW	AVG	**0.04130**	0.05014	0.05228	0.05310	0.05286	0.05089	0.05409	0.04738	0.04608
	STD	0.00526	0.00532	0.00700	0.00702	0.00698	0.00756	0.00711	0.00623	0.00664
Tic-tac-toe	AVG	0.22161	0.20732	0.21500	0.22899	0.21483	**0.20415**	0.22065	0.22114	0.21756
	STD	0.00000	0.00093	0.00477	0.00545	0.01159	0.00595	0.00501	0.00181	0.00665
Vote	AVG	0.05735	0.04847	0.04629	0.05753	0.06864	0.05592	0.04595	0.06721	**0.03806**
	STD	0.00605	0.00538	0.00574	0.00722	0.00668	0.00507	0.00454	0.00571	0.00675
WaveformEW	AVG	**0.26614**	0.27395	0.26713	0.26860	0.27323	0.28225	0.27301	0.27331	0.27360
	STD	0.00587	0.00510	0.00609	0.00504	0.00601	0.00554	0.00471	0.00503	0.00543
WineEW	AVG	0.04276	0.04857	0.01923	0.03019	**0.01294**	0.01351	0.02981	0.01374	0.03633
	STD	0.00387	0.00708	0.00039	0.00776	0.00693	0.00729	0.00083	0.00581	0.00811
Zoo	AVG	0.04376	**0.01257**	0.02057	0.02593	0.12093	0.04339	0.02464	0.06376	0.05092
	STD	0.00055	0.00909	0.00845	0.00092	0.00083	0.00072	0.00062	0.00070	0.00934
clean1	AVG	0.15544	0.14682	0.11538	0.13175	0.15706	0.10596	0.13619	**0.10028**	0.12149
	STD	0.00572	0.00530	0.00616	0.00725	0.01131	0.00856	0.00624	0.00875	0.00803
semeion	AVG	0.02385	**0.02249**	0.03313	0.02872	0.02804	0.02982	0.03108	0.02773	0.03807
	STD	0.00109	0.00159	0.00172	0.00159	0.00152	0.00253	0.00178	0.00163	0.00196
Colon	AVG	0.27648	0.34235	0.32776	0.41346	**0.13261**	0.35391	0.24054	0.32739	0.30188
	STD	0.01807	0.01962	0.01765	0.01349	0.00095	0.00563	0.01518	0.00968	0.02062
Leukemia	AVG	0.13811	**0.03419**	0.14084	0.07819	0.16191	0.15884	0.11704	0.15511	0.10072
	STD	0.01007	0.00664	0.01581	0.01612	0.02303	0.01330	0.02025	0.01717	0.01331
W|T|L		**7|0|13**	3|0|17	2|0|18	0|0|20	2|0|18	2|0|18	1|0|19	2|0|18	1|0|19
F-Test		**3.8**	5.05	4.45	5.15	5.45	5.35	5.25	4.95	5.55

16

(a) Accuracy Results

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(b) Feature Reduction Rates
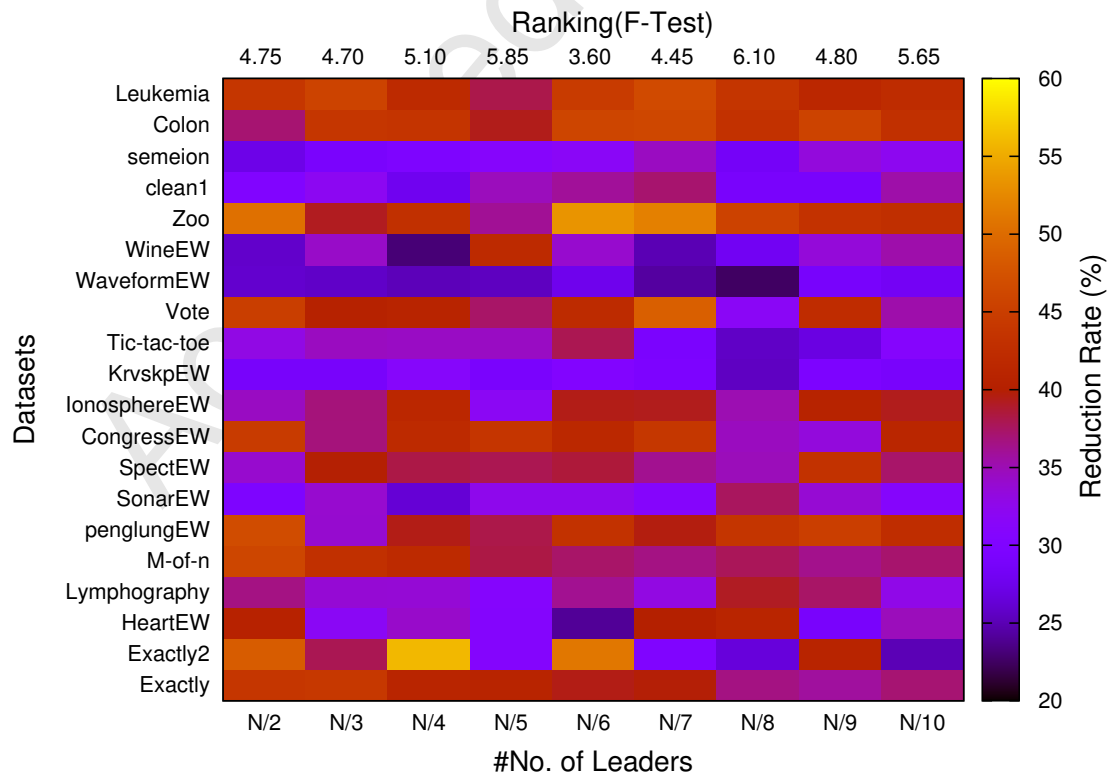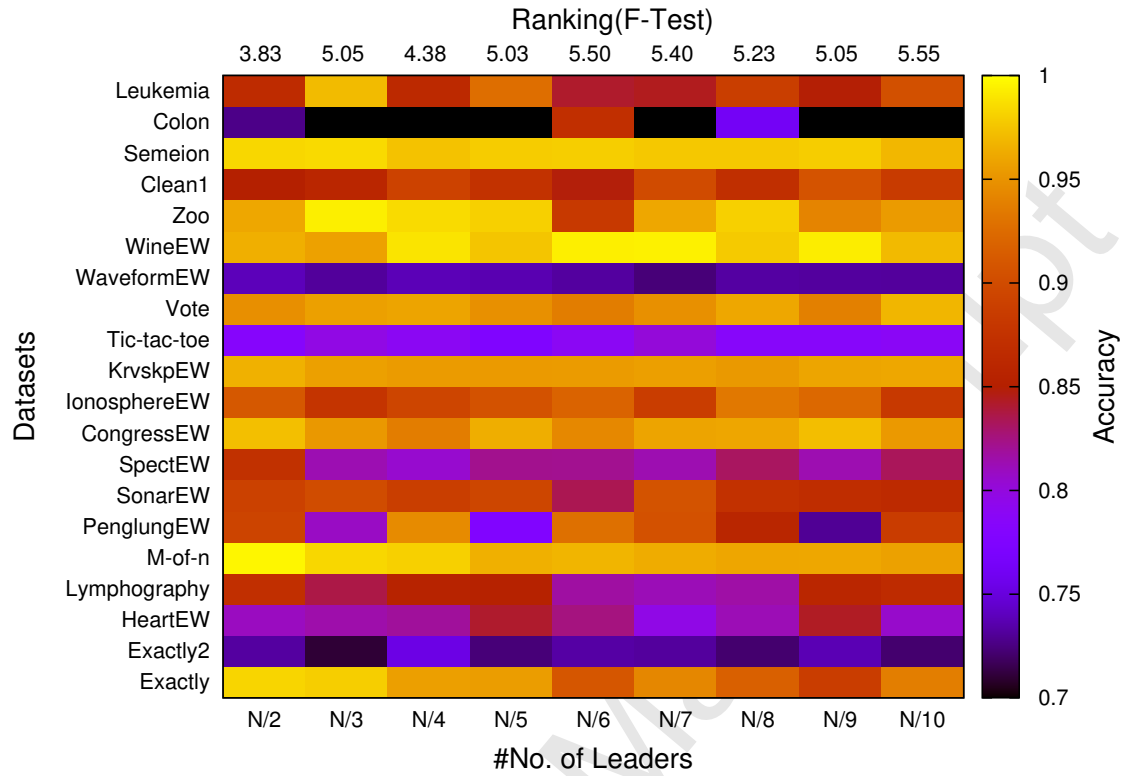
Figure 5: Accuracy and Feature reduction rates of the BSSA with different number of leaders, where N=10.

