**Highlights**

- Two wrapper feature selection approaches using salp swarm algorithm are proposed.
- The crossover operator is utilized in addition to transfer functions to enhance the algorithm.
- The performance is evaluated based on 22 datasets, and compared to five well-known wrapper methods.

# An Efficient Binary Salp Swarm Algorithm with Crossover Scheme for Feature Selection Problems

Hossam Faris[a], Majdi M. Mafarja[b], Ali Asghar Heidari[c], Ibrahim Aljarah[a], Ala' M. Al-Zoubi[a], Seyedali Mirjalili[d], Hamido Fujita[e]

[a]*King Abdullah II School for Information Technology, The University of Jordan, Amman, Jordan*
*{hossam.faris,i.aljarah}@ju.edu.jo , alaah14@gmail.com*
[b]*Department of Computer Science, Birzeit University, Birzeit, Palestine*
*mmafarja@birzeit.edu, mmafarjeh@gmail.com*
[c]*School of Surveying and Geospatial Engineering, University of Tehran, Tehran, Iran*
*as_heidari@ut.ac.ir*
[d]*Institute of Integrated and Intelligent Systems, Griffith University, Nathan, Brisbane, QLD 4111, Australia*
*seyedali.mirjalili@griffithuni.edu.au*
[e]*Faculty of Software and Information Science, Iwate Prefectural University (IPU), Iwate, Japan*
*hfujita-799@acm.org*

**Abstract**

Searching for the (near) optimal subset of features is a challenging problem in the process of Feature Selection (FS). In the literature, Swarm Intelligence (SI) algorithms show superior performance in solving this problem. This motivated our attempts to test the performance of the newly proposed Salp Swarm Algorithm (SSA) in this area. As such, two new wrapper FS approaches that use SSA as the search strategy are proposed. In the first approach, eight transfer functions are employed to convert the continuous version of SSA to binary. In the second approach, the crossover operator is used in addition to the transfer functions to replace the average operator and enhance the exploratory behavior of the algorithm. The proposed approaches are benchmarked on 22 well-known UCI datasets and the results are compared with 5 FS methods: Binary Grey Wolf Optimizer (BGWO), Binary Gravitational Search Algorithms (BGSA), Binary Bat Algorithm (BBA), Binary Particle Swarm Optimization (BPSO), and Genetic Algorithm (GA). The paper also considers an extensive study of the parameter setting for the proposed technique. From the results, it is observed that the proposed approach significantly outperforms others on around 90% of the datasets.

*Keywords:* Wrapper Feature Selection, Salp Swarm Algorithm, Optimization, Classification

## 1. Introduction

Dimensionality is the main challenge that may degrade the performance of the machine learning tasks (e.g., classification). There are many applications in science and engineering fields like medicine, biology, industry, etc. that depend on high dimensional datasets with hundreds or even thousands of features, and some of these features are irrelevant, redundant or noisy [1]. The existence of such features in the dataset may mislead the learning algorithm or cause data over-fit [2]. Feature Selection (FS) is an important pre-processing step that aims to eliminate those types of features to enhance the effectiveness of the learning algorithms (e.g., classification accuracy) and save resources (e.g., CPU time and memory requirement).

FS methods are categorized based on the involvement of a learning algorithm in the selection process. Filter methods (Chi-Square [3], Information Gain [4], Gain Ratio [5], ReliefF [6]) rely on some data properties without involving a specific learning algorithm. On the other hand, wrapper methods depend on a specific learning algorithm (e.g. classifier) in evaluating the selected subset of features [7]. Comparing these families, wrappers are more accurate since they consider the relations between the features themselves. However, they are computationally more expensive than filters and their performances are strongly depend on the employed learning algorithm [8].

Searching for the (near) optimal subset of features is another key issue that must be taken into consideration when designing a FS algorithm. FS is considered as an NP-complete combinatorial optimization problem [9]. Hence, generating all possible subsets using techniques such as brute-force or exhaustive search strategy is impractical. Suppose that a dataset includes $N$ features, then $2^N$ subsets are to be generated and evaluated [10], which is considered as a computationally expensive task especially in the wrapper based methods where the learning algorithm will be executed for each subset.

Since the main aim in FS is to minimize the number of selected features while maintaining the maximum classification accuracy (i.e., minimize the classification error rate), it can be considered as an optimization task. Therefore, metaheuristics, which showed superior performance in solving different optimization scenarios, are potentially suitable solutions for FS problems [11].

Swarm Intelligence (SI) techniques are nature-inspired metaheuristics algorithms that mimic the swarming behavior of ants, bees, schools of fish, flocks of birds, herds of land animals, etc. that live in groups in nature and can cooperate among themselves [12]. Examples of SI algorithms include but not limited to Particle Swarm Optimization (PSO) [13], Ant Colony Optimization (ACO) [14], Dragonfly Algorithm (DA) [15], Whale Optimization Algorithm (WOA) [16], Water Cycle Algorithm (WCA) [17, 18], Krill Herd (KH) [19] algorithm, Fruit Fly Optimization Algorithm (FFOA) [20], Grey Wolf Optimizer (GWO) [21], and Firefly Algorithm (FA) [22]. These algorithms were used in solving many optimization problems including feature selection problems and showed superior performance when compared to several exact methods [10, 23]. For details about the history of metaheuristics, interested readers can refer to [24].

SSA is a recent SI optimizer proposed by Mirjalili *et al.* [25]. SSA mimics the swarming behaviour of salps when navigating and foraging in oceans. It was shown in [25] that SSA significantly outperforms well-regarded and recent metaheursitics. This is due to the several stochastic operators integrated into SSA that allows this algorithm to better avoid local solutions in multi-modal search landscapes. Mirjalili *et al.* also showed that the SSA algorithm performs efficiently on small- and large-scale problems. As a binary problem with a large number of local solutions, the number of parameters of a feature selection problem varies significantly when changing datasets that should be addressed by a reliable stochastic optimization algorithm. This motivated our attempts to propose a feature selection technique using SSA to benefit from the flexibility and highly stochastic nature of this algorithm in handling diverse range of parameter and local solutions.

In this paper, two FS approaches based on SSA are proposed. The native SSA was proposed to deal with continuous problems, so some modifications should be done on SSA to solve FS problems with binary parameters. Mainly, two versions of binary SSA are proposed in this work:

- In the first version, the SSA is converted from continuous to binary using eight different transfer functions (TFs).
- In the second version, a crossover operator is integrated to SSA. In fact, the best search agent of SSA (leader) is updated using the crossover operator to promote exploration while maintaining the main mechanism of this algorithm.

The structure of this paper is as follows: the review of related works is presented in Section 2. Section 3 presents some preliminaries and theoretical background about FS, $k$-NN classifier, and SSA algorithm utilized in this research. The new SSA-based techniques are proposed in Section 4. Section 5 represents the details of binary SSA for FS tasks. Section 6 reports the obtained results and related comparisons and discussions. Finally, the conclusion and several directions for future papers are presented in Section 7.

## 2. Review of related works

In literature, many SI algorithms have been extensively used as search strategies in wrapper FS methods to enhance the results of the classification problems, which are one of the most important data mining tasks. The authors in [26] proposed an ACO-based FS algorithm called (ABACO). A novel FS algorithm based on ABACO has been also proposed in [27] by the same authors. This approach differs from the previous one by giving ants the ability to view the features comprehensively, and helps them to select the most salient features. A hybrid algorithm between two SI algorithms (ACO and ABC) called (AC-ABC Hybrid) has been recently proposed in [28]. In this algorithm, the advantages of both ACO and BCO have combined to produce a better algorithm; the Bees adapt the feature subsets generated by the Ants as their food sources and the Ants use the Bees to determine the best feature subset. Another hybrid model between the ACO and GA has been proposed in [29].

The PSO is a dominant SI algorithm that has been widely used with FS problem. Moradi *et al.* [30] enhanced the performance of PSO by employing a local search to find the salient and less correlated feature subset. Another two different FS approaches based on PSO have been proposed in [31]. In these two approaches a new variable was added to the original PSO which makes it more effective in tackling the FS problem. The PSO for FS has been also utilized in different fields like text clustering [32, 33], text FS [34], disease diagnosis [31, 35]. A FS method using artificial bee colony (ABC) has been proposed for Image steganalysis problem in [36]. A novel ABC based FS approach called wBCO has been proposed in Moayedikia et al. [37]. Two SI based algorithms (namely differential evolution (DE) and ABC) combined in a hybrid FS method in [38]. The Ant Lion Optimizer (ALO) [39] has been employed as a search strategy in a wrapper FS method in [40]. Moreover, three variants of binary ALO algorithm has been presented in [41]. A modified ALO algorithm, where a set of chaotic maps was used to control the balance between exploration and exploitation, has been proposed for FS in [42].

The GWO is a successful SI algorithm that mimics the social hierarchy and hunting traits of the grey wolves [21, 43, 44, 45]. The GWO has successfully been applied to FS problems in a number of works [46, 47]. Moth-flame Optimisation (MFO) [48] also revealed a relatively satisfying efficacy on both optimization and feature selection tasks [42]. The Whale Optimization Algorithm (WOA)-based FS approaches has also been proposed in [49], in which different hybridization models between the WOA and Simulated Annealing (SA) algorithm have been proposed for FS problems. Moreover, many SI-based FS approaches have been proposed in literature such as Genetic Algorithm (GA)-based FS [50, 51, 52], Gravitational Search Algorithm (GSA) [53, 54], DE [55, 56], Harmony Search (HS) [57], Bat Algorithm (BA) [58], Binary Grasshopper Optimization Algorithm (BGOA) [59], Binary Firefly Algorithm (BFA) [60], Binary Harmony Search (BHS) [61], Binary Cuckoo Search (BCS) [62],Binary Charged System Search (BCSS) [63]. For more FS approaches, readers can refer to the available review studies [64, 65]. Referring to No-Free-Lunch (NFL) theorem [66], it can be stated that there is no algorithm that can be the best universal machine for tackling all classes of feature selection problems. Hence, there are many opportunities to propose new algorithms or develop new improved variants of previous algorithms to tackle feature selection problems more efficiently.

## 3. Preliminaries

### *3.1. Feature Selection for Classification*

A dataset (also called training set) usually consists of rows (called objects) and columns (called features) associated with predefined classes (decision features). Classification is a primary task in data mining, it's main role is to to predict the class of an unseen object [64]. The main problem that may affect the the accuracy and the performance of a specific classifier is the large number of features in the dataset which may be redundant or irrelevant. According to [2], the redundant and irrelevant features may negatively affect the classifier's performance in many directions; more features in a dataset raises the need for more instances to be added which costs the classifier longer time to learn. Moreover, the classifier that learns from irrelevant features is less accurate than the one that learns form relevant features. This is because the irrelevant features may mislead the classifier and cause them to overfit data. In addition, the redundant and irrelevant data will increase the complexity of the classifier which make it hard to understand the learned results.

FS usually helps in determining the irrelevant and redundant features and removing them in order to enhance the classifiers performance in terms of learning time and accuracy, and simplify the results to make them understandable. As shown previously, choosing a proper searching strategy in FS methods is very important to enhance the performance of the learning algorithm. By selecting the most informative feature and removing the irrelevant and redundant features, the dimensionality of the feature space will be reduced and the convergence speed of the learning algorithm will be improved [30]. In this regard, the SSA was selected to be utilized as an efficient optimization engine in a wrapper FS method since it has proven a satisfactory efficacy in tackling many optimization problems compared against other SI-based optimizers.

### 3.2. k-Nearest Neighbor Classifier (k-NN)

The $k$-NN algorithm is a simple non-parametric and instance-based classifier that relies on classifying unlabeled instances by measuring the distance between a given unlabeled instance and its closest $k$ instances ($k$ neighbors) [67]. The basic idea of this algorithm is that the label of some point in a given space is more likely to be similar to its closest points. There are different distance measurements utilized in the literature for $k$-NN. However, the most widely used measurement is the Euclidean distance which can be given as shown in Eq. 1.

$$dist(X_1 - X_2) = (\sum_{i=1}^{n}(x_{1i} - x_{2i})^2)^{0.5} \tag{1}$$

where $X_1$ and $X_2$ are two points with $n$ dimensions.

### 3.3. Salp Swarm Algorithm

The main inspiration of SSA is the swarming behavior of sea organisms called salps. The salps are barrel-shaped, free floating tunicates from the family of Salpidae. Salps often float together in a form known as salp chain when navigating and foraging in oceans and seas as shown in Fig. 1. It is thought that a colony of salps move in this form for better locomotion and foraging.

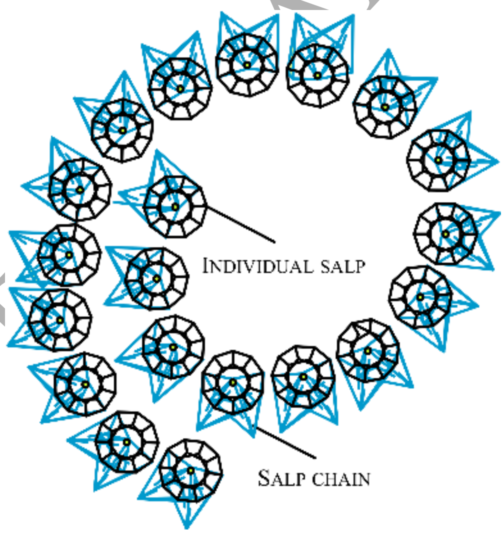



Figure 1: The demonstration of the salp chain

Similarly to other swarm intelligent algorithms, SSA is a population-based algorithm and starts by randomly initializing a predefined number of individuals. Each of these individuals represent a candidate solution for the targeted problem. There are two types of individuals in the swarm of the salps: a leader and followers. The leader is the first salp in the chain which guides the followers in their movement. A swarm $X$ of $n$ salps can be represented by a two-dimensional matrix as shown in Eq. 2. The target of this swarm is a food source in the search space called $F$.

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

The mathematical model that describes the salps chain is presented as follows. As mentioned before, the population is divided into two types of slaps, the leader and the followers. The leader position is updated using Eq. 3.

$$x_j^1 = \begin{cases} F_j + c_1\left((ub_j - lb_j)\, c_2 + lb_j\right) & c_3 \geq 0.5 \\ F_j - c_1\left((ub_j - lb_j)\, c_2 + lb_j\right) & c_3 < 0.5 \end{cases} \tag{3}$$

where $x_j^1$ and $F_j$ are the positions of leaders and food source in the $j^{th}$ dimension, respectively. $c_1$ is a variable that is gradually decreased over the course of iterations, and calculated as given in Eq. 4, where $l$ and $L$ are the current iteration and the maximum number of iterations, respectively. The other $c_2$ and $c_3$ variables in Eq. 3 are two numbers randomly drawn from the interval [0, 1]. The latter two variables are very important factors in SSA as they direct the next position in $j^{th}$ dimension towards $+\infty$ or $-\infty$ as well as dictating the step size. The $ub_j$ and $lb_j$ are the upper and lower bounds of $j^{th}$ dimension.

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

The positions of the followers salps are updated using Eq. 5.

$$x_j^i = \frac{1}{2}\left(x_j^i + x_j^{i-1}\right) \tag{5}$$

where $i \geq 2$ and $x_j^i$ represents the position of the $i^{th}$ follower at the $j^{th}$ dimension.

The pseudocode of the basic SSA is presented in 1.

**Algorithm 1** Pseudo-code of the SSA algorithm

```
Initialize the salp population x_i (i = 1, 2, ..., n) considering ub and lb
while (end condition is not satisfied) do
    Calculate the fitness of each search agent (salp)
    Set F as the best search agent
    Update c_1 by Eq. 4
    for (each salp (x_i)) do
        if (i == 1) then
            Update the position of the leading salp by Eq. 3
        else
            Update the position of the follower salp by Eq. 5
    Update the salps based on the upper and lower bounds of variables
Return F
```

Like other SI algorithms, SSA starts the optimization process by generating a population of solutions (salps) randomly. Then, the generated solution is evaluated using an objective function. In SSA, the fittest solution is denoted as the Food Source $F$ which will be chased by other solutions (follower salps). At each iteration, $c_1$ variable is updated using Eq. 4, and each dimension in the leader (best salp) is updated using Eq. 3, while the positions of the followers salps are updated using Eq. 5. All the previous steps are repeated till a stopping criterion is satisfied. Since the solutions in population are very likely to be improved due to the exploration and exploitation processes, $F$ should be updated during the optimization.

## 4. The Proposed Approaches

The SSA is a recent optimizer that has not been employed to tackle FS problems yet. It has many unique characteristics that make it favorable to be utilized as the searching engine in global optimization and FS problems. Initially, the SSA is efficient, flexible, simple and easy to implement. As a bonus, SSA has only one parameter to balance exploration and exploitation. This parameter is adaptively decreased over the course of iterations, which allows the SSA to explore most of the search space at the begging of the searching process and then exploit the promising areas at the final stages. Moreover, the positions of follower salps are updated gradually with respect to other members of the swarm, which helps the SSA to avoid trapping at local optima. Gradual movements of follower agents can avoid the SSA from effortlessly decaying in local solutions. The SSA retains the finest agent found so far and ascribes it to the food variable, consequently, it never get lost even if the entire agents get weaken. In the SSA, the leader salp moves based on the position of the food source only, which is the best salp attained so far, so the leader continually is capable of exploring and exploiting the space nearby the food source.

In the next section, two SSA approaches are proposed in a wrapper FS method. The first step is to prepare the SSA for tackling the FS by converting it to binary form since it is originally designed to deal with the continuous optimization problems. In the continuous SSA, salps can change their positions to any point in the search space, while in FS the movement is restricted to 0 and 1 values. Moreover, in the original SSA, the positions of the follower salps are updated by applying an average operator between a solution and its neighbor. In the second approaches, this average operator is replaced by a simple crossover operator which plays the same role in enhancing the exploratory behaviour of SSA.