17

(a) Exactly   (b) Exactly2   (c) HeartEW   (d) Lymphography

(e) M-of-n   (f) penglungEW   (g) SonarEW   (h) SpectEW

(i) CongressEW   (j) IonosphereEW   (k) KrvskpEW   (l) Tic-tac-toe

(m) Vote   (n) WaveformEW   (o) WineEW   (p) Zoo

(q) Clean1   (r) Semeion   (s) Colon   (t) Leukemia
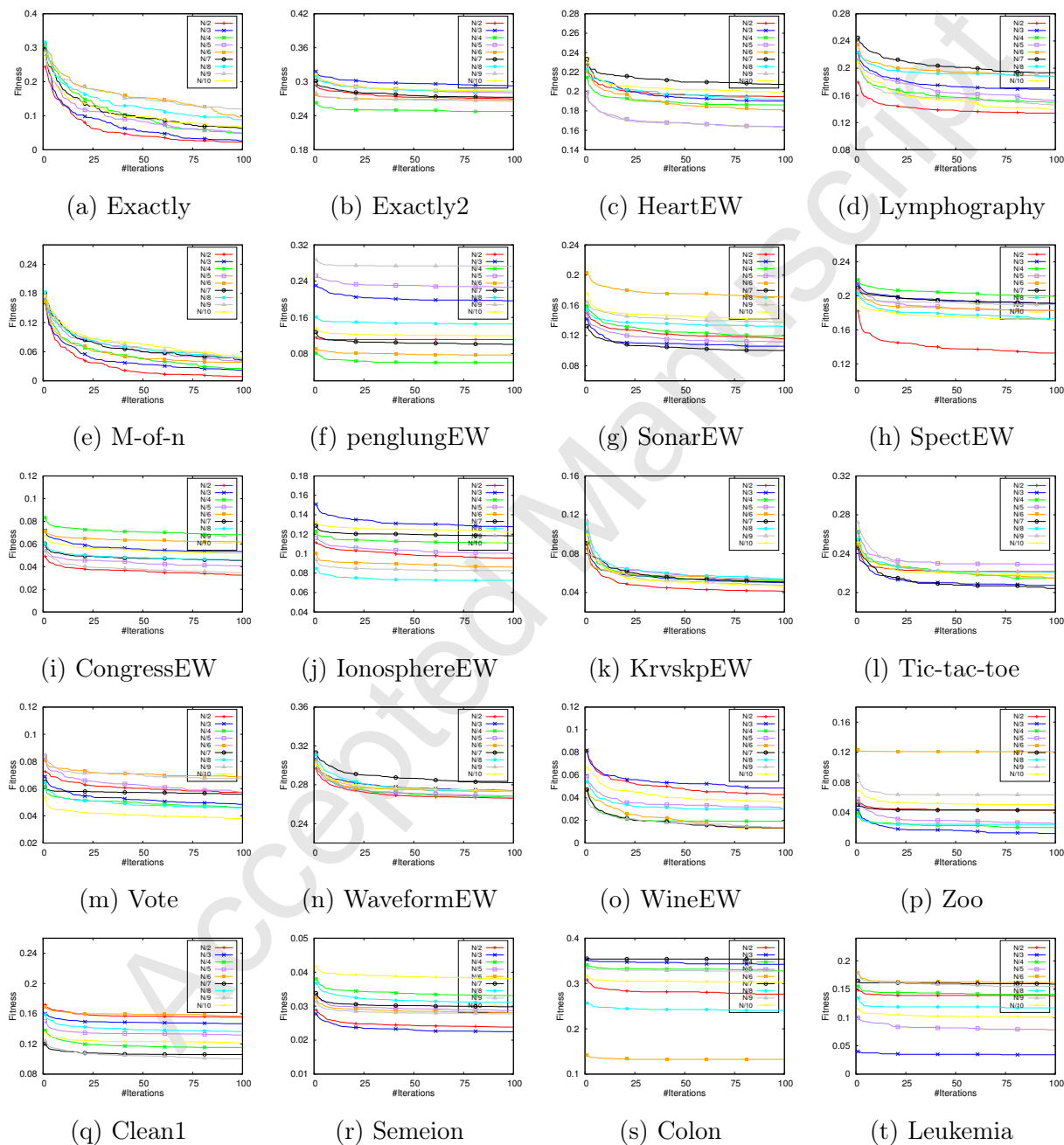
Figure 6: Convergence curves for BSSA with different number of leaders for all benchmark datasets.

18

0.95% only on three cases studies: semeion, Zoo, and WineEW datasets. However, in these cases, the classification rates of TCSSA3 are still higher than those of the bGWO. The average convergence speeds of different techniques can also be seen in Fig. 8. It can be detected that the TCSSA3 is capable of dominating other optimizers in the convergence accelerations on 18 datasets.

The main reason for the improved convergences and results is that the updating strategies in the TCSSA3 and the designed leadership structure can assist the binary algorithm in making a good balance between the exploratory and exploitative propensities. The faster convergence is due to the improved exploratory and exploitative capabilities of the TCSSA3 in exploiting the neighborhood of some leaders, while other leaders can travel to other fruitful regions of the feature space. As the results, SSA can discover better solutions quicker than other competitors. The notable improvements in the results have been achieved just by distributing the salp agents to a number of asynchronous cooperative teams by a variety of updating patterns instead of a single formulation for the main parameter in the SSA.

In Table 11, the average running time for the best TCSSA versions (i.e TCSSA1 and TCSSA3), bGWO, BGSA, and BBA is reported for each dataset. It can be seen that TCSSA3 is very competitive with the fastest algorithm which is BGSA. TCSSA3 has the second rank after BGSA over all datasets. This slight run time overhead in TCSSA variants is due to the incorporated mechanisms of updating rules and the new leadership structure.

19

Table 6: The results of the proposed BSSA with different updating approaches

Benchmark	Metric	BSSA			TCSSA1			TCSSA2			TCSSA3		
		Fitness	Accuracy	Red. Rate	Fitness	Accuracy	Red. Rate	Fitness	Accuracy	Red. Rate	Fitness	Accuracy	Red. Rate
Exactly	AVG	0.02278	0.98253	43.88995	0.00881	0.99633	48.20513	**0.00643**	**0.99873**	48.20513	0.00811	0.99693	**49.23077**
	STD	0.02347	0.02323	7.38679	0.00880	0.00860	4.48686	0.00567	0.00552	4.00639	0.00404	0.00381	3.83287
Exactly2	AVG	0.26964	0.73240	48.43495	0.24397	0.75973	38.97436	0.27167	0.73227	33.84615	**0.23355**	**0.76720**	**69.23077**
	STD	0.00656	0.00620	12.21012	0.00311	0.00146	26.71831	0.00448	0.00435	5.92409	0.01406	0.01241	21.18698
HeartEW	AVG	0.19466	0.80938	40.51164	0.17317	0.83111	40.25641	0.18855	0.81457	**50.25641**	**0.17253**	**0.83309**	27.17949
	STD	0.00726	0.00699	6.88479	0.00530	0.00492	7.74078	0.01040	0.00962	12.24342	0.00715	0.00747	10.04648
Lymphography	AVG	**0.13389**	**0.87117**	36.54285	0.13901	0.86486	**47.77778**	0.16338	0.84279	22.59259	0.16069	0.84437	33.88889
	STD	0.00830	0.00850	7.89841	0.01339	0.01328	11.35742	0.00957	0.00971	4.36064	0.00812	0.00851	7.62996
M-of-n	AVG	0.00899	0.99633	45.95979	0.00708	0.99827	46.41026	0.00590	0.99907	50.25641	**0.00589**	**0.99920**	48.97436
	STD	0.00830	0.00812	4.44349	0.00370	0.00339	4.73037	0.00515	0.00511	3.90320	0.00332	0.00304	4.73037
penglungEW	AVG	0.11125	0.89279	**46.67115**	**0.08634**	**0.91892**	39.27179	0.08650	0.91885	38.45128	0.09777	0.90721	40.93333
	STD	0.00523	0.00493	5.25327	0.01380	0.01420	5.22264	0.00966	0.01005	5.85507	0.01643	0.01692	6.76753
SonarEW	AVG	0.11559	0.89039	29.70496	0.07546	0.93045	**34.00000**	0.07235	0.93365	33.33333	**0.05859**	**0.94808**	28.16667
	STD	0.01041	0.01059	6.66712	0.00812	0.00825	5.94676	0.01047	0.01052	6.94808	0.00577	0.00597	5.94273
SpectEW	AVG	0.13271	0.87264	34.03079	0.17891	0.82537	39.69697	**0.13190**	**0.87289**	39.39394	0.17055	0.83333	**44.54545**
	STD	0.00884	0.00875	7.01343	0.00760	0.00798	8.51911	0.01171	0.01151	11.53219	0.00712	0.00715	7.20185
CongressEW	AVG	**0.03243**	**0.97263**	44.51875	0.04220	0.96223	**51.87500**	0.03246	0.97232	49.37500	0.03419	0.97049	50.20833
	STD	0.00473	0.00458	8.02875	0.00421	0.00375	12.72957	0.00472	0.00458	8.26390	0.00473	0.00462	6.66375
IonosphereEW	AVG	0.09549	0.91004	34.48902	0.12898	0.87519	**45.78431**	0.10324	0.90133	44.50980	**0.06776**	**0.93769**	39.31373
	STD	0.00775	0.00805	8.28840	0.00936	0.00913	8.89703	0.00842	0.00850	7.97971	0.00542	0.00527	11.01797
KrvskpEW	AVG	0.04130	0.96554	28.79408	0.04410	0.96197	**35.46296**	0.04147	0.96510	30.83333	**0.03747**	**0.96923**	29.90741
	STD	0.00526	0.00523	4.17537	0.00563	0.00566	4.98419	0.00378	0.00381	6.41569	0.00470	0.00460	5.72925
Tic-tac-toe	AVG	0.22161	0.78288	32.95411	**0.20604**	**0.79749**	44.44444	0.22257	0.78079	**44.44444**	0.20826	0.79749	22.22222
	STD	0.00000	0.00000	2.02751	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000
Vote	AVG	0.05735	0.94733	44.93523	0.05840	0.94667	43.95833	0.06007	0.94422	**51.45833**	**0.05037**	**0.95489**	42.91667
	STD	0.00605	0.00590	9.91560	0.00661	0.00655	14.81598	0.00523	0.00567	12.78588	0.00435	0.00417	8.32615
WaveformEW	AVG	0.26614	**0.73893**	25.98109	**0.26579**	0.73852	**30.75000**	0.26619	0.73835	28.50000	0.26795	0.73643	29.83333
	STD	0.00587	0.00547	6.96457	0.00498	0.00498	6.05827	0.00469	0.00462	6.45275	0.00407	0.00406	7.36761
WineEW	AVG	0.04276	0.96442	25.88054	0.01547	0.98914	**52.82051**	0.01419	0.99138	43.33333	**0.00810**	**0.99775**	41.28205
	STD	0.00387	0.00426	4.87576	0.00487	0.00465	8.26350	0.00842	0.00869	7.68789	0.00445	0.00457	6.54067
Zoo	AVG	0.04376	0.96078	**50.43375**	0.07530	0.92941	45.83333	0.04965	0.95490	50.00000	**0.01251**	**0.99281**	46.04167
	STD	0.00055	0.00000	5.65014	0.00892	0.00977	10.16212	0.00870	0.00914	7.34025	0.00905	0.00961	7.60759
clean1	AVG	0.15544	0.85014	30.31798	0.09826	0.90728	**35.26104**	0.12070	0.88515	30.02008	**0.09267**	**0.91359**	28.79518
	STD	0.00572	0.00566	6.87348	0.00526	0.00551	5.72750	0.00500	0.00510	4.82728	0.00558	0.00581	5.34240
semeion	AVG	0.02385	0.98344	27.28256	**0.02146**	**0.98519**	**31.93711**	0.02935	0.97737	30.50314	0.02726	0.97996	25.69811
	STD	0.00109	0.00125	7.08537	0.00127	0.00141	4.62325	0.00157	0.00149	5.34592	0.00151	0.00149	5.15730
Colon	AVG	0.27648	0.72689	37.07359	0.22822	0.77527	42.62167	**0.19582**	**0.80753**	**47.32333**	0.34495	0.65699	46.31833
	STD	0.01807	0.01843	8.24942	0.00578	0.00589	4.29187	0.00569	0.00589	4.04031	0.01519	0.01581	6.69491
Leukemia	AVG	0.13811	0.86574	43.89360	0.09259	0.91204	44.90345	0.11796	0.88704	38.74036	**0.05450**	**0.95092**	40.81919
	STD	0.01007	0.01053	6.57479	0.01016	0.01053	5.71851	0.01403	0.01447	7.49406	0.01140	0.01195	7.36320
W|T|L		2|0|18	3|0|17	2|0|18	4|0|16	11|1|18	9|1|10	3|0|17	3|0|17	4|1|15	11|0|10	11|1|18	3|0|17
F-Test		2.8500	2.8000	2.9500	2.5500	2.6250	**1.9000**	2.7000	2.7000	2.4000	**1.9000**	**1.8750**	2.7500