### *4.1. Binary SSA (BSSA) with Transfer Functions*

According to Mirjalili and Lewis [68], one of the most efficient ways to convert a continuous algorithm to a binary version is to utilize transfer functions (TF). In this work, eight TFs are used to convert the continuous SSA to binary version. These TFs belong to two different families, S-shaped and V-shaped. The purpose of a TF is to define a probability for updating an element in the feature subset (solution) to be 1 (selected) or 0 (not selected) as in Eq. 6, which was proposed by Kennedy and Eberhart [69] to covert the original PSO to a binary version.

$$T(x_j^i(t)) = \frac{1}{1 + \exp^{-x_j^i(t)}} \tag{6}$$

where $x_j^i$ is the $j-th$ element in $x$ solution in the $j-th$ dimension, and $t$ is the current iteration.

Table 1: S-shaped and V-shaped transfer functions

| S-shaped family | | V-shaped family | |
|---|---|---|---|
| Name | Transfer function | Name | Transfer function |
| S1 | $T(x) = \frac{1}{1+e^{-2x}}$ | V1 | $T(x) = \lvert \mathrm{erf}(\frac{\sqrt{\Pi}}{2}x)\rvert = \lvert \frac{\sqrt{2}}{\Pi}\int_0^{(\sqrt{\Pi}/2)x} e^{-t^2}dt\rvert$ |
| S2 | $T(x) = \frac{1}{1+e^{-x}}$ | V2 | $T(x) = \lvert\tanh(x)\rvert$ |
| S3 | $T(x) = \frac{1}{1+e^{(-x/2)}}$ | V3 | $T(x) = \lvert(x)/\sqrt{1+x^2}\rvert$ |
| S4 | $T(x) = \frac{1}{1+e^{(-x/3)}}$ | V4 | $T(x) = \lvert\frac{2}{\Pi}\mathrm{arc}\tan(\frac{\Pi}{2}x)\rvert$ |

In S-shaped family, an element of solution in the next iteration can be updated by Eq. 7

$$x_i^k(t+1) = \begin{cases} 0 & \text{If } rand < T(v_i^k(t+1)) \\ 1 & \text{If } rand \geq T(v_i^k(t+1)) \end{cases} \tag{7}$$

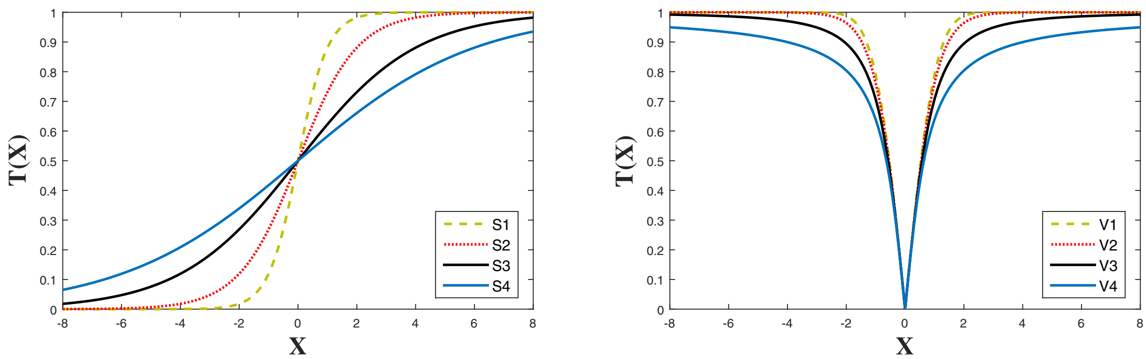
where $X_i^d(t+1)$ is the $i-th$ element at $d^{th}$ dimension in $X$ solution, $T(x_j^i(t))$ is the probability value, which can be obtained via Eq. 6.

In V-shaped family, an element of solution in the next iteration can be updated by Eq. 9, depending on the probability values obtained from Eq. 8, which was defined by Rashedi *et al.* [70] to covert the original GSA to a binary version.

$$T(x_j^i(t)) = \lvert\tanh(x_j^i(t))\rvert \tag{8}$$

$$X_{t+1} = \begin{cases} \neg X_t & r < T(\Delta x_{t+1}) \\ X_t & r \geq T(\Delta x_{t+1}) \end{cases} \tag{9}$$

Table 1 shows the mathematical formulation of all transfer functions used in this paper and Fig. 2 shows these two families of transfer functions.




(a) (b)

Figure 2: Transfer functions families (a) S-shaped and (b) V-shaped.

The flowchart of the the SSA algorithm with Transfer Functions is demonstrated in Fig. 3.

*4.2. The BSSA with crossover scheme*

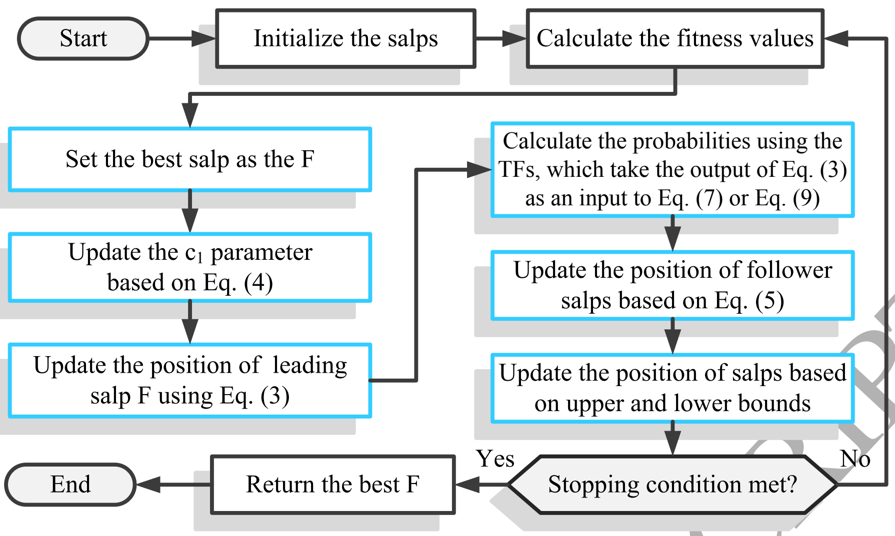



Figure 3: The flowchart of the SSA algorithm with Transfer Functions

In the proposed BSSA, the leader's position is updated by using a TF, while the followers' positions are updated using Eq. 5. This equation calculates a solution between two given solutions, which is helpful when the variables are continuous. This equation is useless for binary problems since there are only two values for the variables. To address this issue, we employ a crossover operator to combine solutions as shown in Eq. 10.

$$x_i^{t+1} = \bowtie (x_i, x_{i-1}) \tag{10}$$

where $\bowtie$ is an operator that performs the crossover scheme on two binary solutions, and $x_i$ is the $i^{th}$ follower salp. An example of this process can be seen in Fig. 4.

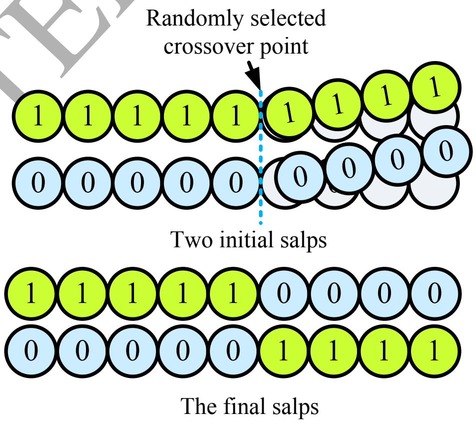



Figure 4: The crossover process

It can be seen in Fig. 4 that the binary bits are exchanged between two solutions, which causes abrupt changes in both solution. This is the main mechanism of global search and exploration in the proposed BSSA algorithm. Note that the crossover operator aims to obtain an intermediate solution in a binary search space to mimic the concept of finding a solution between two solutions in Eq. 5. The crossover operator switches between two input vector with the same probability as given in Eq. 11.

$$x^d = \begin{cases} x_1^d & rand \geq 0.5 \\ x_2^d & otherwise \end{cases} \tag{11}$$

where $x^d$ is the value of the $d^{th}$ dimension in the resulted vector after applying the crossover operator on $x_i$ and $x_{i-1}$.

The pseudocode of the proposed optimizer is presented in Algorithm 2

**Algorithm 2** Pseudo-code of the SSA algorithm with Crossover operator

```
Initialize the salp population x_i (i = 1, 2, ..., n) considering ub and lb
while (end condition is not satisfied) do
    Calculate the fitness of each search agent (salp)
    Set F as the best search agent
    Update c_1 by Eq. 4
    for (each salp (x_i)) do
        if (i == 1) then
            Update the position of the leading salp by Eq. 3
            Calculate the probabilities using a TF which takes the output
            of Eq. 3 as its input (as in Eq. 7 (S-Shaped) or Eq. 9 (V-Shaped))
        else
            Update the position of the follower salp by performing a
            Crossover operator between x_i and x_{i-1} using Eq. 10.

    Update the salps based on the upper and lower bounds of variables
Return the best found solution F
```

## 5. Binary SSA for FS Problem

Two wrapper FS approaches that use SSA as a search algorithm and $k$-NN classifier as an evaluator were proposed. To formulate FS as an optimization problem, two key points should be taken into consideration; how to represent a solution and how to evaluate it. In this work, a feature subset is represented as a binary vector with a length equals to the number of features in the dataset. If a feature is set to 1, this means that it has been selected, otherwise it has not. The goodness of a feature subset is measured depending on two criteria; the maximum classification accuracy (minimum error rate) and simultaneously the minimal number of selected features. These two contradict objectives are represented in one fitness function that is shown in Eq. 12:

$$\downarrow Fitness = \alpha \gamma_R(D) + \beta \frac{|R|}{|C|} \tag{12}$$

where $\gamma_R(D)$ represents the classification error rate obtained by a specific classifier, |R| is the number of selected features in a reduct, and |C| is the number of conditional features in the original dataset, and $\alpha \in [0, 1]$, $\beta = (1 - \alpha)$ are two parameters corresponding to the importance of classification quality and subset length as per recommendations in [41].

## 6. Experimental results and discussions

In this section, a comparative study is presented to carefully examine the exploratory and exploitative behavior of the proposed BSSA algorithms compared to several other well-established and novel metaheuristics. As case studies, 22 practical benchmark datasets are utilized. Table 2 describes these datasets in terms of number of features and number of instances. These datasets include several properties and cover various sizes and dimensions. For complete details about the origin and structure of these datasets, readers can refer to the sources available at UCI repository [71]. These problems can reveal the competency of the experienced optimizers in managing the exploration and exploitation trends and realizing more satisfactory results.

Table 2: List of used datasets

| No. | Dataset | No. of Features | No. of instances |
|---|---|---|---|
| 1. | Breastcancer | 9 | 699 |
| 2. | BreastEW | 30 | 596 |
| 3. | Exactly | 13 | 1000 |
| 4. | Exactly2 | 13 | 1000 |
| 5. | HeartEW | 13 | 270 |
| 6. | Lymphography | 18 | 148 |
| 7. | M-of-n | 13 | 1000 |
| 8. | PenglungEW | 325 | 73 |
| 9. | SonarEW | 60 | 208 |
| 10. | SpectEW | 22 | 267 |
| 11. | CongressEW | 16 | 435 |
| 12. | IonosphereEW | 34 | 351 |
| 13. | KrvskpEW | 36 | 3196 |
| 14. | Tic-tac-toe | 9 | 958 |
| 15. | Vote | 16 | 300 |
| 16. | WaveformEW | 40 | 5000 |
| 17. | WineEW | 13 | 178 |
| 18. | Zoo | 16 | 101 |
| 19. | Clean1 | 166 | 476 |
| 20. | Semeion | 265 | 1593 |
| 21. | Colon | 2000 | 62 |
| 22. | Leukemia | 7129 | 72 |

The developed variants of BSSA are implemented to discover the superior reduct in terms of error rate using KNN classifier with a Euclidean distance metric ($K = 5$ [41]). To validate the optimality of the results and substantiate the capabilities of algorithms, we use hold-out strategy where each dataset is randomly split into 80% for training and 20% for testing. To obtain statistically meaningful results, this split is repeated 30 independent times. Therefore, the statistical measurements are collected based on the overall capabilities and final results throughout 30 independent runs.The dimensions of the tackled problems are equal to number of features in the datasets.

All the tabulated evaluations and analyzed behaviors of the proposed BSSA are recorded and compared to other optimizers using a PC with Intel Core(TM) i5-5200U 2.2GHz CPU and 4.0GB RAM. All algorithms are tested using the MATLAB 2013 software. To have fair comparisons, all algorithms have been carefully implemented in the same programming language and by the same computing platform that can use the same global settings for all algorithms. That is, all algorithms are uniformly randomly initialized. Moreover, for all algorithms the population size is set to 10 search agents, and the number of iterations is set to 100. These values are selected after conducting an initial empirical study by experimenting different values for the population size and number of iterations based on Leukemia dataset. This dataset was selected because it showed more sensitivity in comparison with other datasets. That is, significant changes in the performance of classifiers are noticed for slight changes in the parameter values [72]. As it can be seen in Table 3, a population size of 10 with 100 iterations managed to show very competitive results compared to larger population sizes and more iterations, which the latter require much more running time.

Table 3: Average accuracy results when using different combinations of population sizes and number of iterations based on Leukemia dataset.

| Population size | 10 | 50 | 100 |
|---|---|---|---|
| Number of iterations | 100 | 150 | 200 |
| BSSA_S1 | **0.9311** | 0.8667 | 0.8667 |
| BSSA_S2 | 0.9733 | **1.0000** | **1.0000** |
| BSSA_S3 | **1.0000** | 0.9978 | **1.0000** |
| BSSA_S4 | **1.0000** | **1.0000** | **1.0000** |
| BSSA_V1 | **1.0000** | **1.0000** | **1.0000** |
| BSSA_V2 | **1.0000** | **1.0000** | **1.0000** |
| BSSA_V3 | **1.0000** | 0.9800 | **1.0000** |
| BSSA_V4 | 0.9622 | 0.9378 | **1.0000** |

### *6.1. Assessment of the impact of $\alpha$ and $\beta$ on the fitness function*

The values of $\alpha$ and $\beta$ in the fitness function reflect the weight of their corresponding terms for the user. That is, $\alpha$ determines the weight of the classification accuracy, while $\beta$ corresponds to the weight of the features reduction rate. In majority of the previous works in literature, values of these parameters are set arbitrary. Traditionally, $\alpha$ is set to high value (i.e. $\alpha \geq 0.90$) and $\beta$ is set to a very small value (i.e. $\beta \leq 0.5$). This experiment is conducted to study the influence of $\alpha$ and $\beta$ on the performance of the basic BSSA with different TFs. The accuracy and the feature reduction rates are measured for different combinations of $\alpha$ and $\beta$ values. These experiments are conducted based on Leukemia dataset because this dataset showed more sensitivity in comparison with other datasets. That is, significant changes in the performance of classifiers are noticed for slight changes in the parameter values [72]. The resulted accuracy rates are shown in Table 4, while the reduction rates are shown in Table 5. As it can be seen in the table, the accuracy rates are increased along with increasing the value of the $\alpha$. On the other side, the impact of $\alpha$ and $\beta$ on the feature reduction rate is shown in Table 5. In general, there is a decrease in the reduction rate by decreasing the value of $\beta$.

In order to make fair comparisons with the obtained results in previous works, we will set $\alpha = 0.99$ and $\beta = 0.01$ which are commonly used in the literature [41, 73].

### *6.2. Assessment of the proposed BSSA without crossover*

In this subsection, the proposed BSSA-based algorithms are benchmarked on the 22 datasets to find the best version in dealing with FS problems. These binary versions utilize

Table 4: Impact of $\alpha$ and $\beta$ on the accuracy rates based on Leukemia dataset.

| $\alpha$ | **0.5** | **0.7** | **0.9** | **0.99** |
|---|---|---|---|---|
| $\beta$ | **0.5** | **0.3** | **0.1** | **0.01** |
| Transfer Functions | AVE | AVE | AVE | AVE |
| BSSA_S1 | 0.8156 | 0.8578 | 0.8911 | **0.9311** |
| BSSA_S2 | 0.9267 | 0.9578 | 0.9400 | **0.9733** |
| BSSA_S3 | 0.9578 | 0.9778 | **1.0000** | **1.0000** |
| BSSA_S4 | 0.8667 | 0.9333 | 0.9422 | **1.0000** |
| BSSA_V1 | 0.8756 | 0.9422 | 0.9733 | **1.0000** |
| BSSA_V2 | 0.8222 | 0.8867 | 0.9667 | **1.0000** |
| BSSA_V3 | 0.9311 | 0.9689 | 0.9978 | **1.0000** |
| BSSA_V4 | 0.9333 | 0.9578 | 0.9578 | **0.9622** |

Table 5: Impact of $\alpha$ and $\beta$ on the feature reduction rate based on Leukemia dataset.

| $\alpha$ | **0.5** | **0.7** | **0.9** | **0.99** |
|---|---|---|---|---|
| $\beta$ | **0.5** | **0.3** | **0.1** | **0.01** |
| Transfer Functions | AVE | AVE | AVE | AVE |
| BSSA_S1 | 0.5066 | 0.4495 | 0.4706 | 0.3852 |
| BSSA_S2 | 0.5019 | 0.4671 | 0.4979 | 0.4166 |
| BSSA_S3 | 0.4510 | 0.4572 | 0.4707 | 0.5102 |
| BSSA_S4 | 0.4733 | 0.5014 | 0.5002 | 0.5088 |
| BSSA_V1 | 0.5042 | 0.4934 | 0.4501 | 0.4796 |
| BSSA_V2 | 0.5041 | 0.5055 | 0.4309 | 0.5086 |
| BSSA_V3 | 0.5028 | 0.4879 | 0.5063 | 0.5081 |
| BSSA_V4 | 0.5038 | 0.4917 | 0.4824 | 0.4455 |

different S-shaped and V-shaped transfer functions, which were reported in Table 1. The efficacy of the BSSA-based versions are evaluated in using the average classification accuracy measure, selection size, average fitness, running time, and convergence behaviors on different problems. The accuracy is studied based on the selected features of the evaluated cases. The standard deviation (STD) of the versions in realizing the datasets is reported as well for all comparisons. To compare the effectiveness of multiple transfer functions in BSSA optimizer and detect significant improvements, the average ranking of the Friedman test is utilized here.

Table 6 shows the average fitness (AVE) and STD results for eight versions of BSSA.Tables 7-9 similarly demonstrate the accuracy results, average number of features, and running time records accompanied by the STD and ranking results of all versions of the BSSA optimizer. From Table 6, it is seen that the BSSA_S1 can provide the best fitness results on roughly 27% of the datasets. According to overall rankings, the best algorithm is the BSSA_V3, while the BSSA_S3, BSSA_S1, BSSA_S4, BSSA_V2, BSSA_S2, BSSA_V1, and BSSA_V4 are in the next stages.

Table 7 lists the results in terms of average accuracies. For the best and worst obtained accuracies we refer the reader to Table 25 in the appendix of tables. From Table 7, it can be seen that, in terms of classification accuracy, the BSSA with the first S-function outperforms all variants on around 27% of the datasets. The accuracy results of the binary version with V3 function are superior to those of other competitors according to overall rankings. According to the F-test results, those versions that utilize the S2, V1, and S4 transfer functions are in

Table 6: Comparison between different versions of BSSA (without crossover) based on S-shaped and V-shaped transfer functions in terms of average fitness results

| Benchmark | Stat. Measure | BSSA_S1 | BSSA_S2 | BSSA_S3 | BSSA_S4 | BSSA_V1 | BSSA_V2 | BSSA_V3 | BSSA_V4 |
|---|---|---|---|---|---|---|---|---|---|
| Breastcancer | AVE | **0.0293** | 0.0476 | 0.0308 | 0.0364 | 0.0393 | 0.0347 | 0.0377 | 0.0382 |
| | STD | 0.0000 | 0.0005 | 0.0015 | 0.0011 | 0.0022 | 0.0011 | 0.0017 | 0.0009 |
| BreastEW | AVE | 0.0583 | 0.0496 | **0.0466** | 0.0505 | 0.0528 | 0.0489 | 0.0487 | 0.0508 |
| | STD | 0.0041 | 0.0035 | 0.0044 | 0.0034 | 0.0040 | 0.0050 | 0.0057 | 0.0037 |
| Exactly | AVE | **0.0121** | 0.0162 | 0.0390 | 0.0211 | 0.0679 | 0.0740 | 0.0522 | 0.0771 |
| | STD | 0.0135 | 0.0171 | 0.0333 | 0.0229 | 0.0665 | 0.0630 | 0.0560 | 0.0626 |
| Exactly2 | AVE | 0.2804 | 0.2649 | 0.2431 | 0.2379 | 0.2402 | 0.2748 | **0.2336** | 0.2538 |
| | STD | 0.0153 | 0.0089 | 0.0006 | 0.0056 | 0.0275 | 0.0125 | 0.0033 | 0.0233 |
| HeartEW | AVE | **0.1572** | 0.1780 | 0.1939 | 0.1641 | 0.1826 | 0.1939 | 0.1734 | 0.1769 |
| | STD | 0.0078 | 0.0116 | 0.0095 | 0.0105 | 0.0091 | 0.0103 | 0.0064 | 0.0100 |
| Lymphography | AVE | **0.1326** | 0.1924 | 0.1551 | 0.1585 | 0.1393 | 0.1557 | 0.1824 | 0.1923 |
| | STD | 0.0085 | 0.0109 | 0.0109 | 0.0128 | 0.0120 | 0.0150 | 0.0125 | 0.0146 |
| M-of-n | AVE | 0.0093 | **0.0077** | 0.0186 | 0.0167 | 0.0304 | 0.0299 | 0.0277 | 0.0213 |
| | STD | 0.0075 | 0.0050 | 0.0184 | 0.0119 | 0.0316 | 0.0319 | 0.0278 | 0.0209 |
| PenglungEW | AVE | 0.1592 | 0.1041 | 0.1882 | 0.1773 | **0.0621** | 0.1497 | 0.1048 | 0.1184 |
| | STD | 0.0117 | 0.0162 | 0.0141 | 0.0151 | 0.0093 | 0.0158 | 0.0115 | 0.0162 |
| SonarEW | AVE | 0.1403 | 0.1310 | 0.1159 | 0.1298 | 0.1044 | **0.0679** | 0.1126 | 0.1566 |
| | STD | 0.0097 | 0.0110 | 0.0136 | 0.0094 | 0.0104 | 0.0084 | 0.0117 | 0.0115 |
| SpectEW | AVE | 0.1896 | 0.1456 | **0.1307** | 0.1551 | 0.1707 | 0.1570 | 0.1550 | 0.1790 |
| | STD | 0.0077 | 0.0084 | 0.0090 | 0.0074 | 0.0052 | 0.0105 | 0.0090 | 0.0089 |
| CongressEW | AVE | 0.0463 | 0.0395 | 0.0437 | 0.0335 | 0.0482 | **0.0249** | 0.0416 | 0.0302 |
| | STD | 0.0050 | 0.0046 | 0.0050 | 0.0036 | 0.0039 | 0.0053 | 0.0042 | 0.0044 |
| IonosphereEW | AVE | 0.1027 | 0.0807 | 0.0786 | 0.1139 | 0.0704 | 0.0728 | **0.0550** | 0.1006 |
| | STD | 0.0054 | 0.0049 | 0.0067 | 0.0074 | 0.0074 | 0.0114 | 0.0053 | 0.0083 |
| KrvskpEW | AVE | 0.0439 | **0.0348** | 0.0487 | 0.0450 | 0.0523 | 0.0518 | 0.0567 | 0.0500 |
| | STD | 0.0048 | 0.0040 | 0.0038 | 0.0056 | 0.0081 | 0.0071 | 0.0067 | 0.0073 |
| Tic-tac-toe | AVE | 0.2175 | 0.2120 | **0.1972** | 0.2247 | 0.1998 | 0.2154 | 0.2091 | 0.2114 |
| | STD | 0.0000 | 0.0026 | 0.0041 | 0.0034 | 0.0063 | 0.0023 | 0.0029 | 0.0076 |
| Vote | AVE | 0.0471 | 0.0541 | 0.0456 | **0.0337** | 0.0709 | 0.0597 | 0.0542 | 0.0493 |
| | STD | 0.0058 | 0.0054 | 0.0035 | 0.0060 | 0.0052 | 0.0046 | 0.0036 | 0.0078 |
| WaveformEW | AVE | **0.2671** | 0.2722 | 0.2703 | 0.2718 | 0.2773 | 0.2734 | 0.2838 | 0.2751 |
| | STD | 0.0039 | 0.0057 | 0.0066 | 0.0052 | 0.0068 | 0.0081 | 0.0073 | 0.0071 |
| WineEW | AVE | **0.0140** | 0.0412 | 0.0354 | 0.0256 | 0.0253 | 0.0279 | 0.0190 | 0.0288 |
| | STD | 0.0049 | 0.0048 | 0.0044 | 0.0035 | 0.0069 | 0.0054 | 0.0087 | 0.0065 |
| Zoo | AVE | 0.0704 | 0.0446 | **0.0047** | 0.0609 | 0.0486 | 0.0440 | 0.0427 | 0.0438 |
| | STD | 0.0092 | 0.0005 | 0.0005 | 0.0064 | 0.0080 | 0.0006 | 0.0117 | 0.0009 |
| Clean1 | AVE | 0.1592 | 0.1083 | 0.1100 | **0.1048** | 0.1327 | 0.1240 | 0.1080 | 0.1224 |
| | STD | 0.0053 | 0.0049 | 0.0059 | 0.0059 | 0.0049 | 0.0073 | 0.0056 | 0.0081 |
| Semeion | AVE | 0.0286 | 0.0299 | 0.0289 | 0.0369 | 0.0274 | 0.0304 | **0.0246** | 0.0259 |
| | STD | 0.0014 | 0.0017 | 0.0012 | 0.0018 | 0.0016 | 0.0018 | 0.0018 | 0.0018 |
| Colon | AVE | 0.1635 | 0.2630 | 0.2184 | 0.2894 | 0.2463 | 0.1670 | 0.2037 | **0.1570** |
| | STD | 0.0058 | 0.0079 | 0.0152 | 0.0097 | 0.0242 | 0.0379 | 0.0248 | 0.0216 |
| Leukemia | AVE | 0.0743 | 0.0322 | **0.0049** | **0.0049** | 0.0052 | **0.0049** | **0.0049** | 0.0429 |
| | STD | 0.0118 | 0.0326 | 0.0000 | 0.0000 | 0.0006 | 0.0000 | 0.0000 | 0.0326 |
| **Ranking** | **W\|T\|L** | **6\|0\|16** | 2\|0\|22 | 4\|1\|17 | 2\|1\|19 | 1\|0\|21 | 2\|1\|19 | 3\|1\|18 | 1\|0\|21 |
| **Overall Ranking** | **F-Test** | 4.4091 | 4.7727 | 3.9318 | 4.5455 | 4.9091 | 4.75 | **3.7273** | 4.9545 |

Table 7: Comparison between different versions of BSSA (without crossover) based on S-shaped and V-shaped transfer functions in terms of average accuracy.

| Benchmark | Stat. Measure | BSSA_S1 | BSSA_S2 | BSSA_S3 | BSSA_S4 | BSSA_V1 | BSSA_V2 | BSSA_V3 | BSSA_V4 |
|---|---|---|---|---|---|---|---|---|---|
| Breastcancer | AVE | **0.9771** | 0.9571 | 0.9743 | 0.9686 | 0.9659 | 0.9707 | 0.9678 | 0.9684 |
| | STD | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0025 | 0.0018 | 0.0018 | 0.0007 |
| BreastEW | AVE | 0.9478 | 0.9557 | **0.9584** | 0.9544 | 0.9516 | 0.9551 | 0.9554 | 0.9528 |
| | STD | 0.0041 | 0.0036 | 0.0046 | 0.0033 | 0.0042 | 0.0046 | 0.0053 | 0.0038 |
| Exactly | AVE | **0.9932** | 0.9891 | 0.9663 | 0.9843 | 0.9374 | 0.9313 | 0.9533 | 0.9281 |
| | STD | 0.0132 | 0.0169 | 0.0332 | 0.0227 | 0.0665 | 0.0629 | 0.0558 | 0.0625 |
| Exactly2 | AVE | 0.7239 | 0.7392 | 0.7560 | 0.7611 | 0.7589 | 0.7277 | **0.7655** | 0.7467 |
| | STD | 0.0134 | 0.0087 | 0.0000 | 0.0047 | 0.0270 | 0.0119 | 0.0029 | 0.0212 |
| HeartEW | AVE | **0.8467** | 0.8257 | 0.8104 | 0.8395 | 0.8217 | 0.8089 | 0.8299 | 0.8272 |
| | STD | 0.0071 | 0.0113 | 0.0096 | 0.0107 | 0.0101 | 0.0104 | 0.0071 | 0.0109 |
| Lymphography | AVE | **0.8734** | 0.8113 | 0.8491 | 0.8455 | 0.8644 | 0.8473 | 0.8203 | 0.8099 |
| | STD | 0.0090 | 0.0109 | 0.0113 | 0.0131 | 0.0125 | 0.0155 | 0.0129 | 0.0154 |
| M-of-n | AVE | 0.9960 | **0.9977** | 0.9869 | 0.9887 | 0.9753 | 0.9758 | 0.9777 | 0.9843 |
| | STD | 0.0072 | 0.0047 | 0.0181 | 0.0116 | 0.0315 | 0.0315 | 0.0274 | 0.0205 |
| PenglungEW | AVE | 0.8450 | 0.9009 | 0.8153 | 0.8261 | **0.9414** | 0.8523 | 0.8973 | 0.8838 |
| | STD | 0.0122 | 0.0164 | 0.0143 | 0.0154 | 0.0102 | 0.0154 | 0.0110 | 0.0161 |
| SonarEW | AVE | 0.8654 | 0.8744 | 0.8885 | 0.8740 | 0.8997 | **0.9365** | 0.8910 | 0.8465 |
| | STD | 0.0098 | 0.0113 | 0.0137 | 0.0096 | 0.0106 | 0.0086 | 0.0119 | 0.0117 |
| SpectEW | AVE | 0.8139 | 0.8585 | **0.8741** | 0.8483 | 0.8306 | 0.8465 | 0.8478 | 0.8239 |
| | STD | 0.0078 | 0.0084 | 0.0091 | 0.0072 | 0.0056 | 0.0109 | 0.0091 | 0.0093 |
| CongressEW | AVE | 0.9584 | 0.9645 | 0.9593 | 0.9699 | 0.9535 | **0.9795** | 0.9624 | 0.9723 |
| | STD | 0.0050 | 0.0047 | 0.0051 | 0.0035 | 0.0036 | 0.0056 | 0.0042 | 0.0044 |
| IonosphereEW | AVE | 0.9028 | 0.9241 | 0.9258 | 0.8892 | 0.9331 | 0.9305 | **0.9487** | 0.9021 |
| | STD | 0.0055 | 0.0048 | 0.0068 | 0.0076 | 0.0074 | 0.0110 | 0.0053 | 0.0081 |
| KrvskpEW | AVE | 0.9629 | **0.9711** | 0.9570 | 0.9606 | 0.9523 | 0.9529 | 0.9479 | 0.9546 |
| | STD | 0.0048 | 0.0037 | 0.0036 | 0.0055 | 0.0086 | 0.0072 | 0.0068 | 0.0074 |
| Tic-tac-toe | AVE | 0.7871 | 0.7926 | **0.8086** | 0.7789 | 0.8052 | 0.7895 | 0.7947 | 0.7933 |
| | STD | 0.0000 | 0.0026 | 0.0045 | 0.0029 | 0.0074 | 0.0020 | 0.0027 | 0.0076 |
| Vote | AVE | 0.9571 | 0.9491 | 0.9584 | **0.9696** | 0.9324 | 0.9433 | 0.9500 | 0.9536 |
| | STD | 0.0057 | 0.0057 | 0.0042 | 0.0060 | 0.0057 | 0.0045 | 0.0042 | 0.0075 |
| WaveformEW | AVE | **0.7379** | 0.7315 | 0.7328 | 0.7316 | 0.7255 | 0.7291 | 0.7190 | 0.7271 |
| | STD | 0.0039 | 0.0056 | 0.0067 | 0.0052 | 0.0068 | 0.0077 | 0.0072 | 0.0071 |
| WineEW | AVE | **0.9918** | 0.9633 | 0.9704 | 0.9794 | 0.9794 | 0.9768 | 0.9858 | 0.9753 |
| | STD | 0.0051 | 0.0051 | 0.0055 | 0.0043 | 0.0073 | 0.0051 | 0.0093 | 0.0069 |
| Zoo | AVE | 0.9340 | 0.9608 | **1.0000** | 0.9438 | 0.9562 | 0.9608 | 0.9621 | 0.9608 |
| | STD | 0.0096 | 0.0000 | 0.0000 | 0.0068 | 0.0084 | 0.0000 | 0.0114 | 0.0000 |
| Clean1 | AVE | 0.8462 | 0.8969 | 0.8945 | **0.8996** | 0.8706 | 0.8793 | 0.8955 | 0.8805 |
| | STD | 0.0057 | 0.0050 | 0.0060 | 0.0060 | 0.0050 | 0.0071 | 0.0055 | 0.0079 |
| Semeion | AVE | 0.9783 | 0.9762 | 0.9764 | 0.9681 | 0.9774 | 0.9742 | **0.9801** | 0.9789 |
| | STD | 0.0014 | 0.0018 | 0.0012 | 0.0018 | 0.0017 | 0.0019 | 0.0019 | 0.0017 |
| Colon | AVE | 0.8398 | 0.7398 | 0.7849 | 0.7129 | 0.7538 | 0.8344 | 0.7978 | **0.8441** |
| | STD | 0.0059 | 0.0082 | 0.0155 | 0.0098 | 0.0232 | 0.0367 | 0.0239 | 0.0209 |
| Leukemia | AVE | 0.9311 | 0.9733 | **1.0000** | **1.0000** | **1.0000** | **1.0000** | **1.0000** | 0.9622 |
| | STD | 0.0122 | 0.0332 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0336 |
| **Ranking** | **W\|T\|L** | **6\|0\|16** | 2\|0\|20 | 4\|1\|17 | 2\|1\|19 | 2\|1\|19 | 2\|1\|19 | 3\|1\|18 | 1\|0\|21 |
| **Overall Ranking** | **F-Test** | 4.3182 | 4.5455 | 3.9091 | 4.5 | 4.9773 | 4.8182 | **3.8636** | 5.0682 |

the next places.