20

Table 7: The actual features selected by the TCSSA3 algorithm for Exactly dataset (NSF: Number of selected features)

Feature ID	1	2	3	4	5	6	7	8	9	10	11	12	13	NSF
Run 1	1	0	1	0	1	0	1	0	1	0	1	0	0	6
Run 2	1	0	1	0	1	0	1	0	1	0	1	0	0	6
Run 3	1	0	1	0	1	0	1	0	1	0	1	0	0	6
Run 4	1	0	1	0	1	0	1	0	1	0	1	0	0	6
Run 5	1	0	1	0	1	0	1	0	1	0	1	0	0	6
Run 6	1	0	1	0	1	0	1	0	1	0	1	0	0	6
Run 7	1	0	1	0	1	0	1	0	1	0	1	0	0	6
Run 8	1	0	1	0	1	0	1	0	1	0	1	0	0	6
Run 9	1	0	1	0	1	0	1	0	1	0	1	0	0	6
Run 10	1	0	1	0	1	0	1	0	1	0	1	0	0	6
Frequency	**10**	**0**	**10**	**0**	**10**	**0**	**10**	**0**	**10**	**0**	**10**	**0**	**0**	**Avg. [6]**

Table 8: The actual features selected by the TCSSA3 algorithm for SpectEW dataset

Feature ID	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	NSF
Run 1	0	0	0	0	0	0	1	0	0	1	1	0	1	0	0	0	0	1	0	1	1	0	6
Run 2	0	1	0	0	0	0	0	0	0	1	1	0	1	0	0	0	0	1	1	0	1	1	7
Run 3	0	1	0	0	0	1	0	0	0	1	0	0	1	0	0	0	0	0	0	0	1	1	4
Run 4	0	0	0	0	1	0	0	1	0	1	0	0	0	0	0	1	1	0	0	1	1	1	6
Run 5	0	1	0	1	0	0	1	0	1	1	1	0	1	0	0	0	0	1	0	0	1	0	5
Run 6	0	0	0	0	0	1	0	0	0	1	0	0	1	0	0	0	0	0	0	0	1	1	4
Run 7	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	1	0	0	1	1	1	5
Run 8	0	0	1	0	0	0	0	1	0	1	1	0	0	0	0	0	0	0	1	0	1	1	5
Run 9	0	0	0	0	1	0	0	1	0	1	1	0	0	0	0	1	1	1	1	1	1	1	9
Run 10	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	1	0	0	0	1	1	5
Frequency	**0**	**3**	**1**	**1**	**2**	**2**	**2**	**4**	**1**	**10**	**5**	**0**	**6**	**0**	**0**	**2**	**4**	**4**	**3**	**4**	**10**	**8**	**Avg. [5.6]**

Table 9: The actual features selected by the TCSSA3 algorithm for Zoo dataset

Feature ID	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	NSF
Run 1	0	0	0	1	0	1	0	0	1	0	0	0	1	1	0	0	5
Run 2	1	0	0	0	0	1	0	0	1	0	0	0	1	1	0	0	4
Run 3	1	0	0	1	0	1	0	0	1	0	0	0	1	1	0	0	5
Run 4	0	0	0	1	0	1	0	0	1	0	0	0	1	1	0	0	5
Run 5	1	0	0	0	0	1	0	0	1	0	0	0	1	1	0	0	4
Run 6	0	0	0	1	0	1	0	0	1	0	0	0	1	1	0	0	5
Run 7	0	0	1	1	0	1	0	0	1	0	0	0	1	1	0	0	5
Run 8	0	0	0	1	0	1	0	0	1	0	0	0	1	1	0	0	5
Run 9	1	0	0	0	0	1	0	0	1	0	0	0	1	1	0	0	4
Run 10	0	0	0	1	0	1	0	0	1	0	0	0	1	1	0	0	5
Frequency	**4**	**0**	**1**	**7**	**0**	**10**	**0**	**0**	**10**	**0**	**0**	**0**	**10**	**10**	**0**	**0**	**Avg. [4.7]**