Table 8: Comparison between different versions of BSSA (without crossover) based on S-shaped and V-shaped transfer functions in terms of average number of features

| Benchmark | Stat. Measure | BSSA_S1 | BSSA_S2 | BSSA_S3 | BSSA_S4 | BSSA_V1 | BSSA_V2 | BSSA_V3 | BSSA_V4 |
|---|---|---|---|---|---|---|---|---|---|
| Breastcancer | AVE | 6.0000 | **4.6333** | 4.8000 | 4.7333 | 5.0000 | 5.0667 | 5.2333 | 6.2333 |
| | STD | 0.0000 | 0.4901 | 1.3493 | 0.9803 | 0.7428 | 0.9072 | 0.5040 | 0.4302 |
| BreastEW | AVE | 19.8333 | 17.2000 | 16.0000 | 16.0667 | 14.5333 | 13.4333 | 13.8333 | **11.9333** |
| | STD | 2.1669 | 2.5380 | 2.3342 | 2.6121 | 2.8129 | 3.4309 | 3.6111 | 3.2898 |
| Exactly | AVE | **6.9667** | 7.0000 | 7.4000 | 7.2000 | 7.7000 | 7.8667 | 7.7000 | 7.7333 |
| | STD | 0.6687 | 0.6433 | 0.7701 | 0.6644 | 1.0222 | 0.9371 | 1.0875 | 1.0483 |
| Exactly2 | AVE | 9.2000 | 8.7333 | 2.0333 | **1.8000** | 1.9000 | 6.7667 | 1.8667 | 3.8667 |
| | STD | 2.7342 | 0.7397 | 0.7649 | 1.2972 | 1.0619 | 2.4591 | 0.8996 | 3.3501 |
| HeartEW | AVE | 6.9667 | 7.0000 | 8.0333 | 6.8333 | 7.9333 | **6.1000** | 6.4667 | 7.5000 |
| | STD | 1.6291 | 1.4622 | 1.2726 | 1.2058 | 1.8182 | 1.5166 | 1.7564 | 1.4081 |
| Lymphography | AVE | 13.1333 | 9.9000 | 10.2333 | 9.9667 | 9.1667 | 8.1333 | 8.1000 | **7.3333** |
| | STD | 1.1366 | 1.3734 | 1.7357 | 1.5196 | 2.8416 | 3.0820 | 2.9167 | 2.1227 |
| M-of-n | AVE | **6.9333** | 7.0333 | 7.2667 | 7.2000 | 7.7333 | 7.7333 | 7.3333 | 7.4333 |
| | STD | 0.6915 | 0.5561 | 0.6397 | 0.7144 | 0.8683 | 1.0148 | 1.0283 | 0.9353 |
| PenglungEW | AVE | 189.5000 | 195.4333 | 172.7333 | 167.7000 | 133.8667 | 111.0333 | **103.1333** | 109.1667 |
| | STD | 25.5920 | 10.7405 | 9.1234 | 7.9791 | 40.3431 | 54.1113 | 55.9715 | 50.0221 |
| SonarEW | AVE | 42.2667 | 39.8667 | 32.7333 | 30.7667 | 30.3667 | 30.6667 | 28.1667 | **27.6333** |
| | STD | 3.0954 | 4.4313 | 2.6253 | 3.3081 | 3.2641 | 4.3417 | 4.2757 | 4.7524 |
| SpectEW | AVE | 11.8000 | 12.0000 | 13.3000 | 10.6333 | **6.5000** | 11.1667 | 9.3333 | 10.2667 |
| | STD | 2.1877 | 2.3342 | 2.0703 | 2.3413 | 3.6742 | 2.2907 | 2.5371 | 2.0331 |
| CongressEW | AVE | 8.1333 | 7.0333 | 5.4333 | 5.9333 | **3.5333** | 7.3333 | 6.9000 | 4.4667 |
| | STD | 1.2521 | 2.2047 | 1.4547 | 1.4840 | 2.2854 | 1.9885 | 1.6474 | 1.9954 |
| IonosphereEW | AVE | 22.0333 | 18.9000 | 17.2667 | 14.3667 | 14.2667 | 13.7000 | 14.2667 | **12.5000** |
| | STD | 3.5862 | 2.3831 | 3.0731 | 2.3706 | 2.7535 | 3.5926 | 3.3107 | 3.5307 |
| KrvskpEW | AVE | 25.6667 | 22.2667 | 21.9000 | 21.6000 | **18.2000** | 18.4667 | 18.3000 | **18.2000** |
| | STD | 2.1549 | 2.1324 | 2.3976 | 2.4719 | 4.4443 | 3.0141 | 3.4356 | 3.4978 |
| Tic-tac-toe | AVE | 6.0000 | 6.0000 | 6.9000 | **5.2667** | 6.2333 | 6.3000 | **5.2667** | 6.0667 |
| | STD | 0.0000 | 0.0000 | 0.3051 | 0.6915 | 0.8584 | 0.9154 | 0.5208 | 0.3651 |
| Vote | AVE | 7.4667 | 5.9667 | 7.1333 | 5.7667 | 6.3667 | 5.7000 | 7.4667 | **5.3333** |
| | STD | 1.2521 | 1.5862 | 2.1772 | 1.8696 | 2.0592 | 2.4233 | 2.7759 | 2.0734 |
| WaveformEW | AVE | 30.4333 | 25.4000 | 23.3333 | 24.0667 | 22.0667 | 20.7000 | 22.4333 | **19.6333** |
| | STD | 2.0457 | 2.8357 | 2.6305 | 2.7409 | 3.7318 | 4.1369 | 4.1163 | 3.2322 |
| WineEW | AVE | 7.6333 | 6.3667 | 7.9667 | 6.8333 | 6.4333 | 6.3667 | 6.4000 | **5.6333** |
| | STD | 0.8087 | 1.1592 | 2.0924 | 1.3917 | 1.6333 | 1.8286 | 1.5669 | 1.0662 |
| Zoo | AVE | 8.1333 | 9.2667 | **7.5667** | 8.3333 | 8.4333 | 8.2667 | 8.2000 | 7.9667 |
| | STD | 0.8996 | 0.7849 | 0.7739 | 1.0613 | 1.4308 | 0.9444 | 1.4239 | 1.3767 |
| Clean1 | AVE | 115.5667 | 103.5667 | 93.2333 | 89.5000 | 76.7000 | 75.1000 | 75.5000 | **68.9667** |
| | STD | 13.1193 | 7.4772 | 8.7678 | 5.6614 | 13.0758 | 14.8982 | 16.6604 | 16.7507 |
| Semeion | AVE | 190.0333 | 166.2333 | 148.1333 | 140.8000 | 134.4000 | **129.4667** | 131.4000 | 132.2333 |
| | STD | 23.1181 | 8.0288 | 7.3940 | 9.7994 | 7.7797 | 17.6728 | 7.3700 | 13.6904 |
| Colon | AVE | 984.9000 | 1079.4333 | 1093.0000 | 1044.6667 | **502.8333** | 608.8000 | 710.2333 | 533.2333 |
| | STD | 17.4224 | 105.4853 | 36.7283 | 31.5391 | 426.8525 | 418.4239 | 393.4634 | 381.6319 |
| Leukemia | AVE | 4382.8000 | 4159.2670 | **3491.8670** | 3501.6670 | 3709.9670 | 3503.2670 | 3506.8670 | 3953.0670 |
| | STD | 415.7237 | 346.0309 | 31.9145 | 23.3036 | 398.4409 | 25.7266 | 25.2870 | 632.9743 |
| Ranking | W\|T\|L | 2\|0\|20 | 1\|0\|21 | 1\|0\|21 | 2\|0\|20 | 4\|0\|18 | 2\|0\|20 | 2\|0\|20 | 9\|0\|13 |
| Overall Ranking | F-Test | 6.3182 | 5.6818 | 5.5909 | 4.3864 | 3.9545 | 3.7727 | 3.3636 | **2.9318** |

Inspecting the results in Table 8, it can be spotted that the proposed BSSA with V4 transfer function provides the lower number of features than others in around 41% of the datasets with the best ranking. Regarding the ranks, the BSSA with V-shaped transfer functions can provide better results than those with S-shaped functions.

From Table 9, it is evident that the V4 can decrease the running time of the algorithm more than other choices. The transfer functions V2, V3, V1, S4, S3, S1, and S2 can be the next choices, respectively.

### *6.3. Assessment of the proposed BSSA with crossover*

In this section we assess the performance of BSSA combined with crossover and compare its performance to the basic BSSA that has no crossover operator.

Table 10 reveals the average fitness results of the BSSA with S-shaped TFs and the proposed BSSA with crossover operator and S-shaped TFs. From this table, it is seen

Table 9: Comparison between different versions of BSSA (without crossover) based on S-shaped and V-shaped transfer functions in terms of average running time

| Benchmark | Stat. Measure | BSSA_S1 | BSSA_S2 | BSSA_S3 | BSSA_S4 | BSSA_V1 | BSSA_V2 | BSSA_V3 | BSSA_V4 |
|---|---|---|---|---|---|---|---|---|---|
| Breastcancer | AVE | 6.3419 | 6.1287 | 6.0900 | 6.0691 | 6.0650 | 6.0793 | **6.0087** | 6.0535 |
| | STD | 0.2242 | 0.1176 | 0.1593 | 0.1416 | 0.1542 | 0.1310 | 0.1391 | 0.1472 |
| BreastEW | AVE | 6.9568 | 6.8192 | 6.7886 | 6.7479 | 6.7490 | 6.7242 | 6.7241 | **6.7204** |
| | STD | 0.1544 | 0.1412 | 0.1368 | 0.1365 | 0.1548 | 0.1054 | 0.1468 | 0.1474 |
| Exactly | AVE | 9.1079 | 8.8297 | 8.7315 | 8.5636 | 8.4290 | 8.3918 | **8.3905** | 8.4522 |
| | STD | 0.1820 | 0.1895 | 0.1461 | 0.1479 | 0.1691 | 0.1605 | 0.1509 | 0.1756 |
| Exactly2 | AVE | 9.2486 | 8.9892 | 8.6881 | 8.6479 | 8.5800 | 8.5698 | 8.6158 | **8.5339** |
| | STD | 0.2807 | 0.1765 | 0.1530 | 0.1408 | 0.2083 | 0.1446 | 0.1493 | 0.1533 |
| HeartEW | AVE | 4.8109 | 4.7856 | 4.8080 | 4.7876 | 4.7885 | 4.7795 | 4.8058 | **4.7629** |
| | STD | 0.1153 | 0.1266 | 0.1547 | 0.1490 | 0.1485 | 0.1241 | 0.1435 | 0.1143 |
| Lymphography | AVE | **4.5691** | 4.6016 | 4.5918 | 4.5776 | 4.5928 | 4.5818 | 4.5852 | 4.5817 |
| | STD | 0.1373 | 0.1310 | 0.1321 | 0.1051 | 0.1266 | 0.1128 | 0.1135 | 0.1230 |
| M-of-n | AVE | 8.9426 | 8.7137 | 8.5289 | 8.4811 | 8.4435 | 8.3370 | 8.3191 | **8.2535** |
| | STD | 0.1567 | 0.1353 | 0.1652 | 0.1800 | 0.1867 | 0.1428 | 0.1603 | 0.1564 |
| PenglungEW | AVE | 6.9319 | 7.0017 | 6.9723 | 6.9908 | 7.0545 | 6.8316 | 6.7966 | **6.7937** |
| | STD | 0.1779 | 0.2111 | 0.1598 | 0.1647 | 0.2331 | 0.1739 | 0.1856 | 0.1474 |
| SonarEW | AVE | 5.2936 | 5.2877 | 5.2625 | 5.2572 | 5.2337 | 5.1985 | **5.1945** | 5.2115 |
| | STD | 0.1417 | 0.1429 | 0.1502 | 0.1306 | 0.1504 | 0.1372 | 0.1408 | 0.1676 |
| SpectEW | AVE | 4.8724 | 4.8749 | 4.9058 | **4.8595** | 4.8817 | 4.8618 | 4.8952 | 4.8630 |
| | STD | 0.1254 | 0.1179 | 0.1166 | 0.0954 | 0.1349 | 0.1129 | 0.0963 | 0.1024 |
| CongressEW | AVE | 5.4705 | 5.4873 | 5.4636 | 5.4580 | 5.4406 | 5.4539 | **5.4404** | 5.4507 |
| | STD | 0.1292 | 0.0989 | 0.0971 | 0.1208 | 0.1466 | 0.1434 | 0.1103 | 0.1372 |
| IonosphereEW | AVE | 5.5331 | 5.5000 | 5.4766 | 5.4798 | 5.5120 | 5.4691 | 5.4667 | **5.4471** |
| | STD | 0.1344 | 0.1397 | 0.1002 | 0.1013 | 0.1217 | 0.1286 | 0.1224 | 0.1224 |
| KrvskpEW | AVE | 90.1701 | 85.5203 | 83.3227 | 82.4860 | 80.9167 | 80.8368 | 80.9479 | **80.7104** |
| | STD | 1.0019 | 0.6986 | 0.7765 | 0.7200 | 0.7489 | 0.9229 | 0.8432 | 0.8994 |
| Tic-tac-toe | AVE | 8.8671 | 8.6742 | 8.4558 | 8.4044 | 8.3256 | **8.2557** | 8.3069 | 8.2683 |
| | STD | 0.1682 | 0.1747 | 0.1625 | 0.1808 | 0.1533 | 0.1268 | 0.1958 | 0.1660 |
| Vote | AVE | 4.9164 | 4.9204 | 4.8939 | 4.9023 | 4.8986 | 4.8907 | 4.8872 | **4.8821** |
| | STD | 0.1268 | 0.1445 | 0.1002 | 0.1203 | 0.1053 | 0.1177 | 0.1121 | 0.1202 |
| WaveformEW | AVE | 233.4317 | 219.4103 | 211.4342 | 209.5122 | 203.5272 | **203.0986** | 203.7187 | 203.3405 |
| | STD | 2.6403 | 2.4184 | 1.5368 | 1.6556 | 2.0957 | 1.9709 | 2.3329 | 2.0857 |
| WineEW | AVE | 4.5797 | 4.5874 | 4.5819 | 4.5683 | 4.5612 | **4.5252** | 4.5425 | 4.5563 |
| | STD | 0.1356 | 0.1068 | 0.1281 | 0.1213 | 0.1273 | 0.0992 | 0.1021 | 0.1120 |
| Zoo | AVE | 4.5614 | 4.5935 | 4.5761 | 4.5770 | 4.5990 | 4.5575 | 4.5501 | **4.5438** |
| | STD | 0.1179 | 0.1361 | 0.1149 | 0.1313 | 0.1089 | 0.1098 | 0.1355 | 0.1457 |
| Clean1 | AVE | 14.5884 | 14.0300 | 13.6366 | 13.5364 | 13.2981 | 13.1682 | 13.2241 | **13.1324** |
| | STD | 0.3487 | 0.3311 | 0.3186 | 0.3236 | 0.3548 | 0.3357 | 0.3146 | 0.3455 |
| Semeion | AVE | 171.5068 | 160.8404 | 152.9361 | 150.4326 | 145.3891 | 145.4128 | 145.8595 | **145.3749** |
| | STD | 2.6292 | 1.4173 | 1.2590 | 1.1394 | 1.8617 | 1.7401 | 1.5058 | 1.5577 |
| Colon | AVE | 18.7257 | 19.0884 | 19.2046 | 19.2324 | 19.3587 | 18.1871 | 18.1081 | **18.0409** |
| | STD | 0.5844 | 0.5838 | 0.6449 | 0.6399 | 0.9240 | 0.5712 | 0.5278 | 0.5719 |
| Leukemia | AVE | 29.0596 | 26.0303 | **24.4623** | 24.5787 | 26.8454 | 26.4626 | 28.1687 | 27.0976 |
| | STD | 2.3031 | 2.4104 | 1.2403 | 1.1275 | 1.3364 | 0.8502 | 2.0315 | 1.3519 |
| **Ranking** | **W\|T\|L** | 1\|0\|21 | 0\|0\|22 | 1\|0\|21 | 1\|0\|21 | 0\|0\|22 | 3\|0\|19 | 4\|0\|18 | 12\|0\|10 |
| **Overall Ranking** | **F-Test** | 6.6364 | 6.8182 | 5.9091 | 4.8636 | 4.6364 | 2.5909 | 2.8182 | 1.7273 |

that the BSSA_S3_CP and BSSA_S2_CP can significantly outperform the BSSA_S3 and BSSA_S3 on 73% of the datasets, respectively. The BSSA_S2_CP can disclose superior results compared to the BSSA_S2 in 54% of the datasets. The BSSA_S4_CP outperforms the BSSA_S4 on 68% problems. The reason is that the embedded crossover operator has enhanced the exploration capacity of BSSA_S3_CP and BSSA_S2_CP compared to those versions that utilize the standard average operator. Hence, in the case of premature convergence the BSSA-based methods with crossover theme have more chance to escape from them by more iteration and then, smoothly, switch from broad exploration to focused exploitation around the food source. Based on the overall ranks at the end of Table 10, the BSSA_S3_CP have attained the best rank among other competitors in terms of the average fitness values.