21
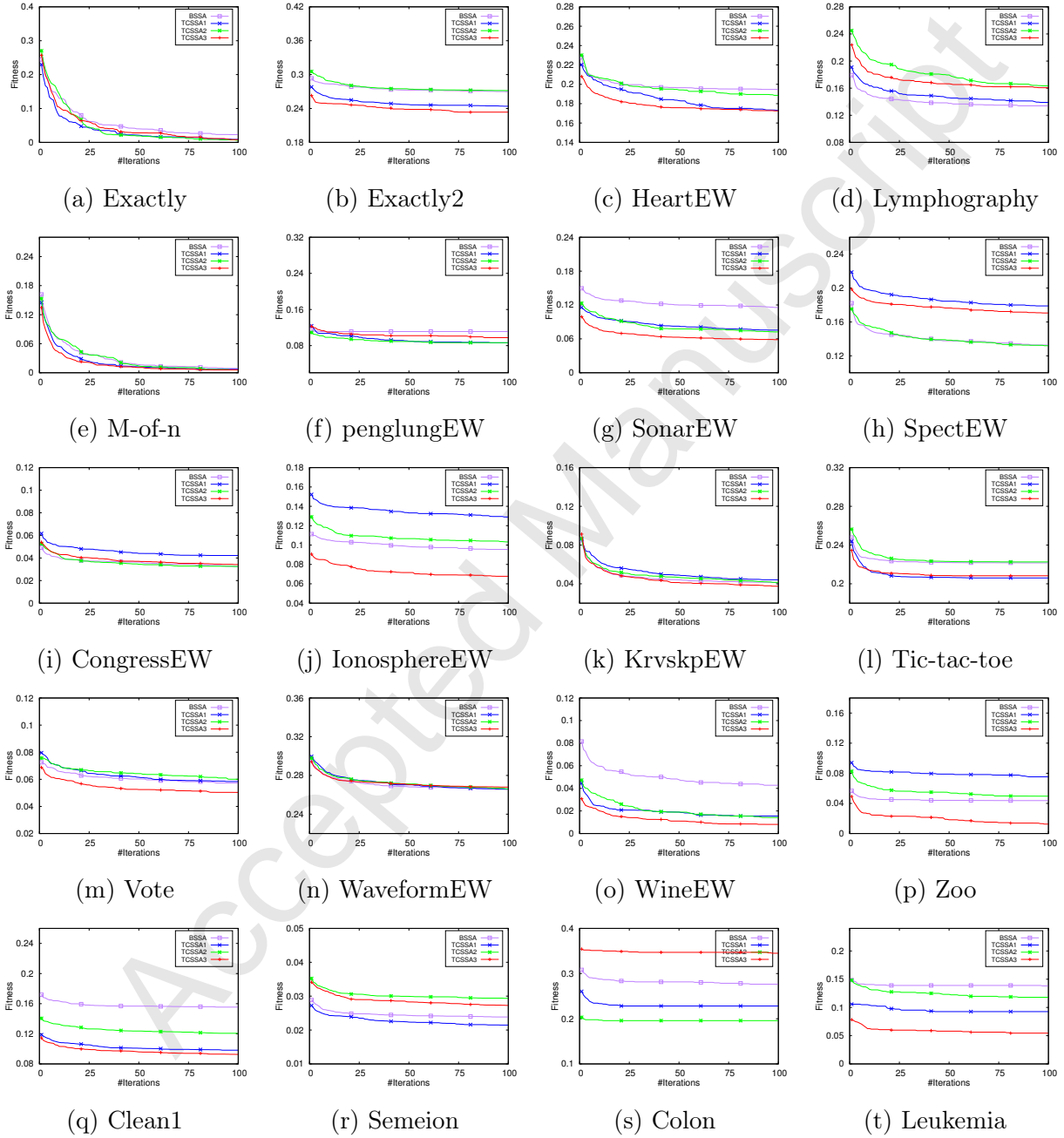
Figure 7: Convergence curves for BSSA with $N/2$ leaders and proposed updating approaches for all benchmark datasets.

22

(a) Exactly   (b) Exactly2   (c) HeartEW   (d) Lymphography

(e) M-of-n   (f) penglungEW   (g) SonarEW   (h) SpectEW

(i) CongressEW   (j) IonosphereEW   (k) KrvskpEW   (l) Tic-tac-toe

(m) Vote   (n) WaveformEW   (o) WineEW   (p) Zoo

(q) Clean1   (r) Semeion   (s) Colon   (t) Leukemia

Figure 8: Convergence curves for BSSA and other state-of-art methods for all benchmark datasets.

23

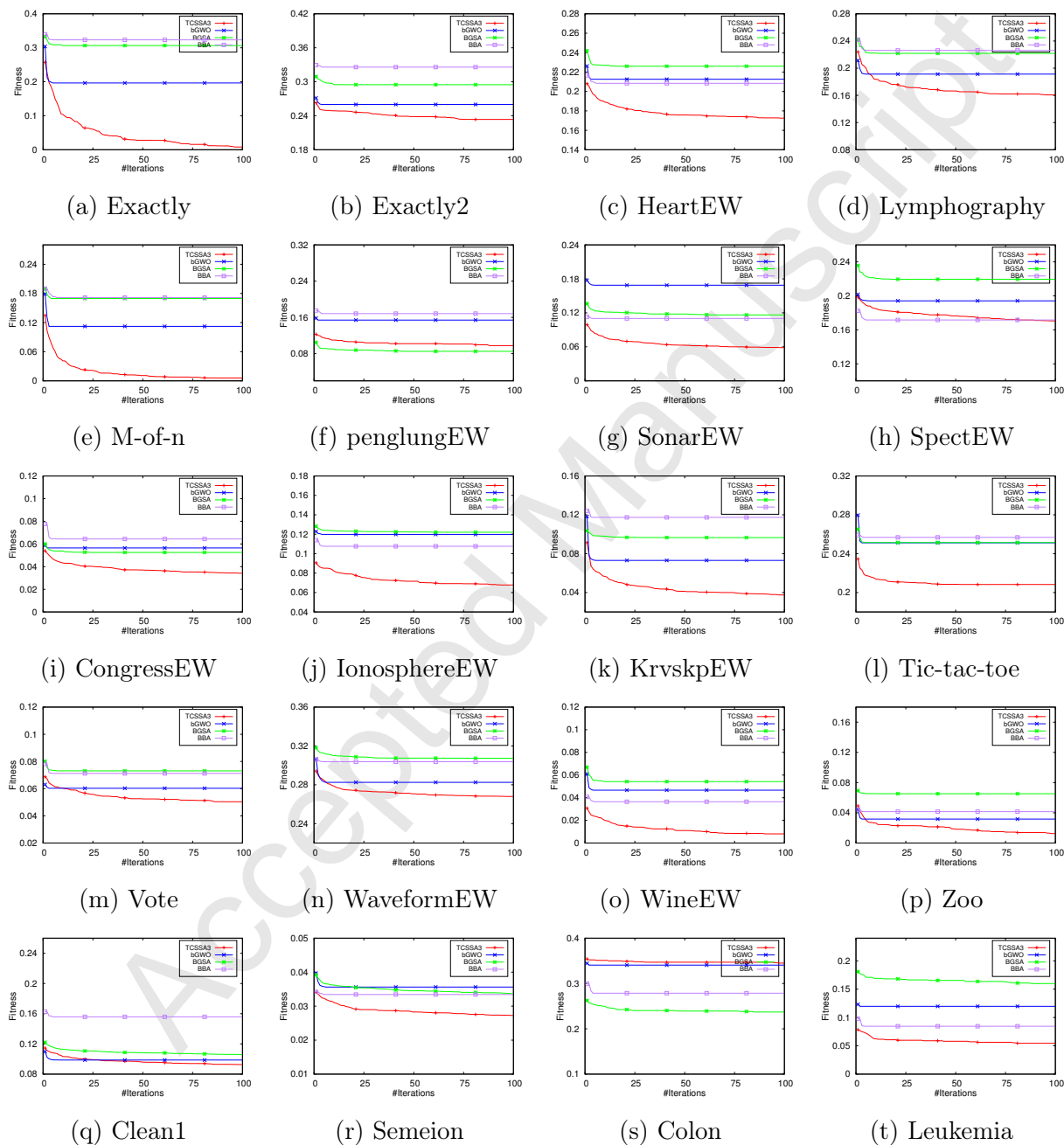Table 10: Comparison between the TCSSA1, TCSSA3 and other metaheuristics approaches based on the average fitness, average accuracy, and average features reduction rate results.