Table 10: Comparison between the BSSA with S-shaped functions (without crossover) and the proposed BSSA combined with CP in terms of average fitness results.

| Benchmark | Stat. Measure | BSSA_S1 | BSSA_S1_CP | BSSA_S2 | BSSA_S2_CP | BSSA_S3 | BSSA_S3_CP | BSSA_S4 | BSSA_S4_CP |
|---|---|---|---|---|---|---|---|---|---|
| Breastcancer | AVE | **0.0293** | 0.0447 | 0.0476 | **0.0312** | 0.0308 | **0.0273** | 0.0364 | **0.0227** |
| | STD | 0.0000 | 0.0019 | 0.0005 | 0.0032 | 0.0015 | 0.0006 | 0.0011 | 0.0005 |
| BreastEW | AVE | 0.0583 | **0.0448** | **0.0496** | 0.0551 | **0.0466** | 0.0566 | 0.0505 | **0.0442** |
| | STD | 0.0041 | 0.0035 | 0.0035 | 0.0056 | 0.0044 | 0.0033 | 0.0034 | 0.0030 |
| Exactly | AVE | **0.0121** | 0.0146 | 0.0162 | **0.0088** | 0.0390 | **0.0251** | **0.0211** | 0.0231 |
| | STD | 0.0135 | 0.0127 | 0.0171 | 0.0047 | 0.0333 | 0.0254 | 0.0229 | 0.0211 |
| Exactly2 | AVE | 0.2804 | **0.2561** | 0.2649 | **0.2512** | 0.2431 | **0.2415** | **0.2379** | 0.2818 |
| | STD | 0.0153 | 0.0081 | 0.0089 | 0.0107 | 0.0006 | 0.0197 | 0.0056 | 0.0073 |
| HeartEW | AVE | **0.1572** | 0.1711 | 0.1780 | **0.1691** | 0.1939 | **0.1426** | 0.1641 | **0.1604** |
| | STD | 0.0078 | 0.0053 | 0.0116 | 0.0075 | 0.0095 | 0.0074 | 0.0105 | 0.0077 |
| Lymphography | AVE | **0.1326** | 0.1674 | 0.1924 | **0.1630** | 0.1551 | **0.1146** | 0.1585 | **0.1332** |
| | STD | 0.0085 | 0.0092 | 0.0109 | 0.0118 | 0.0109 | 0.0108 | 0.0128 | 0.0085 |
| M-of-n | AVE | 0.0093 | **0.0076** | 0.0077 | **0.0064** | 0.0186 | **0.0136** | 0.0167 | **0.0115** |
| | STD | 0.0075 | 0.0068 | 0.0050 | 0.0043 | 0.0184 | 0.0136 | 0.0119 | 0.0079 |
| PenglungEW | AVE | 0.1592 | **0.0853** | **0.1041** | 0.2147 | 0.1882 | **0.1266** | 0.1773 | **0.0816** |
| | STD | 0.0117 | 0.0084 | 0.0162 | 0.0098 | 0.0141 | 0.0134 | 0.0151 | 0.0091 |
| SonarEW | AVE | 0.1403 | **0.0776** | 0.1310 | **0.1100** | 0.1159 | **0.0678** | 0.1298 | **0.1131** |
| | STD | 0.0097 | 0.0076 | 0.0110 | 0.0105 | 0.0136 | 0.0095 | 0.0094 | 0.0098 |
| SpectEW | AVE | 0.1896 | **0.1479** | **0.1456** | 0.1632 | **0.1307** | 0.1673 | **0.1551** | 0.1678 |
| | STD | 0.0077 | 0.0050 | 0.0084 | 0.0067 | 0.0090 | 0.0044 | 0.0074 | 0.0082 |
| CongressEW | AVE | 0.0463 | **0.0375** | 0.0395 | **0.0345** | 0.0437 | **0.0404** | **0.0335** | 0.0386 |
| | STD | 0.0050 | 0.0056 | 0.0046 | 0.0033 | 0.0050 | 0.0037 | 0.0036 | 0.0052 |
| IonosphereEW | AVE | **0.1027** | 0.1413 | 0.0807 | **0.0762** | **0.0786** | 0.0857 | 0.1139 | **0.1000** |
| | STD | 0.0054 | 0.0059 | 0.0049 | 0.0048 | 0.0067 | 0.0080 | 0.0074 | 0.0059 |
| KrvskpEW | AVE | 0.0439 | **0.0411** | **0.0348** | 0.0397 | 0.0487 | **0.0410** | 0.0450 | **0.0446** |
| | STD | 0.0048 | 0.0037 | 0.0040 | 0.0047 | 0.0038 | 0.0058 | 0.0056 | 0.0068 |
| Tic-tac-toe | AVE | 0.2175 | **0.2135** | **0.2120** | 0.2222 | 0.1972 | **0.1844** | 0.2247 | **0.2098** |
| | STD | 0.0000 | 0.0069 | 0.0026 | 0.0028 | 0.0041 | 0.0000 | 0.0034 | 0.0038 |
| Vote | AVE | 0.0471 | **0.0420** | 0.0541 | **0.0523** | **0.0456** | 0.0514 | **0.0337** | 0.0549 |
| | STD | 0.0058 | 0.0093 | 0.0054 | 0.0032 | 0.0035 | 0.0057 | 0.0060 | 0.0042 |
| WaveformEW | AVE | **0.2671** | 0.2709 | 0.2722 | **0.2658** | 0.2703 | **0.2695** | 0.2718 | **0.2711** |
| | STD | 0.0039 | 0.0047 | 0.0057 | 0.0061 | 0.0066 | 0.0071 | 0.0052 | 0.0072 |
| WineEW | AVE | 0.0140 | **0.0077** | 0.0412 | **0.0279** | 0.0354 | **0.0115** | **0.0256** | 0.0350 |
| | STD | 0.0049 | 0.0035 | 0.0048 | 0.0021 | 0.0044 | 0.0057 | 0.0035 | 0.0043 |
| Zoo | AVE | **0.0704** | 0.1015 | 0.0446 | **0.0438** | 0.0047 | **0.0042** | 0.0609 | **0.0401** |
| | STD | 0.0092 | 0.0155 | 0.0005 | 0.0005 | 0.0005 | 0.0004 | 0.0064 | 0.0064 |
| Clean1 | AVE | 0.1592 | **0.1168** | 0.1083 | **0.1051** | **0.1100** | 0.1248 | **0.1048** | 0.1079 |
| | STD | 0.0053 | 0.0068 | 0.0049 | 0.0048 | 0.0059 | 0.0041 | 0.0059 | 0.0067 |
| Semeion | AVE | **0.0286** | 0.0322 | **0.0299** | 0.0338 | 0.0289 | **0.0255** | 0.0369 | **0.0308** |
| | STD | 0.0014 | 0.0017 | 0.0017 | 0.0016 | 0.0012 | 0.0014 | 0.0018 | 0.0015 |
| Colon | AVE | **0.1635** | 0.2464 | 0.2630 | **0.1390** | **0.2184** | 0.3163 | 0.2894 | **0.1255** |
| | STD | 0.0058 | 0.0156 | 0.0079 | 0.0119 | 0.0152 | 0.0185 | 0.0097 | 0.0137 |
| Leukemia | AVE | 0.0743 | **0.0123** | 0.0322 | **0.0051** | **0.0049** | 0.0166 | **0.0049** | 0.0765 |
| | STD | 0.0118 | 0.0199 | 0.0326 | 0.0003 | 0.0000 | 0.0247 | 0.0000 | 0.0165 |
| **Ranking** | W\|T\|L | 9\|0\|13 | 13\|0\|9 | 6\|0\|16 | **16\|0\|6** | 7\|0\|15 | **15\|0\|7** | 8\|0\|14 | 14\|0\|8 |
| **Overall Ranking** | F-Test | 4.8636 | 4.2727 | 5.2273 | 3.8182 | 4.7727 | **3.6818** | 5.0909 | 4.2727 |

In Table 11 we list the fitness results of the proposed BSSA methods with V-shaped TFs.According to this table, it is observed that the BSSA_V2_CP can obtain significantly better fitness measures than the BSSA_V2 on 59% of the datasets. The crossover operator has also improved the fitness values of BSSA_V4 algorithm on 12 cases. The reason is that the crossover operator improves the exploratory characteristic of the BSSA_V2 and BSSA_V4 variants. As such, it can jump out of sub-optimal solutions more efficiently, whereas the other competitors are still disposed to stagnation to local solutions. Based on the overall ranks, the BSSA with V2 and CP has demonstrated a better efficacy than other techniques.

Table 11: Comparison between the BSSA with V-shaped functions and the proposed BSSA with CP regarding the average fitness results.

| Benchmark | Stat. Measure | BSSA_V1 | BSSA_V1_CP | BSSA_V2 | BSSA_V2_CP | BSSA_V3 | BSSA_V3_CP | BSSA_V4 | BSSA_V4_CP |
|---|---|---|---|---|---|---|---|---|---|
| Breastcancer | AVE | 0.0393 | **0.0331** | 0.0347 | **0.0278** | 0.0377 | **0.0324** | 0.0382 | **0.0371** |
| | STD | 0.0022 | 0.0007 | 0.0011 | 0.0016 | 0.0017 | 0.0005 | 0.0009 | 0.0029 |
| BreastEW | AVE | 0.0528 | **0.0435** | 0.0489 | **0.0385** | **0.0487** | 0.0640 | 0.0508 | **0.0445** |
| | STD | 0.0040 | 0.0042 | 0.0050 | 0.0041 | 0.0057 | 0.0049 | 0.0037 | 0.0039 |
| Exactly | AVE | 0.0679 | **0.0390** | 0.0740 | **0.0467** | 0.0522 | **0.0413** | 0.0771 | **0.0294** |
| | STD | 0.0665 | 0.0446 | 0.0630 | 0.0527 | 0.0560 | 0.0370 | 0.0626 | 0.0286 |
| Exactly2 | AVE | **0.2402** | 0.2639 | 0.2748 | **0.2448** | **0.2336** | 0.2838 | **0.2538** | 0.2727 |
| | STD | 0.0275 | 0.0127 | 0.0125 | 0.0005 | 0.0033 | 0.0089 | 0.0233 | 0.0120 |
| HeartEW | AVE | 0.1826 | **0.1767** | 0.1939 | **0.1714** | **0.1734** | 0.1779 | **0.1769** | 0.1820 |
| | STD | 0.0091 | 0.0104 | 0.0103 | 0.0080 | 0.0064 | 0.0099 | 0.0100 | 0.0101 |
| Lymphography | AVE | **0.1393** | 0.1581 | 0.1557 | **0.1382** | **0.1824** | 0.1958 | 0.1923 | **0.1520** |
| | STD | 0.0120 | 0.0142 | 0.0150 | 0.0149 | 0.0125 | 0.0109 | 0.0146 | 0.0169 |
| M-of-n | AVE | 0.0304 | **0.0163** | 0.0299 | **0.0192** | **0.0277** | 0.0318 | **0.0213** | 0.0243 |
| | STD | 0.0316 | 0.0146 | 0.0319 | 0.0236 | 0.0278 | 0.0370 | 0.0209 | 0.0235 |
| PenglungEW | AVE | **0.0621** | 0.1752 | 0.1497 | **0.0844** | **0.1048** | 0.1183 | **0.1184** | 0.1237 |
| | STD | 0.0093 | 0.0185 | 0.0158 | 0.0008 | 0.0115 | 0.0174 | 0.0162 | 0.0135 |
| SonarEW | AVE | **0.1044** | 0.1139 | **0.0679** | 0.1014 | 0.1126 | **0.1021** | 0.1566 | **0.1062** |
| | STD | 0.0104 | 0.0125 | 0.0084 | 0.0075 | 0.0117 | 0.0105 | 0.0115 | 0.0110 |
| SpectEW | AVE | **0.1707** | 0.1948 | **0.1570** | 0.1771 | 0.1550 | **0.1337** | 0.1790 | **0.1693** |
| | STD | 0.0052 | 0.0131 | 0.0105 | 0.0096 | 0.0090 | 0.0061 | 0.0089 | 0.0116 |
| CongressEW | AVE | 0.0482 | **0.0317** | **0.0249** | 0.0438 | **0.0416** | 0.0456 | **0.0302** | 0.0306 |
| | STD | 0.0039 | 0.0036 | 0.0053 | 0.0061 | 0.0042 | 0.0058 | 0.0044 | 0.0095 |
| IonosphereEW | AVE | **0.0704** | 0.0924 | **0.0728** | 0.1089 | **0.0550** | 0.0886 | 0.1006 | **0.0949** |
| | STD | 0.0074 | 0.0066 | 0.0114 | 0.0100 | 0.0053 | 0.0089 | 0.0083 | 0.0076 |
| KrvskpEW | AVE | 0.0523 | **0.0508** | **0.0518** | 0.0604 | 0.0567 | **0.0512** | **0.0500** | 0.0521 |
| | STD | 0.0081 | 0.0095 | 0.0071 | 0.0069 | 0.0067 | 0.0079 | 0.0073 | 0.0069 |
| Tic-tac-toe | AVE | **0.1998** | 0.2170 | **0.2154** | 0.2162 | 0.2091 | **0.2022** | **0.2114** | 0.2245 |
| | STD | 0.0063 | 0.0016 | 0.0023 | 0.0038 | 0.0029 | 0.0085 | 0.0076 | 0.0053 |
| Vote | AVE | 0.0709 | **0.0465** | 0.0597 | **0.0440** | 0.0542 | **0.0336** | 0.0493 | **0.0368** |
| | STD | 0.0052 | 0.0053 | 0.0046 | 0.0063 | 0.0036 | 0.0038 | 0.0078 | 0.0053 |
| WaveformEW | AVE | 0.2773 | **0.2707** | **0.2734** | 0.2767 | 0.2838 | **0.2702** | **0.2751** | 0.2806 |
| | STD | 0.0068 | 0.0059 | 0.0081 | 0.0079 | 0.0073 | 0.0057 | 0.0071 | 0.0083 |
| WineEW | AVE | **0.0253** | 0.0437 | 0.0279 | **0.0228** | **0.0190** | 0.0249 | 0.0288 | **0.0267** |
| | STD | 0.0069 | 0.0052 | 0.0054 | 0.0052 | 0.0087 | 0.0110 | 0.0065 | 0.0056 |
| Zoo | AVE | 0.0486 | **0.0299** | **0.0440** | 0.0605 | **0.0427** | 0.0446 | 0.0438 | **0.0040** |
| | STD | 0.0080 | 0.0137 | 0.0006 | 0.0059 | 0.0117 | 0.0048 | 0.0009 | 0.0006 |
| Clean1 | AVE | 0.1327 | **0.1149** | 0.1240 | **0.1082** | 0.1080 | **0.1020** | **0.1224** | 0.1242 |
| | STD | 0.0049 | 0.0085 | 0.0073 | 0.0077 | 0.0056 | 0.0082 | 0.0081 | 0.0062 |
| Semeion | AVE | **0.0274** | 0.0293 | 0.0304 | **0.0295** | **0.0246** | 0.0336 | 0.0259 | **0.0238** |
| | STD | 0.0016 | 0.0016 | 0.0018 | 0.0021 | 0.0018 | 0.0015 | 0.0018 | 0.0018 |
| Colon | AVE | **0.2463** | 0.2535 | **0.1670** | 0.1875 | 0.2037 | **0.1433** | **0.1570** | 0.3530 |
| | STD | 0.0242 | 0.0503 | 0.0379 | 0.0335 | 0.0248 | 0.0286 | 0.0216 | 0.1000 |
| Leukemia | AVE | 0.0052 | **0.0049** | **0.0049** | 0.0051 | **0.0049** | **0.0049** | 0.0429 | **0.0365** |
| | STD | 0.0006 | 0.0000 | 0.0000 | 0.0004 | 0.0000 | 0.0000 | 0.0326 | 0.0328 |
| **Ranking** | W\|T\|L | 10\|0\|12 | 12\|0\|10 | 10\|0\|12 | **12\|0\|10** | 10\|1\|11 | 10\|1\|11 | 10\|0\|12 | 12\|0\|10 |
| **Overall Ranking** | F-Test | 5 | 4.409 | 4.9091 | **3.8182** | 4.0909 | 4.1364 | 5.0455 | 4.5909 |

Table 12 reveals the average results of proposed methods with S-shaped TFs. The superior accuracies of the BSSA with crossover operator can be detected on majority of datasets. The reason is that it can make a more stable balance between the diversification and intensification leanings due to its effective crossover operator between the candidate salps. Based on the ranking orders, the BSSA with S2 function and crossover strategy is the best algorithm among other optimizers. It is capable of providing higher accuracies than other optimizers on 68% of the datasets when showing acceptable STD values.

Table 12: Comparison between the BSSA with S-Shaped TFs approaches and the proposed method (with CP) based on the average accuracy.