Benchmark	Metric	TCSSA1			TCSSA3			bGWO			BGSA			BBA		
		Fitness	Accuracy	Red. Rate	Fitness	Accuracy	Red. Rate	Fitness	Accuracy	Red. Rate	Fitness	Accuracy	Red. Rate	Fitness	Accuracy	Red. Rate
Exactly	AVG	0.00881	0.99633	48.20513	0.00811	0.99693	49.23077	0.19650	0.80947	21.28205	0.30655	0.69713	32.82051	0.32331	0.60993	55.89744
	STD	0.00880	0.00860	4.48686	0.00404	0.00381	3.83287	0.07663	0.07622	12.72555	0.05933	0.06012	8.06354	0.07446	0.06467	14.55780
Exactly2	AVG	0.24397	0.75973	38.97436	0.23355	0.76720	69.23077	0.25994	0.74313	43.58974	0.29485	0.70613	60.76923	0.32592	0.62820	53.33333
	STD	0.00311	0.00146	26.71831	0.01406	0.01241	21.18698	0.01924	0.01723	31.96186	0.02409	0.02348	16.20492	0.01671	0.05735	17.94745
HeartEW	AVG	0.17317	0.83111	40.25641	0.17253	0.83309	27.17949	0.21259	0.79161	37.17949	0.22599	0.77704	47.43590	0.20840	0.75383	54.61538
	STD	0.00530	0.00492	7.74078	0.00715	0.00747	10.04648	0.01701	0.01693	15.39566	0.02139	0.02160	10.11731	0.01468	0.03259	12.67200
Lymphography	AVG	0.13901	0.86486	47.77778	0.16069	0.84437	33.88889	0.19124	0.81306	38.33333	0.22182	0.78108	49.07407	0.22615	0.70135	56.66667
	STD	0.01339	0.01328	11.35742	0.00812	0.00851	7.62996	0.02813	0.02841	10.95192	0.02151	0.02170	10.52914	0.02365	0.06903	12.24136
M-of-n	AVG	0.00708	0.99827	46.41026	0.00589	0.99920	48.97436	0.11222	0.89413	25.89744	0.16966	0.83520	34.87179	0.17141	0.72187	52.56410
	STD	0.00370	0.00339	4.73037	0.00332	0.00304	4.73037	0.04149	0.04120	7.41773	0.06254	0.06320	11.01525	0.05619	0.07971	16.04464
penglungEW	AVG	0.08634	0.91892	39.27179	0.09777	0.90721	40.93333	0.15406	0.84955	48.82051	0.08511	0.91892	51.64103	0.16835	0.79459	61.17949
	STD	0.01380	0.01420	5.22264	0.01643	0.01692	6.76753	0.01300	0.01362	8.68683	0.00024	0.00000	2.37800	0.01690	0.02892	4.80025
SonarEW	AVG	0.07546	0.93045	34.00000	0.05859	0.94808	28.16667	0.16882	0.83558	39.61111	0.11638	0.88750	49.94444	0.11012	0.84391	58.83333
	STD	0.00812	0.00825	5.94676	0.00577	0.00597	5.94273	0.01594	0.01604	14.35512	0.01483	0.01497	6.16633	0.02095	0.03595	8.96086
SpectEW	AVG	0.17891	0.82537	39.69697	0.17055	0.83333	44.54545	0.19414	0.80970	42.57576	0.21957	0.78259	56.66667	0.17164	0.79975	63.78788
	STD	0.00760	0.00798	8.51911	0.00712	0.00715	7.20185	0.01362	0.01354	11.10093	0.02411	0.02414	10.45648	0.01191	0.02652	10.37096
CongressEW	AVG	0.04220	0.96223	51.87500	0.03419	0.97049	50.20833	0.05648	0.94755	54.37500	0.05252	0.95122	57.70833	0.06443	0.87171	61.04167
	STD	0.00375	0.00375	12.72957	0.00473	0.00462	6.66375	0.01094	0.01069	13.34938	0.00832	0.00812	15.01466	0.01470	0.07533	12.89080
IonosphereEW	AVG	0.12898	0.87519	45.78431	0.06776	0.93769	39.31373	0.11984	0.88466	43.43137	0.12209	0.88125	54.70588	0.10764	0.87652	60.58824
	STD	0.00936	0.00913	8.89703	0.00542	0.00527	11.01797	0.00890	0.00934	14.75010	0.01037	0.01048	7.39239	0.01184	0.01899	7.63066
KrvskpEW	AVG	0.04410	0.96197	35.46296	0.03747	0.96923	29.90741	0.07304	0.93390	23.98148	0.09655	0.90807	44.53704	0.11737	0.81635	58.33333
	STD	0.00563	0.00566	4.98419	0.00470	0.00460	5.72925	0.01500	0.01457	9.41237	0.04729	0.04784	5.90308	0.04677	0.08068	7.92418
Tic-tac-toe	AVG	0.20604	0.79749	44.44444	0.20826	0.79749	22.22222	0.25119	0.75379	25.55556	0.25144	0.75261	34.81481	0.25680	0.66535	47.77778
	STD	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.03221	0.03224	14.92139	0.02366	0.02442	12.62935	0.02374	0.06277	16.54489
Vote	AVG	0.05840	0.94667	43.95833	0.05037	0.95489	42.91667	0.06029	0.94378	53.75000	0.07308	0.93133	48.95833	0.07122	0.85111	61.66667
	STD	0.00661	0.00655	14.81598	0.00435	0.00417	8.32615	0.01033	0.00985	13.88841	0.01093	0.01109	11.38134	0.01298	0.09571	13.60754
WaveformEW	AVG	0.26579	0.73852	30.75000	0.26795	0.73643	29.83333	0.28250	0.72272	20.08333	0.30732	0.69460	50.25000	0.30371	0.66931	58.33333
	STD	0.00498	0.00498	6.05827	0.00407	0.00406	7.36761	0.00725	0.00674	11.53113	0.01399	0.01422	7.29165	0.01354	0.03258	8.26118
WineEW	AVG	0.01547	0.98914	52.82051	0.00810	0.99775	41.28205	0.04666	0.95955	33.84615	0.05424	0.95094	43.33333	0.03647	0.91873	53.33333
	STD	0.00487	0.00465	8.26350	0.00445	0.00457	6.54067	0.01167	0.01165	13.49087	0.01514	0.01547	8.44666	0.01300	0.05193	13.38967
Zoo	AVG	0.07530	0.92941	45.83333	0.01251	0.99281	46.04167	0.03171	0.97451	35.20833	0.06528	0.93922	48.95833	0.04153	0.87386	58.95833
	STD	0.00892	0.00977	10.16212	0.00905	0.00961	7.60759	0.00850	0.00914	15.52627	0.00782	0.00789	7.35553	0.01487	0.09490	15.63003
clean1	AVG	0.09826	0.90728	35.26104	0.09267	0.91359	28.79518	0.09868	0.90770	26.94779	0.10584	0.89818	49.57831	0.15587	0.82647	60.98394
	STD	0.00526	0.00551	5.72750	0.00558	0.00581	5.34240	0.00621	0.00619	12.46469	0.01044	0.01056	3.26580	0.01297	0.02082	6.03382
semeion	AVG	0.02146	0.98519	31.93711	0.02726	0.97996	25.69811	0.03562	0.97164	24.49057	0.03365	0.97110	49.61006	0.03343	0.96219	59.61006
	STD	0.00127	0.00141	4.62325	0.00151	0.00149	5.15730	0.00259	0.00298	11.70644	0.00201	0.00215	2.80073	0.00262	0.00629	4.13076
Colon	AVG	0.22822	0.77527	42.62167	0.34495	0.65699	46.31833	0.34053	0.66129	47.89500	0.23704	0.76559	50.20833	0.27856	0.68172	58.62500
	STD	0.00578	0.00589	4.29187	0.01519	0.01581	6.69491	0.02175	0.02201	6.33605	0.01435	0.01451	1.00104	0.03524	0.03763	2.76853
Leukemia	AVG	0.09259	0.91204	44.90345	0.05450	0.95092	40.81919	0.11972	0.88426	48.60757	0.15990	0.84352	50.13139	0.08452	0.87685	59.88217
	STD	0.01016	0.01053	5.71851	0.01140	0.01195	7.36320	0.01617	0.01645	4.13624	0.01345	0.01362	0.55706	0.02291	0.02889	3.47373
W|T|L		5|0|13	4|2|14	0|0|20	0|0|20	14|1|5	1|0|19	0|0|20	0|0|20	0|0|20	1|0|19	0|1|19	0|0|20	0|0|20	0|0|20	19|0|1
F-Test		2.150	2.050	3.55000	3.500	1.475	3.95000	3.500	3.100	4.05000	4.000	3.675	2.35000	3.850	4.700	1.10000