| Benchmark | Stat. Measure | BSSA_S1 | BSSA_S1_CP | BSSA_S2 | BSSA_S2_CP | BSSA_S3 | BSSA_S3_CP | BSSA_S4 | BSSA_S4_CP |
|---|---|---|---|---|---|---|---|---|---|
| **Breastcancer** | **AVE** | **0.9771** | 0.9608 | 0.9571 | **0.9724** | 0.9743 | **0.9768** | 0.9686 | **0.9829** |
| | **STD** | 0.0000 | 0.0017 | 0.0000 | 0.0027 | 0.0000 | 0.0010 | 0.0000 | 0.0000 |
| **BreastEW** | **AVE** | 0.9478 | **0.9616** | **0.9557** | 0.9505 | **0.9584** | 0.9484 | 0.9544 | **0.9603** |
| | **STD** | 0.0041 | 0.0036 | 0.0036 | 0.0056 | 0.0046 | 0.0035 | 0.0033 | 0.0029 |
| **Exactly** | **AVE** | **0.9932** | 0.9905 | 0.9891 | **0.9963** | 0.9663 | **0.9803** | **0.9843** | 0.9823 |
| | **STD** | 0.0132 | 0.0125 | 0.0169 | 0.0046 | 0.0332 | 0.0253 | 0.0227 | 0.0209 |
| **Exactly2** | **AVE** | 0.7239 | **0.7480** | 0.7392 | **0.7509** | 0.7560 | **0.7582** | **0.7611** | 0.7224 |
| | **STD** | 0.0134 | 0.0078 | 0.0087 | 0.0092 | 0.0000 | 0.0183 | 0.0047 | 0.0078 |
| **HeartEW** | **AVE** | **0.8467** | 0.8336 | 0.8257 | **0.8338** | 0.8104 | **0.8605** | 0.8395 | **0.8432** |
| | **STD** | 0.0071 | 0.0050 | 0.0113 | 0.0072 | 0.0096 | 0.0070 | 0.0107 | 0.0073 |
| **Lymphography** | **AVE** | **0.8734** | 0.8369 | 0.8113 | **0.8410** | 0.8491 | **0.8900** | 0.8455 | **0.8707** |
| | **STD** | 0.0090 | 0.0093 | 0.0109 | 0.0121 | 0.0113 | 0.0110 | 0.0131 | 0.0085 |
| **M-of-n** | **AVE** | 0.9960 | **0.9976** | 0.9977 | **0.9987** | 0.9869 | **0.9918** | 0.9887 | **0.9941** |
| | **STD** | 0.0072 | 0.0066 | 0.0047 | 0.0041 | 0.0181 | 0.0133 | 0.0116 | 0.0076 |
| **PenglungEW** | **AVE** | 0.8450 | **0.9198** | **0.9009** | 0.7883 | 0.8153 | **0.8775** | 0.8261 | **0.9225** |
| | **STD** | 0.0122 | 0.0086 | 0.0164 | 0.0102 | 0.0143 | 0.0137 | 0.0154 | 0.0093 |
| **SonarEW** | **AVE** | 0.8654 | **0.9285** | 0.8744 | **0.8949** | 0.8885 | **0.9372** | 0.8740 | **0.8910** |
| | **STD** | 0.0098 | 0.0079 | 0.0113 | 0.0107 | 0.0137 | 0.0097 | 0.0096 | 0.0099 |
| **SpectEW** | **AVE** | 0.8139 | **0.8565** | **0.8585** | 0.8418 | **0.8741** | 0.8361 | **0.8483** | 0.8356 |
| | **STD** | 0.0078 | 0.0051 | 0.0084 | 0.0072 | 0.0091 | 0.0054 | 0.0072 | 0.0082 |
| **CongressEW** | **AVE** | 0.9584 | **0.9668** | 0.9645 | **0.9697** | 0.9593 | **0.9628** | **0.9699** | 0.9645 |
| | **STD** | 0.0050 | 0.0053 | 0.0047 | 0.0037 | 0.0051 | 0.0035 | 0.0035 | 0.0048 |
| **IonosphereEW** | **AVE** | **0.9028** | 0.8634 | 0.9241 | **0.9286** | **0.9258** | 0.9182 | 0.8892 | **0.9034** |
| | **STD** | 0.0055 | 0.0059 | 0.0048 | 0.0051 | 0.0068 | 0.0081 | 0.0076 | 0.0058 |
| **KrvskpEW** | **AVE** | 0.9629 | **0.9657** | **0.9711** | 0.9661 | 0.9570 | **0.9644** | 0.9606 | **0.9607** |
| | **STD** | 0.0048 | 0.0036 | 0.0037 | 0.0046 | 0.0036 | 0.0059 | 0.0055 | 0.0067 |
| **Tic-tac-toe** | **AVE** | 0.7871 | **0.7902** | **0.7926** | 0.7822 | 0.8086 | **0.8205** | 0.7789 | **0.7939** |
| | **STD** | 0.0000 | 0.0065 | 0.0026 | 0.0031 | 0.0045 | 0.0000 | 0.0029 | 0.0033 |
| **Vote** | **AVE** | 0.9571 | **0.9629** | 0.9491 | **0.9529** | **0.9584** | 0.9511 | **0.9696** | 0.9489 |
| | **STD** | 0.0057 | 0.0092 | 0.0057 | 0.0035 | 0.0042 | 0.0059 | 0.0060 | 0.0040 |
| **WaveformEW** | **AVE** | **0.7379** | 0.7337 | 0.7315 | **0.7381** | 0.7328 | **0.7335** | 0.7316 | **0.7321** |
| | **STD** | 0.0039 | 0.0045 | 0.0056 | 0.0060 | 0.0067 | 0.0069 | 0.0052 | 0.0072 |
| **WineEW** | **AVE** | 0.9918 | **0.9985** | 0.9633 | **0.9772** | 0.9704 | **0.9933** | **0.9794** | 0.9708 |
| | **STD** | 0.0051 | 0.0039 | 0.0051 | 0.0021 | 0.0055 | 0.0056 | 0.0043 | 0.0056 |
| **Zoo** | **AVE** | **0.9340** | 0.9026 | **0.9608** | **0.9608** | **1.0000** | **1.0000** | 0.9438 | **0.9634** |
| | **STD** | 0.0096 | 0.0159 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0068 | 0.0068 |
| **Clean1** | **AVE** | 0.8462 | **0.8894** | 0.8969 | **0.8999** | **0.8945** | 0.8796 | **0.8996** | 0.8962 |
| | **STD** | 0.0057 | 0.0067 | 0.0050 | 0.0049 | 0.0060 | 0.0042 | 0.0060 | 0.0068 |
| **Semeion** | **AVE** | **0.9783** | 0.9749 | **0.9762** | 0.9721 | 0.9764 | **0.9799** | 0.9681 | **0.9744** |
| | **STD** | 0.0014 | 0.0018 | 0.0018 | 0.0018 | 0.0012 | 0.0015 | 0.0018 | 0.0015 |
| **Colon** | **AVE** | **0.8398** | 0.7570 | 0.7398 | **0.8656** | **0.7849** | 0.6860 | 0.7129 | **0.8785** |
| | **STD** | 0.0059 | 0.0164 | 0.0082 | 0.0122 | 0.0155 | 0.0188 | 0.0098 | 0.0139 |
| **Leukemia** | **AVE** | 0.9311 | **0.9933** | 0.9733 | **1.0000** | **1.0000** | 0.9889 | **1.0000** | 0.9289 |
| | **STD** | 0.0122 | 0.0203 | 0.0332 | 0.0000 | 0.0000 | 0.0253 | 0.0000 | 0.0169 |
| Ranking | W\|T\|L | 9\|0\|13 | 13\|0\|9 | 6\|1\|15 | 15\|1\|6 | 7\|1\|14 | 14\|1\|7 | 8\|0\|14 | 14\|0\|8 |
| Overall Ranking | F-Test | 4.7955 | 4.0909 | 5.0455 | **3.75** | 4.7955 | 3.9091 | 5.1818 | 4.4318 |

Table 13 tabulates the average accuracy results of the proposed methods with V-shaped TFs. For the best and worst obtained accuracies we refer the reader to Table 25 in the appendix of tables. From Table 13, it is observed that the accuracies have been increased in those cases that utilize both crossover operator and V-shaped transfer formula. For instance, the BSSA_V1_CP, BSSA_V2_CP and BSSA_V4_CP show higher classification rates than those of their competitors on Breastcancer, BreastEW, and Exactly datasets. The enriched searching patterns of algorithms with crossover scheme can be detected from their improved results on different datasets compared to other binary versions. By comparing the BSSA_V3 with BSSA_V3_CP, it is seen that each method has outperformed other one on 11 datasets and both methods have achieved to a similar rank. Regarding the overall ranks, the BSSA_V2_CP can be selected as the best version.

The average number of features found by BSSA-based techniques with S-shaped TFs are revealed in Table 14. As it can be seen, both BSSA_S4 and BSSA_S4_CP are similarly

Table 13: Comparison between the BSSA with V-Shaped TFs approaches and the related version with CP based on average accuracy.

| Benchmark | Stat. Measure | BSSA_V1 | BSSA_V1_CP | BSSA_V2 | BSSA_V2_CP | BSSA_V3 | BSSA_V3_CP | BSSA_V4 | BSSA_V4_CP |
|---|---|---|---|---|---|---|---|---|---|
| **Breastcancer** | **AVE** | 0.9659 | **0.9713** | 0.9707 | **0.9767** | 0.9678 | **0.9735** | 0.9684 | **0.9695** |
| | **STD** | 0.0025 | 0.0005 | 0.0018 | 0.0017 | 0.0018 | 0.0013 | 0.0007 | 0.0026 |
| **BreastEW** | **AVE** | 0.9516 | **0.9608** | 0.9551 | **0.9661** | **0.9554** | 0.9400 | 0.9528 | **0.9601** |
| | **STD** | 0.0042 | 0.0040 | 0.0046 | 0.0044 | 0.0053 | 0.0049 | 0.0038 | 0.0042 |
| **Exactly** | **AVE** | 0.9374 | **0.9663** | 0.9313 | **0.9586** | 0.9533 | **0.9640** | 0.9281 | **0.9759** |
| | **STD** | 0.0665 | 0.0445 | 0.0629 | 0.0526 | 0.0558 | 0.0369 | 0.0625 | 0.0284 |
| **Exactly2** | **AVE** | **0.7589** | 0.7354 | 0.7277 | **0.7540** | **0.7655** | 0.7203 | **0.7467** | 0.7302 |
| | **STD** | 0.0270 | 0.0106 | 0.0119 | 0.0000 | 0.0029 | 0.0089 | 0.0212 | 0.0129 |
| **HeartEW** | **AVE** | 0.8217 | **0.8262** | 0.8089 | **0.8316** | **0.8299** | 0.8252 | **0.8272** | 0.8215 |
| | **STD** | 0.0101 | 0.0108 | 0.0104 | 0.0080 | 0.0071 | 0.0102 | 0.0109 | 0.0104 |
| **Lymphography** | **AVE** | **0.8644** | 0.8459 | 0.8473 | **0.8650** | **0.8203** | 0.8068 | 0.8099 | **0.8509** |
| | **STD** | 0.0125 | 0.0153 | 0.0155 | 0.0151 | 0.0129 | 0.0113 | 0.0154 | 0.0172 |
| **M-of-n** | **AVE** | 0.9753 | **0.9891** | 0.9758 | **0.9863** | **0.9777** | 0.9735 | **0.9843** | 0.9813 |
| | **STD** | 0.0315 | 0.0141 | 0.0315 | 0.0233 | 0.0274 | 0.0368 | 0.0205 | 0.0231 |
| **PenglungEW** | **AVE** | **0.9414** | 0.8270 | 0.8523 | **0.9189** | **0.8973** | 0.8847 | **0.8838** | 0.8793 |
| | **STD** | 0.0102 | 0.0182 | 0.0154 | 0.0000 | 0.0110 | 0.0173 | 0.0161 | 0.0137 |
| **SonarEW** | **AVE** | **0.8997** | 0.8894 | **0.9365** | 0.9022 | 0.8910 | **0.9016** | 0.8465 | **0.8974** |
| | **STD** | 0.0106 | 0.0126 | 0.0086 | 0.0076 | 0.0119 | 0.0106 | 0.0117 | 0.0114 |
| **SpectEW** | **AVE** | **0.8306** | 0.8072 | **0.8465** | 0.8236 | 0.8478 | **0.8699** | 0.8239 | **0.8331** |
| | **STD** | 0.0056 | 0.0132 | 0.0109 | 0.0101 | 0.0091 | 0.0064 | 0.0093 | 0.0117 |
| **CongressEW** | **AVE** | 0.9535 | **0.9708** | **0.9795** | 0.9587 | **0.9624** | 0.9564 | **0.9723** | 0.9713 |
| | **STD** | 0.0036 | 0.0039 | 0.0056 | 0.0058 | 0.0042 | 0.0055 | 0.0044 | 0.0089 |
| **IonosphereEW** | **AVE** | **0.9331** | 0.9106 | **0.9305** | 0.8938 | **0.9487** | 0.9136 | 0.9021 | **0.9078** |
| | **STD** | 0.0074 | 0.0067 | 0.0110 | 0.0097 | 0.0053 | 0.0086 | 0.0081 | 0.0069 |
| **KrvskpEW** | **AVE** | 0.9523 | **0.9540** | **0.9529** | 0.9447 | 0.9479 | **0.9536** | **0.9546** | 0.9525 |
| | **STD** | 0.0086 | 0.0097 | 0.0072 | 0.0071 | 0.0068 | 0.0081 | 0.0074 | 0.0072 |
| **Tic-tac-toe** | **AVE** | **0.8052** | 0.7868 | **0.7895** | 0.7875 | 0.7947 | **0.8025** | **0.7933** | 0.7800 |
| | **STD** | 0.0074 | 0.0011 | 0.0020 | 0.0034 | 0.0027 | 0.0086 | 0.0076 | 0.0054 |
| **Vote** | **AVE** | 0.9324 | **0.9558** | 0.9433 | **0.9589** | 0.9500 | **0.9696** | 0.9536 | **0.9662** |
| | **STD** | 0.0057 | 0.0054 | 0.0045 | 0.0063 | 0.0042 | 0.0042 | 0.0075 | 0.0055 |
| **WaveformEW** | **AVE** | 0.7255 | **0.7321** | **0.7291** | 0.7256 | 0.7190 | **0.7323** | **0.7271** | 0.7219 |
| | **STD** | 0.0068 | 0.0058 | 0.0077 | 0.0077 | 0.0072 | 0.0058 | 0.0071 | 0.0082 |
| **WineEW** | **AVE** | **0.9794** | 0.9610 | 0.9768 | **0.9820** | **0.9858** | 0.9794 | 0.9753 | **0.9779** |
| | **STD** | 0.0073 | 0.0057 | 0.0051 | 0.0056 | 0.0093 | 0.0111 | 0.0069 | 0.0055 |
| **Zoo** | **AVE** | 0.9562 | **0.9739** | **0.9608** | 0.9431 | **0.9621** | 0.9595 | 0.9608 | **1.0000** |
| | **STD** | 0.0084 | 0.0139 | 0.0000 | 0.0060 | 0.0114 | 0.0050 | 0.0000 | 0.0000 |
| **Clean1** | **AVE** | 0.8706 | **0.8882** | 0.8793 | **0.8955** | 0.8955 | **0.9020** | **0.8805** | 0.8793 |
| | **STD** | 0.0050 | 0.0082 | 0.0071 | 0.0076 | 0.0055 | 0.0084 | 0.0079 | 0.0061 |
| **Semeion** | **AVE** | **0.9774** | 0.9754 | 0.9742 | **0.9751** | **0.9801** | 0.9710 | 0.9789 | **0.9808** |
| | **STD** | 0.0017 | 0.0016 | 0.0019 | 0.0021 | 0.0019 | 0.0013 | 0.0017 | 0.0018 |
| **Colon** | **AVE** | **0.7538** | 0.7473 | **0.8344** | 0.8140 | 0.7978 | **0.8581** | **0.8441** | 0.6462 |
| | **STD** | 0.0232 | 0.0495 | 0.0367 | 0.0325 | 0.0239 | 0.0276 | 0.0209 | 0.0993 |
| **Leukemia** | **AVE** | **1.0000** | **1.0000** | **1.0000** | **1.0000** | **1.0000** | **1.0000** | 0.9622 | **0.9689** |
| | **STD** | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0336 | 0.0338 |
| Ranking | W\|T\|L | 10\|1\|11 | 11\|1\|10 | 9\|1\|12 | 12\|1\|9 | 11\|1\|10 | 10\|1\|11 | 10\|0\|12 | 12\|0\|10 |
| Overall Ranking | F-Test | 4.9318 | 4.4545 | 4.9091 | **3.8409** | 4.1591 | 4.1591 | 4.9318 | 4.6136 |

the best choices in terms of selected features.

Table 14: Comparison between the BSSA based S-Shaped transfer functions approaches and the proposed method (with CP) based on average number of features.

| Benchmark | Stat. Measure | BSSA_S1 | BSSA_S1_CP | BSSA_S2 | BSSA_S2_CP | BSSA_S3 | BSSA_S3_CP | BSSA_S4 | BSSA_S4_CP |
|---|---|---|---|---|---|---|---|---|---|
| **Breastcancer** | **AVE** | 6.0000 | **5.2333** | 4.6333 | **3.4333** | 4.8000 | **3.8667** | **4.7333** | 5.2000 |
| | **STD** | 0.0000 | 0.4302 | 0.4901 | 0.5040 | 1.3493 | 0.3457 | 0.9803 | 0.4068 |
| **BreastEW** | **AVE** | **19.8333** | 20.5000 | **17.2000** | 18.3667 | **16.0000** | 16.7000 | 16.0667 | **14.8333** |
| | **STD** | 2.1669 | 1.7568 | 2.5380 | 2.8099 | 2.3342 | 2.3364 | 2.6121 | 1.8770 |
| **Exactly** | **AVE** | 6.9667 | **6.8000** | 7.0000 | **6.7000** | 7.4000 | **7.2000** | **7.2000** | 7.3333 |
| | **STD** | 0.6687 | 0.5509 | 0.6433 | 0.4661 | 0.7701 | 0.6644 | 0.6644 | 0.6065 |
| **Exactly2** | **AVE** | 9.2000 | **8.6333** | 8.7333 | **6.0333** | **2.0333** | 2.7333 | **1.8000** | 9.1333 |
| | **STD** | 2.7342 | 1.6291 | 0.7397 | 2.6193 | 0.7649 | 2.3916 | 1.2972 | 1.0743 |
| **HeartEW** | **AVE** | **6.9667** | 8.3000 | 7.0000 | **6.0000** | 8.0333 | **5.8000** | 6.8333 | **6.6667** |
| | **STD** | 1.6291 | 0.5350 | 1.4622 | 1.3646 | 1.2726 | 1.4239 | 1.2058 | 1.3218 |
| **Lymphography** | **AVE** | 13.1333 | **10.8000** | **9.9000** | 10.0000 | **10.2333** | 10.2667 | 9.9667 | **9.4667** |
| | **STD** | 1.1366 | 0.9613 | 1.3734 | 1.2318 | 1.7357 | 1.9286 | 1.5196 | 1.8333 |
| **M-of-n** | **AVE** | 6.9333 | **6.8333** | 7.0333 | **6.7333** | 7.2667 | **7.1000** | **7.2000** | 7.3000 |
| | **STD** | 0.6915 | 0.5307 | 0.5561 | 0.6397 | 0.6397 | 0.6618 | 0.7144 | 0.6513 |
| **PenglungEW** | **AVE** | **189.5000** | 193.5000 | 195.4333 | **166.8333** | 172.7333 | **171.6000** | 167.7000 | **159.9000** |
| | **STD** | 25.5920 | 19.3333 | 10.7405 | 15.1887 | 9.1234 | 9.9329 | 7.9791 | 5.9385 |
| **SonarEW** | **AVE** | 42.2667 | **41.1333** | 39.8667 | **35.6667** | **32.7333** | 33.3667 | **30.7667** | 31.1000 |
| | **STD** | 3.0954 | 3.6173 | 4.4313 | 2.9866 | 2.6253 | 2.8585 | 3.3081 | 2.6044 |
| **SpectEW** | **AVE** | **11.8000** | 12.7667 | **12.0000** | 14.4667 | 13.3000 | **10.9333** | **10.6333** | 11.0333 |
| | **STD** | 2.1877 | 1.6121 | 2.3342 | 2.4457 | 2.0703 | 3.5809 | 2.3413 | 1.6709 |
| **CongressEW** | **AVE** | 8.1333 | **7.4000** | **7.0333** | 7.2000 | **5.4333** | 5.7333 | 5.9333 | **5.5333** |
| | **STD** | 1.2521 | 1.6103 | 2.2047 | 1.8644 | 1.4547 | 1.3629 | 1.4840 | 1.6965 |
| **IonosphereEW** | **AVE** | 22.0333 | **20.8333** | 18.9000 | **18.8333** | 17.2667 | **15.8667** | **14.3667** | 14.9333 |
| | **STD** | 3.5862 | 2.4925 | 2.3831 | 2.5875 | 3.0731 | 2.5829 | 2.3706 | 2.4486 |
| **KrvskpEW** | **AVE** | **25.6667** | 25.7333 | 22.2667 | **21.9667** | 21.9000 | **20.4667** | 21.6000 | **20.5667** |
| | **STD** | 2.1549 | 2.1324 | 2.1324 | 2.3706 | 2.3976 | 2.5560 | 2.4719 | 2.3735 |
| **Tic-tac-toe** | **AVE** | 6.0000 | **5.2333** | 6.0000 | **5.9000** | 6.9000 | **6.0000** | 5.2667 | **5.2000** |
| | **STD** | 0.0000 | 0.5040 | 0.0000 | 0.3051 | 0.3051 | 0.0000 | 0.6915 | 0.4842 |
| **Vote** | **AVE** | **7.4667** | 8.4667 | **5.9667** | 9.0333 | 7.1333 | **4.8333** | **5.7667** | 6.9000 |
| | **STD** | 1.2521 | 1.4077 | 1.5862 | 1.5421 | 2.1772 | 1.4875 | 1.8696 | 1.8634 |
| **WaveformEW** | **AVE** | 30.4333 | **28.7667** | **25.4000** | 25.8333 | 23.3333 | **22.9000** | 24.0667 | **23.6000** |
| | **STD** | 2.0457 | 2.6997 | 2.8357 | 2.6663 | 2.6305 | 3.3255 | 2.7409 | 3.0468 |
| **WineEW** | **AVE** | **7.6333** | 8.1333 | **6.3667** | 6.8333 | 7.9667 | **6.3333** | **6.8333** | 7.8667 |
| | **STD** | 0.8087 | 1.6554 | 1.1592 | 1.2617 | 2.0924 | 0.9589 | 1.3917 | 2.1772 |
| **Zoo** | **AVE** | **8.1333** | 8.2000 | 9.2667 | **7.9333** | 7.5667 | **6.7000** | 8.3333 | **6.1667** |
| | **STD** | 0.8996 | 1.1567 | 0.7849 | 0.7397 | 0.7739 | 0.7022 | 1.0613 | 0.8743 |
| **Clean1** | **AVE** | **115.5667** | 120.0667 | 103.5667 | **99.7333** | 93.2333 | **92.1667** | 89.5000 | **86.4000** |
| | **STD** | 13.1193 | 8.4115 | 7.4772 | 6.6381 | 8.7678 | 6.2427 | 5.6614 | 7.2853 |
| **Semeion** | **AVE** | **190.0333** | 196.9000 | 166.2333 | **165.9000** | 148.1333 | **147.5000** | **140.8000** | 143.2000 |
| | **STD** | 23.1181 | 10.3968 | 8.0288 | 14.5705 | 7.3940 | 8.7168 | 9.7994 | 7.2844 |
| **Colon** | **AVE** | **984.9000** | 1160.8333 | **1079.4333** | 1180.7000 | **1093.0000** | 1097.4333 | **1044.6667** | 1049.2333 |
| | **STD** | 17.4224 | 152.8493 | 105.4853 | 85.4312 | 36.7283 | 44.7165 | 31.5391 | 22.2272 |
| **Leukemia** | **AVE** | 4382.8000 | **4063.0333** | 4159.2670 | **3642.5000** | **3491.8670** | 3959.9333 | **3501.6670** | 4326.3667 |
| | **STD** | 415.7237 | 482.5962 | 346.0309 | 235.9664 | 31.9145 | 530.6809 | 23.3036 | 515.6235 |
| Ranking | W\|T\|L | 11\|0\|11 | 11\|0\|11 | 8\|0\|14 | 14\|0\|8 | 7\|0\|15 | 15\|0\|7 | 12\|0\|10 | 10\|0\|12 |
| Overall Ranking | F-Test | 6.1364 | 6.2727 | 5.1818 | 4.5227 | 4.5455 | 3.2500 | **3.0455** | **3.0455** |

Inspecting the average number of features attained by BSSA-based algorithms with V-shaped TFs in Table 15, we can notice that the BSSA_V2_CP version has obtained the best place among other versions. The reason is that the crossover operator has enhanced the searching competences of the BSSA_V2_CP on majority of tasks.

Average running time of BSSA-based optimizers with S-shaped TFs are shown in Table 16. Inspecting the results in in this table, the BSSA_S3_CP is the best approach among others. On the other hand, Table 17 compares the the running time of the BSSA-based algorithms with V-shaped TFs.It can be noticed that the BSSA_V4_CP algorithm has the lowest average running time. From the running time results in Tables 16 and 17, it is evident that BSSA-based versions that utilize the crossover strategy beside the S-shaped and V-shaped TFs can perform the exploration and exploitation phases better and quicker than other binary versions that still employ the average operator of the basic SSA.

Table 15: Comparison between the BSSA based V-Shaped transfer functions approaches and the proposed method (with CP) based on average number of features.

| Benchmark | Stat. Measure | BSSA_V1 | BSSA_V1_CP | BSSA_V2 | BSSA_V2_CP | BSSA_V3 | BSSA_V3_CP | BSSA_V4 | BSSA_V4_CP |
|---|---|---|---|---|---|---|---|---|---|
| **Breastcancer** | **AVE** | 5.0000 | **4.2667** | 5.0667 | **4.2000** | **5.2333** | 5.5667 | **6.2333** | 6.2667 |
| | **STD** | 0.7428 | 0.4498 | 0.9072 | 0.5509 | 0.5040 | 0.7739 | 0.4302 | 0.4498 |
| **BreastEW** | **AVE** | 14.5333 | **14.0000** | **13.4333** | 14.8333 | 13.8333 | **13.6667** | **11.9333** | 15.1667 |
| | **STD** | 2.8129 | 2.5052 | 3.4309 | 3.1082 | 3.6111 | 2.9165 | 3.2898 | 2.4925 |
| **Exactly** | **AVE** | 7.7000 | **7.3333** | 7.8667 | **7.4000** | 7.7000 | **7.4000** | 7.7333 | **7.3000** |
| | **STD** | 1.0222 | 0.8023 | 0.9371 | 0.9685 | 1.0875 | 0.7701 | 1.0483 | 0.7497 |
| **Exactly2** | **AVE** | **1.9000** | 2.4667 | 6.7667 | **1.6000** | **1.8667** | 9.0333 | **3.8667** | 7.2667 |
| | **STD** | 1.0619 | 2.9212 | 2.4591 | 0.6215 | 0.8996 | 1.0334 | 3.3501 | 2.1961 |
| **HeartEW** | **AVE** | 7.9333 | **6.0000** | **6.1000** | **6.1000** | 6.4667 | **6.2333** | 7.5000 | **6.8667** |
| | **STD** | 1.8182 | 1.2318 | 1.5166 | 0.9948 | 1.7564 | 0.8584 | 1.4081 | 1.0743 |
| **Lymphography** | **AVE** | **9.1667** | 10.0333 | **8.1333** | 8.2667 | 8.1000 | **8.0333** | **7.3333** | 7.9000 |
| | **STD** | 2.8416 | 2.4980 | 3.0820 | 1.8742 | 2.9167 | 1.9911 | 2.1227 | 1.9538 |
| **M-of-n** | **AVE** | 7.7333 | **7.1667** | 7.7333 | **7.2667** | 7.3333 | **7.2333** | **7.4333** | 7.4667 |
| | **STD** | 0.8683 | 0.9129 | 1.0148 | 0.8683 | 1.0283 | 0.9714 | 0.9353 | 0.8604 |
| **PenglungEW** | **AVE** | 133.8667 | **127.2000** | **111.0333** | 133.3333 | **103.1333** | 133.7000 | **109.1667** | 137.4333 |
| | **STD** | 40.3431 | 44.5633 | 54.1113 | 26.1116 | 55.9715 | 37.5014 | 50.0221 | 32.8210 |
| **SonarEW** | **AVE** | 30.3667 | **26.7667** | 30.6667 | **27.9667** | **28.1667** | 28.3333 | **27.6333** | 28.1667 |
| | **STD** | 3.2641 | 4.8187 | 4.3417 | 3.3475 | 4.2757 | 4.2209 | 4.7524 | 3.5143 |
| **SpectEW** | **AVE** | **6.5000** | 8.7000 | 11.1667 | **5.5667** | **9.3333** | 10.8667 | 10.2667 | **8.9000** |
| | **STD** | 3.6742 | 1.8597 | 2.2907 | 2.8367 | 2.5371 | 2.4031 | 2.0331 | 2.3831 |
| **CongressEW** | **AVE** | **3.5333** | 4.5333 | 7.3333 | **4.6333** | 6.9000 | **4.0000** | 4.4667 | **3.4667** |
| | **STD** | 2.2854 | 1.7953 | 1.9885 | 1.8659 | 1.6474 | 2.1335 | 1.9954 | 1.4794 |
| **IonosphereEW** | **AVE** | 14.2667 | **13.3000** | 13.7000 | **12.6333** | 14.2667 | **10.5333** | 12.5000 | **12.2000** |
| | **STD** | 2.7535 | 4.1784 | 3.5926 | 3.4887 | 3.3107 | 3.5597 | 3.5307 | 4.6416 |
| **KrvskpEW** | **AVE** | **18.2000** | 18.9667 | **18.4667** | 20.2333 | **18.3000** | 18.8667 | **18.2000** | 18.3000 |
| | **STD** | 4.4443 | 3.0680 | 3.0141 | 2.5688 | 3.4356 | 3.0820 | 3.4978 | 4.0442 |
| **Tic-tac-toe** | **AVE** | 6.2333 | **5.3000** | 6.3000 | **5.2000** | **5.2667** | 6.0000 | 6.0667 | **6.0333** |
| | **STD** | 0.8584 | 0.5960 | 0.9154 | 0.4068 | 0.5208 | 0.0000 | 0.3651 | 0.3198 |
| **Vote** | **AVE** | 6.3667 | **4.4000** | 5.7000 | **5.3000** | 7.4667 | **5.4667** | **5.3333** | 5.3667 |
| | **STD** | 2.0592 | 2.1592 | 2.4233 | 1.3684 | 2.7759 | 1.5698 | 2.0734 | 2.6972 |
| **WaveformEW** | **AVE** | 22.0667 | **21.9667** | 20.7000 | **20.0667** | 22.4333 | **20.7333** | **19.6333** | 21.2000 |
| | **STD** | 3.7318 | 3.0680 | 4.1369 | 3.1724 | 4.1163 | 4.2825 | 3.2322 | 3.9862 |
| **WineEW** | **AVE** | **6.4333** | 6.6667 | **6.3667** | 6.5667 | 6.4000 | **5.8000** | **5.6333** | 6.2667 |
| | **STD** | 1.6333 | 1.2130 | 1.8286 | 1.6121 | 1.5669 | 1.1861 | 1.0662 | 1.8742 |
| **Zoo** | **AVE** | 8.4333 | **6.4333** | 8.2667 | **6.7000** | 8.2000 | **7.1667** | 7.9667 | **6.4667** |
| | **STD** | 1.4308 | 1.0400 | 0.9444 | 0.9879 | 1.4239 | 1.5775 | 1.3767 | 0.8996 |
| **Clean1** | **AVE** | 76.7000 | **70.8333** | **75.1000** | 78.7667 | **75.5000** | 81.4333 | **68.9667** | 77.6667 |
| | **STD** | 13.0758 | 17.5540 | 14.8982 | 13.3563 | 16.6604 | 8.3900 | 16.7507 | 9.8483 |
| **Semeion** | **AVE** | 134.4000 | **130.1333** | 129.4667 | **128.8000** | 131.4000 | **129.2000** | 132.2333 | **127.8667** |
| | **STD** | 7.7797 | 13.9747 | 17.6728 | 14.5232 | 7.3700 | 12.9679 | 13.6904 | 12.5003 |
| **Colon** | **AVE** | **502.8333** | 675.1333 | **608.8000** | 660.2333 | 710.2333 | **562.2000** | **533.2333** | 552.6333 |
| | **STD** | 426.8525 | 394.4688 | 418.4239 | 367.4116 | 393.4634 | 391.4070 | 381.6319 | 441.3998 |
| **Leukemia** | **AVE** | 3709.9670 | **3524.5333** | **3503.2670** | 3629.9000 | 3506.8670 | **3496.7000** | **3953.0670** | 4070.5667 |
| | **STD** | 398.4409 | 27.50643 | 25.7266 | 279.0204 | 25.2870 | 31.9160 | 632.9743 | 608.5844 |
| Ranking | W\|T\|L | 7\|0\|15 | 15\|0\|7 | 8\|1\|13 | 13\|1\|8 | 8\|0\|14 | 14\|0\|8 | 14\|0\|8 | 8\|0\|14 |
| Overall Ranking | F-Test | 5.5000 | 4.0000 | 5.1818 | **3.8182** | 4.8636 | 4.4773 | 3.8864 | 4.2727 |

Table 16: Comparison between the BSSA with S-shaped TFs and the related version with CP based on the average running time.

| Benchmark | Stat. Measure | BSSA_S1 | BSSA_S1_CP | BSSA_S2 | BSSA_S1_CP | BSSA_S3 | BSSA_S3_CP | BSSA_S4 | BSSA_S4_CP |
|---|---|---|---|---|---|---|---|---|---|
| **Breastcancer** | **AVE** | 6.3419 | **6.0842** | 6.1287 | **5.8927** | 6.0900 | **5.8258** | 6.0691 | **5.8422** |
| | **STD** | 0.2242 | 0.1260 | 0.1176 | 0.1250 | 0.1593 | 0.1478 | 0.1416 | 0.1384 |
| **BreastEW** | **AVE** | 6.9568 | **6.6689** | 6.8192 | **6.4934** | 6.7886 | **6.4352** | 6.7479 | **6.4043** |
| | **STD** | 0.1544 | 0.1272 | 0.1412 | 0.1214 | 0.1368 | 0.1305 | 0.1365 | 0.1298 |
| **Exactly** | **AVE** | 9.1079 | **8.3701** | 8.8297 | **7.9362** | 8.7315 | **8.1474** | 8.5636 | **7.5922** |
| | **STD** | 0.1820 | 0.2866 | 0.1895 | 0.1775 | 0.1461 | 0.1931 | 0.1479 | 0.1858 |
| **Exactly2** | **AVE** | 9.2486 | **9.0258** | 8.9892 | **8.4106** | 8.6881 | **7.9427** | 8.6479 | **8.0397** |
| | **STD** | 0.2807 | 0.3479 | 0.1765 | 0.2986 | 0.1530 | 0.2523 | 0.1408 | 0.2022 |
| **HeartEW** | **AVE** | **4.8109** | 4.9190 | **4.7856** | 4.9095 | **4.8080** | 4.8747 | **4.7876** | 4.8858 |
| | **STD** | 0.1153 | 0.1310 | 0.1266 | 0.1480 | 0.1547 | 0.1283 | 0.1490 | 0.1209 |
| **Lymphography** | **AVE** | **4.5691** | 4.6471 | **4.6016** | 4.6431 | **4.5918** | 4.6382 | **4.5776** | 4.6911 |
| | **STD** | 0.1373 | 0.0935 | 0.1310 | 0.1394 | 0.1321 | 0.1233 | 0.1051 | 0.1106 |
| **M-of-n** | **AVE** | 8.9426 | **8.8660** | 8.7137 | **7.9496** | 8.5289 | **7.6689** | 8.4811 | **7.5729** |
| | **STD** | 0.1567 | 0.2029 | 0.1353 | 0.2322 | 0.1652 | 0.2028 | 0.1800 | 0.1634 |
| **PenglungEW** | **AVE** | 6.9319 | **6.9308** | 7.0017 | **6.9442** | 6.9723 | **6.9286** | 6.9908 | **6.9542** |
| | **STD** | 0.1779 | 0.1783 | 0.2111 | 0.1706 | 0.1598 | 0.1928 | 0.1647 | 0.1729 |
| **SonarEW** | **AVE** | 5.2936 | **5.2555** | 5.2877 | **5.2270** | 5.2625 | **5.1872** | 5.2572 | **5.1788** |
| | **STD** | 0.1417 | 0.1166 | 0.1429 | 0.1409 | 0.1502 | 0.1487 | 0.1306 | 0.1277 |
| **SpectEW** | **AVE** | **4.8724** | 4.9135 | **4.8749** | 4.9194 | **4.9058** | 4.9259 | **4.8595** | 4.9371 |
| | **STD** | 0.1254 | 0.1146 | 0.1179 | 0.1217 | 0.1166 | 0.1282 | 0.0954 | 0.1070 |
| **CongressEW** | **AVE** | **5.4705** | 5.5734 | **5.4873** | 5.5849 | **5.4636** | 5.5814 | **5.4580** | 5.5357 |
| | **STD** | 0.1292 | 0.1390 | 0.0989 | 0.1287 | 0.0971 | 0.1323 | 0.1208 | 0.1162 |
| **IonosphereEW** | **AVE** | 5.5331 | **5.4944** | 5.5000 | **5.4048** | 5.4766 | **5.3749** | 5.4798 | **5.3395** |
| | **STD** | 0.1344 | 0.1425 | 0.1397 | 0.1628 | 0.1002 | 0.1283 | 0.1013 | 0.1139 |
| **KrvskpEW** | **AVE** | 90.1701 | **77.9537** | 85.5203 | **68.7881** | 83.3227 | **64.0376** | 82.4860 | **63.1520** |
| | **STD** | 1.0019 | 1.8611 | 0.6986 | 1.4156 | 0.7765 | 0.9309 | 0.7200 | 0.6287 |
| **Tic-tac-toe** | **AVE** | 8.8671 | **7.6934** | 8.6742 | **7.3372** | 8.4558 | **7.0290** | 8.4044 | **6.8724** |
| | **STD** | 0.1682 | 0.2195 | 0.1747 | 0.1880 | 0.1625 | 0.1509 | 0.1808 | 0.1567 |
| **Vote** | **AVE** | **4.9164** | 4.9854 | **4.9204** | 4.9754 | **4.8939** | 4.9979 | **4.9023** | 4.9976 |
| | **STD** | 0.1268 | 0.1245 | 0.1445 | 0.1381 | 0.1002 | 0.1326 | 0.1203 | 0.1325 |
| **WaveformEW** | **AVE** | 233.4317 | **200.5977** | 219.4103 | **175.3999** | 211.4342 | **158.3204** | 209.5122 | **155.2800** |
| | **STD** | 2.6403 | 6.1824 | 2.4184 | 2.7815 | 1.5368 | 2.0943 | 1.6556 | 2.0963 |
| **WineEW** | **AVE** | **4.5797** | 4.6636 | **4.5874** | 4.6801 | **4.5819** | 4.6498 | **4.5683** | 4.6587 |
| | **STD** | 0.1356 | 0.1263 | 0.1068 | 0.1127 | 0.1281 | 0.1167 | 0.1213 | 0.1074 |
| **Zoo** | **AVE** | **4.5614** | 4.6952 | **4.5935** | 4.6181 | **4.5761** | 4.5942 | **4.5770** | 4.6478 |
| | **STD** | 0.1179 | 0.1546 | 0.1361 | 0.0939 | 0.1149 | 0.1210 | 0.1313 | 0.1266 |
| **Clean1** | **AVE** | 14.5884 | **13.1172** | 14.0300 | **11.9863** | 13.6366 | **11.2840** | 13.5364 | **11.0792** |
| | **STD** | 0.3487 | 0.4052 | 0.3311 | 0.3728 | 0.3186 | 0.2966 | 0.3236 | 0.2654 |
| **Semeion** | **AVE** | 171.5068 | **147.1775** | 160.8404 | **124.0739** | 152.9361 | **109.3973** | 150.4326 | **105.0623** |
| | **STD** | 2.6292 | 2.1649 | 1.4173 | 2.3551 | 1.2590 | 1.2306 | 1.1394 | 1.0139 |
| **Colon** | **AVE** | 18.7257 | **18.4842** | 19.0884 | **18.7992** | 19.2046 | **18.7866** | 19.2324 | **18.8292** |
| | **STD** | 0.5844 | 0.6246 | 0.5838 | 0.6407 | 0.6449 | 0.6070 | 0.6399 | 0.5785 |
| **Leukemia** | **AVE** | 29.0596 | **26.5747** | 26.0303 | **23.4061** | 24.4623 | **22.6561** | 24.5787 | **23.5067** |
| | **STD** | 2.3031 | 1.5675 | 2.4104 | 1.3921 | 1.2403 | 0.8432 | 1.1275 | 1.3120 |
| Ranking | W\|T\|L | 7\|0\|15 | 15\|0\|7 | 7\|0\|15 | 15\|0\|7 | 7\|0\|15 | 15\|0\|7 | 7\|0\|15 | 15\|0\|7 |
| Overall Ranking | F-Test | 5.5455 | 5 | 5.8182 | 4.2273 | 4.7727 | **3.1818** | 4.1364 | 3.3182 |