24

Table 11: Comparison between the TCSSA1, TCSSA3 and other metaheuristics approaches based on the average running time results.

Benchmark	TCSSA1		TCSSA3		bGWO		BGSA		BBA	
	AVG	STD	AVG	STD	AVG	STD	AVG	STD	AVG	STD
Exactly	5.5835	0.2267	6.0734	0.3506	6.1544	0.2753	**4.8760**	0.3113	4.9563	0.2719
Exactly2	5.8795	0.4261	5.5584	0.4304	6.0499	0.3798	**5.0329**	0.3743	5.2239	0.3941
HeartEW	2.8059	0.1323	**2.6691**	0.1525	2.7390	0.1737	2.8118	0.1822	2.7666	0.2005
Lymphography	2.5142	0.1165	**2.3768**	0.1149	2.6023	0.1607	2.5885	0.1496	2.6343	0.1452
M-of-n	5.5922	0.2521	5.5850	0.2444	6.1569	0.2410	5.1377	0.2934	**4.8916**	0.3614
penglungEW	4.0432	0.1659	4.0211	0.2190	7.7166	0.4321	**3.0602**	0.1707	4.1657	0.2384
SonarEW	2.9612	0.1461	2.8761	0.1465	3.6772	0.1928	**2.7028**	0.1462	2.8501	0.1910
SpectEW	**2.6541**	0.1526	2.7215	0.1789	2.8694	0.1757	2.7225	0.1621	2.8089	0.1613
CongressEW	3.2748	0.1734	3.3135	0.2262	3.3091	0.1719	**3.2168**	0.1878	3.2435	0.1582
IonosphereEW	3.1135	0.1653	3.2154	0.2275	3.5639	0.1838	**2.9213**	0.1445	3.0184	0.1479
KrvskpEW	62.5567	2.6913	66.8095	2.2950	78.1132	4.6058	49.5337	2.5273	**47.9225**	2.5762
Tic-tac-toe	4.9093	0.2508	5.2740	0.2704	6.2078	0.6220	4.3440	0.2784	**4.2372**	0.2775
Vote	2.8021	0.1291	**2.6335**	0.1352	2.8512	0.1536	2.8243	0.1516	2.8343	0.1783
WaveformEW	166.6715	4.8928	175.5412	6.1130	213.9553	13.6071	125.8036	6.7701	**119.9900**	8.1688
WineEW	2.5566	0.1297	**2.4475**	0.1276	2.6282	0.1734	2.5852	0.1706	2.6238	0.1408
Zoo	2.5131	0.1158	**2.3792**	0.1176	2.6234	0.1358	2.5473	0.1579	2.7774	0.1923
clean1	9.7487	0.2374	10.1214	0.3580	13.6825	0.6475	**7.3968**	0.2884	7.5886	0.4673
semeion	126.3091	1.9589	135.8338	2.6086	169.5376	9.1906	90.6010	2.2118	**82.7761**	5.5785
Colon	11.9469	0.4566	11.7073	0.5344	36.6944	1.9980	**5.1536**	0.2417	12.1760	0.7744
Leukemia	41.8940	1.8276	41.2598	1.7718	130.8780	6.3655	**16.4414**	0.6832	39.3789	2.4179
W|T|L	1|0|19		5|0|15		0|0|20		9|0|11		5|0|15	
F-Test	2.950		2.800		4.700		**1.950**		2.600	

Comparison with other meta-heuristics in literature: After analyzing the results of the proposed approaches, a comparison with similar approaches from the literature is given based on classification accuracy rates. The results for those approaches were obtained from two well-known research works that used the same datasets. In Table 12, we compared the performance of TCSSA3 with the results of GA and PSO from [37] executed using the source code from the same authors, the results of the bGWO1, bGWO2, GA, and PSO obtained from the paper [16], and a similar approach that uses the same updating strategy for the PSO algorithm (i.e., AGPSO3) proposed in [55].

Table 12 shows that TCSSA3 provides a superior performance in comparison with other approaches. It obtained the best results in 70% of the datasets with a significant difference according to the F-Test. Compared to the PSO1 and PSO2 approaches, TCSSA3 can outperform both approaches in all datasets. The AGPSO3, which is an enhanced PSO approach that uses a similar updating strategy used in TCSSA3, comes in the second place after TCSSA3. It can be seen that AGPSO3 performs better than both PSO approaches on fourteen datasets, which means that using different updating strategies with the PSO can enhance the performance of this algorithm on feature selection tasks. At the same time, AGPSO3 can outperform TCSSA3 in only four datasets. The previous results clearly prove the influence of different updating strategies on the capabilities of SSA in searching for the most informative features. The proposed SSA-based method can reveal the highest classification accuracies for different datasets with different dimensions.

The proposed asynchronous team behaviors of agents allow them to have a variety of randomized patterns in performing the socio-random exploration and exploitation phases for all search agents. This results in enhancements in local solutions avoidance of the TCSSA3 algorithm. We think that the proposed updating mechanisms and considering multi-leader structure can also expand the exploratory and exploitative capacities of the other stochastic optimizers. Interpretation of these effects for other population-based optimizers would

25

Table 12: Comparison between the TCSSA3 and other meta-heuristics from the literature in terms of accuracy

Benchmark	TCSSA3	GA1 [37]	PSO1 [37]	bGWO1 [15]	bGWO2 [15]	GA2 [15]	PSO2 [15]	AGPSO3 [53]
Exactly	0.99693	0.82200	0.97327	0.70800	0.77600	0.67400	0.68800	**1.00000**
Exactly2	**0.76720**	0.67720	0.66640	0.74500	0.75000	0.74600	0.73000	0.76083
HeartEW	**0.83309**	0.73235	0.74469	0.77600	0.77600	0.78000	0.78700	0.79259
Lymphography	**0.84437**	0.75766	0.75946	0.74400	0.70000	0.69600	0.74400	0.82508
M-of-n	0.99920	0.91600	0.99620	0.90800	0.96300	0.86100	0.92100	**1.00000**
penglungEW	**0.90721**	0.67207	0.87928	0.60000	0.58400	0.58400	0.58400	0.83556
SonarEW	**0.94808**	0.83333	0.80353	0.73100	0.72900	0.75400	0.73700	0.88571
SpectEW	**0.83333**	0.75597	0.73806	0.82000	0.82200	0.79300	0.82200	0.70308
CongressEW	**0.97049**	0.89771	0.93746	0.93500	0.93800	0.93200	0.92800	0.96130
IonosphereEW	**0.93769**	0.86269	0.87614	0.80700	0.83400	0.81400	0.81900	0.89202
KrvskpEW	**0.96923**	0.94026	0.94875	0.94400	0.95600	0.92000	0.94100	0.96422
Tic-tac-toe	0.79749	0.76388	0.75024	0.72800	0.72700	0.71900	0.73500	**0.81250**
Vote	0.95489	0.80844	0.88844	0.91200	0.92000	0.90400	0.90400	**0.96556**
WaveformEW	0.73643	0.71207	0.73168	0.78600	**0.78900**	0.77300	0.76200	0.73827
WineEW	**0.99775**	0.94719	0.93670	0.93000	0.92000	0.93700	0.93300	0.96852
Zoo	**0.99281**	0.94575	0.96275	0.87900	0.87900	0.85500	0.86100	0.97059
W|T|L	11|0|5	0|0|16	0|0|16	0|0|16	1|0|15	0|0|16	0|0|16	4|0|12
F-Test	**1.563**	5.438	4.625	5.469	4.844	6.156	5.531	2.375

need deeper insight into the exploration and exploitation mechanisms of those algorithms supported by some experiments and analyses and will go far outside the core scope of this research.

6. Conclusion and future directions

In this work, an asynchronous binary SSA algorithm with several updating rules was proposed to tackle the FS problems. First, tests were performed to determine the best leadership structure of the artificial salp chains. SSA with the best leadership structure ($N/2$ salps as leaders) was then used as the basic algorithm (BSSA) to implement the following approaches. The whole chain was divided to several sub-chains, where the salps in each sub-chain could follow a different strategy to adaptively update their locations inside the search space. Three different updating strategies (TCSSA1, TCSSA2, TCSSA3) were used. In each strategy, each subchain of the salps followed an updating mechanism. The proposed algorithm was benchmarked on 20 datasets from UCI repository. The statistical results confirm the superiority of the proposed TCSSA3 in dealing with exploration and exploitation of the feature space for the majority of datasets. The discussions and analyses of results showed that idea of asynchronous tuning of the main parameter of the SSA with different leading salp for different regions of the salp chain is beneficial in alleviating the possible drawbacks of the conventional algorithm.

Future researches can investigate the optimum number of updating rules and utilize the proposed structure for other population-based algorithms.

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26

8. References

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29