Table 17: Comparison between the BSSA with V-shaped TFs and the related version with CP based on the average running time.

| Benchmark | Stat. Measure | BSSA_V1 | BSSA_V1_CP | BSSA_V2 | BSSA_V2_CP | BSSA_V3 | BSSA_V3_CP | BSSA_V4 | BSSA_V4_CP |
|---|---|---|---|---|---|---|---|---|---|
| **Breastcancer** | **AVE** | 6.0650 | **5.7544** | 6.0793 | **5.7602** | 6.0087 | **5.7671** | 6.0535 | **5.7707** |
| | **STD** | 0.1542 | 0.1289 | 0.1310 | 0.1426 | 0.1391 | 0.1570 | 0.1472 | 0.1640 |
| **BreastEW** | **AVE** | 6.7490 | **6.3354** | 6.7242 | **6.3116** | 6.7241 | **6.3232** | 6.7204 | **6.3470** |
| | **STD** | 0.1548 | 0.1459 | 0.1054 | 0.1351 | 0.1468 | 0.1484 | 0.1474 | 0.1219 |
| **Exactly** | **AVE** | 8.4290 | **7.6049** | 8.3918 | **7.4452** | 8.3905 | **7.4395** | 8.4522 | **7.4230** |
| | **STD** | 0.1691 | 0.2045 | 0.1605 | 0.2518 | 0.1509 | 0.2402 | 0.1756 | 0.2597 |
| **Exactly2** | **AVE** | 8.5800 | **7.5672** | 8.5698 | **7.8250** | 8.6158 | **7.7201** | 8.5339 | **7.6678** |
| | **STD** | 0.2083 | 0.3811 | 0.1446 | 0.2409 | 0.1493 | 0.2561 | 0.1533 | 0.2616 |
| **HeartEW** | **AVE** | **4.7885** | 4.8539 | **4.7795** | 4.8300 | **4.8058** | 4.8155 | **4.7629** | 4.8385 |
| | **STD** | 0.1485 | 0.1311 | 0.1241 | 0.1015 | 0.1435 | 0.1115 | 0.1143 | 0.1123 |
| **Lymphography** | **AVE** | **4.5928** | 4.6688 | **4.5818** | 4.6317 | **4.5852** | 4.6490 | **4.5817** | 4.6382 |
| | **STD** | 0.1266 | 0.1233 | 0.1128 | 0.1087 | 0.1135 | 0.1077 | 0.1230 | 0.0884 |
| **M-of-n** | **AVE** | 8.4435 | **7.2751** | 8.3370 | **7.4175** | 8.3191 | **7.2508** | 8.2535 | **7.6105** |
| | **STD** | 0.1867 | 0.1895 | 0.1428 | 0.2362 | 0.1603 | 0.1931 | 0.1564 | 0.2569 |
| **PenglungEW** | **AVE** | 7.0545 | **6.9564** | 6.8316 | **6.7616** | 6.7966 | **6.7419** | 6.7937 | **6.6936** |
| | **STD** | 0.2331 | 0.2646 | 0.1739 | 0.1747 | 0.1856 | 0.1600 | 0.1474 | 0.1582 |
| **SonarEW** | **AVE** | 5.2337 | **5.1523** | 5.1985 | **5.0872** | 5.1945 | **5.0950** | 5.2115 | **5.0919** |
| | **STD** | 0.1504 | 0.1522 | 0.1372 | 0.1406 | 0.1408 | 0.1247 | 0.1676 | 0.1285 |
| **SpectEW** | **AVE** | **4.8817** | 4.9277 | **4.8618** | 4.8828 | **4.8952** | 4.9308 | **4.8630** | 4.9191 |
| | **STD** | 0.1349 | 0.1027 | 0.1129 | 0.1766 | 0.0963 | 0.1359 | 0.1024 | 0.1295 |
| **CongressEW** | **AVE** | **5.4406** | 5.5259 | **5.4539** | 5.5105 | **5.4404** | 5.5259 | **5.4507** | 5.5099 |
| | **STD** | 0.1466 | 0.1534 | 0.1434 | 0.1330 | 0.1103 | 0.1333 | 0.1372 | 0.1388 |
| **IonosphereEW** | **AVE** | 5.5120 | **5.2989** | 5.4691 | **5.2922** | 5.4667 | **5.3063** | 5.4471 | **5.2993** |
| | **STD** | 0.1217 | 0.1163 | 0.1286 | 0.1378 | 0.1224 | 0.1478 | 0.1224 | 0.1135 |
| **KrvskpEW** | **AVE** | 80.9167 | **60.0669** | 80.8368 | **60.1490** | 80.9479 | **60.1087** | 80.7104 | **59.9048** |
| | **STD** | 0.7489 | 1.9395 | 0.9229 | 1.3245 | 0.8432 | 1.6498 | 0.8994 | 1.7692 |
| **Tic-tac-toe** | **AVE** | 8.3256 | **6.7029** | 8.2557 | **6.6715** | 8.3069 | **6.7194** | 8.2683 | **6.6701** |
| | **STD** | 0.1533 | 0.1740 | 0.1268 | 0.2075 | 0.1958 | 0.2127 | 0.1660 | 0.2105 |
| **Vote** | **AVE** | **4.8986** | 4.9969 | **4.8907** | 4.9518 | **4.8872** | 4.9493 | **4.8821** | 4.9461 |
| | **STD** | 0.1053 | 0.1116 | 0.1177 | 0.0960 | 0.1121 | 0.1186 | 0.1202 | 0.1339 |
| **WaveformEW** | **AVE** | 203.5272 | **145.8042** | 203.0986 | **143.8175** | 203.7187 | **144.2169** | 203.3405 | **145.0240** |
| | **STD** | 2.0957 | 4.3338 | 1.9709 | 4.7723 | 2.3329 | 4.6742 | 2.0857 | 5.2775 |
| **WineEW** | **AVE** | **4.5612** | 4.6379 | **4.5252** | 4.6144 | **4.5425** | 4.6346 | **4.5563** | 4.6068 |
| | **STD** | 0.1273 | 0.1251 | 0.0992 | 0.1138 | 0.1021 | 0.1100 | 0.1120 | 0.1015 |
| **Zoo** | **AVE** | **4.5990** | 4.6112 | **4.5575** | 4.5993 | **4.5501** | 4.5919 | **4.5438** | 4.6045 |
| | **STD** | 0.1089 | 0.1086 | 0.1098 | 0.1000 | 0.1355 | 0.1224 | 0.1457 | 0.1091 |
| **Clean1** | **AVE** | 13.2981 | **10.3848** | 13.1682 | **10.3065** | 13.2241 | **10.3193** | 13.1324 | **10.3543** |
| | **STD** | 0.3548 | 0.2905 | 0.3357 | 0.2838 | 0.3146 | 0.3637 | 0.3455 | 0.3244 |
| **Semeion** | **AVE** | 145.3891 | **93.8624** | 145.4128 | **94.7978** | 145.8595 | **94.1344** | 145.3749 | **93.3334** |
| | **STD** | 1.8617 | 4.2413 | 1.7401 | 3.6139 | 1.5058 | 3.1943 | 1.5577 | 3.7049 |
| **Colon** | **AVE** | 19.3587 | **18.8523** | 18.1871 | **17.6476** | 18.1081 | **17.5061** | 18.0409 | **17.5174** |
| | **STD** | 0.9240 | 0.9281 | 0.5712 | 0.5006 | 0.5278 | 0.4838 | 0.5719 | 0.5925 |
| **Leukemia** | **AVE** | 26.8454 | **22.7709** | 26.4626 | **23.9507** | 28.1687 | **22.3894** | 27.0976 | **25.0805** |
| | **STD** | 1.3364 | 1.0506 | 0.8502 | 2.1127 | 2.0315 | 1.6292 | 1.3519 | 1.8981 |
| Ranking | W\|T\|L | 7\|0\|15 | 15\|0\|7 | 7\|0\|15 | 15\|0\|7 | 7\|0\|15 | 15\|0\|7 | 7\|0\|15 | 15\|0\|7 |
| Overall Ranking | F-Test | 6.2727 | 4.75 | 5.0455 | 3.4545 | 5.1818 | 3.7045 | 4.2273 | **3.3636** |

To detect the best binary variant among the evaluated versions, the overall ranks are considered here. Table 18 shows the ranks of different binary approaches in terms of different measures based on F-test.

Based on the overall ranks in Table 18, it can be observed that the BSSA_S3_CP has achieved to the lowest rank among others in terms of fitness and accuracy measures over all 22 datasets. According to the number of features and running time results, the BSSA_V2_CP has outperformed other versions. The notable changes in the results show the noteworthy effect of the TF on the effectiveness of the investigated versions. In addition, from the overall results, it can be noticed that the crossover scheme has heightened the efficacy of the related algorithms with both S-shaped and V-shaped TFs in terms of fitness and accuracy measures. The reason is that it has avoided the algorithms from converging towards local solutions to some extent and increased the exploration capacities of proposed BSSA-based approaches in tackling more complex scenarios. Hence, they can establish a more stable tradeoff between the exploration and exploitation trends.

Table 18: Overall Ranking results using the F-test for all proposed approaches based on fitness, accuracy, Number of features and running time.

| Algorithm | Fitness | Accuracy | Features | Time |
|---|---|---|---|---|
| BSSA-S1 | 8.9545 | 8.6136 | 12.8636 | 11.7727 |
| BSSA-S1-CP | 7.7273 | 7.1364 | 12.9091 | 11.3636 |
| BSSA-S2 | 9.5227 | 8.9091 | 11.4545 | 12.2273 |
| BSSA-S2-CP | 6.9545 | 6.8864 | 10.4545 | 9.7273 |
| BSSA-S3 | 8.1364 | 8.0682 | 11.2500 | 11.2727 |
| BSSA-S3-CP | **6.1364** | **6.2500** | 8.4773 | 8.3864 |
| BSSA-S4 | 9.2727 | 9.2273 | 8.9773 | 10.1364 |
| BSSA-S4-CP | 7.1818 | 7.2500 | 9.2045 | 8.8182 |
| BSSA-V1 | 9.6364 | 9.6818 | 7.6364 | 9.9545 |
| BSSA-V1-CP | 8.8864 | 9.2727 | 5.2273 | 6.9318 |
| BSSA-V2 | 9.5455 | 9.7727 | 7.5227 | 7.0909 |
| BSSA-V2-CP | 8.0909 | 8.3409 | **4.8864** | **4.7273** |
| BSSA-V3 | 8.2273 | 8.4091 | 6.9091 | 7.3636 |
| BSSA-V3-CP | 8.5682 | 8.8409 | 6.2045 | 5.2045 |
| BSSA-V4 | 10.1591 | 10.2273 | 5.9318 | 6.2273 |
| BSSA-V4-CP | 9.0000 | 9.1136 | 6.0909 | 4.7955 |

Table 19 reveals the attained p-values for the BSSA_S3_CP compared to other optimizers.

Table 19: The p-values of the Wilcoxon test of BSSA_S3_CP fitness results vs. other approaches (p $\geq$ 0.05 are underlined).

| Benchmark | BSSA_S1 | BSSA_S1_CP | BSSA_S2 | BSSA_S2_CP | BSSA_S3 | BSSA_S4 | BSSA_S4_CP | BSSA_V1 | BSSA_V1_CP | BSSA_V2 | BSSA_V2_CP | BSSA_V3 | BSSA_V3_CP | BSSA_V4 | BSSA_V4_CP |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Breastcancer | 8.64E-14 | 2.69E-12 | 1.43E-12 | 4.92E-11 | 9.50E-13 | 1.43E-12 | 6.33E-13 | 2.90E-12 | 1.15E-12 | 2.35E-12 | 7.76E-02 | 2.05E-12 | 9.99E-13 | 9.90E-13 | 1.90E-12 |
| BreastEW | 9.88E-02 | 3.77E-11 | 2.22E-09 | 6.20E-01 | 5.12E-11 | 1.94E-08 | 2.90E-11 | 1.28E-03 | 2.92E-11 | 1.05E-09 | 2.93E-11 | 1.80E-07 | 3.14E-08 | 7.26E-08 | 2.94E-11 |
| Exactly | 1.34E-03 | 3.02E-01 | 1.16E-01 | 1.92E-02 | 1.10E-01 | 1.72E-01 | 5.07E-01 | 1.62E-02 | 5.82E-01 | 3.97E-03 | 1.69E-01 | 4.08E-01 | 4.04E-02 | 1.02E-03 | 6.50E-01 |
| Exactly2 | 1.57E-09 | 5.94E-04 | 4.50E-05 | 2.71E-02 | 3.35E-04 | 2.95E-04 | 3.19E-09 | 4.20E-05 | 3.22E-05 | 2.52E-07 | 3.13E-04 | 3.34E-04 | 2.42E-09 | 9.09E-06 | 5.69E-07 |
| HeartEW | 9.73E-07 | 1.32E-11 | 5.15E-11 | 1.05E-10 | 2.72E-11 | 4.13E-10 | 1.08E-09 | 2.74E-11 | 4.97E-11 | 2.78E-11 | 6.57E-11 | 3.05E-11 | 3.97E-11 | 4.09E-11 | 3.17E-11 |
| Lymphography | 5.60E-10 | 2.84E-11 | 2.92E-11 | 2.91E-11 | 4.84E-11 | 4.40E-11 | 2.67E-07 | 1.83E-08 | 2.90E-11 | 6.95E-11 | 5.54E-07 | 2.95E-11 | 2.94E-11 | 2.96E-11 | 1.98E-09 |
| M-of-n | 4.49E-01 | 8.91E-02 | 3.81E-01 | 1.20E-02 | 1.74E-01 | 1.19E-01 | 5.09E-01 | 9.87E-03 | 8.20E-01 | 2.93E-02 | 6.22E-01 | 8.33E-02 | 4.83E-02 | 2.19E-01 | 8.08E-02 |
| PenglungEW | 6.65E-11 | 3.48E-11 | 6.22E-03 | 2.97E-11 | 6.61E-11 | 4.25E-11 | 2.94E-11 | 2.99E-11 | 2.12E-09 | 9.50E-04 | 2.97E-11 | 2.99E-11 | 4.07E-05 | 1.69E-05 | 6.89E-04 |
| SonarEW | 2.98E-11 | 8.09E-07 | 2.98E-11 | 3.28E-11 | 3.45E-11 | 2.97E-11 | 2.96E-11 | 3.98E-11 | 4.03E-11 | 2.83E-01 | 2.95E-11 | 4.02E-11 | 5.41E-11 | 2.99E-11 | 3.29E-11 |
| SpectEW | 9.13E-11 | 2.89E-11 | 2.93E-11 | 2.40E-02 | 2.89E-11 | 4.02E-09 | 4.82E-01 | 1.18E-03 | 2.78E-10 | 1.84E-05 | 2.23E-05 | 3.10E-09 | 2.92E-11 | 1.08E-06 | 4.96E-01 |
| CongressEW | 4.28E-06 | 9.71E-02 | 3.70E-01 | 4.84E-07 | 1.59E-02 | 3.17E-08 | 8.00E-02 | 4.23E-09 | 4.09E-10 | 5.18E-11 | 2.89E-02 | 5.10E-02 | 1.44E-04 | 2.81E-10 | 2.33E-05 |
| IonosphereEW | 2.69E-10 | 2.98E-11 | 5.75E-03 | 4.37E-06 | 4.08E-04 | 5.18E-11 | 1.23E-08 | 9.57E-09 | 3.17E-03 | 5.04E-06 | 3.31E-09 | 2.97E-11 | 3.25E-01 | 5.26E-08 | 1.10E-04 |
| KrvskpEW | 3.09E-02 | 5.69E-01 | 3.15E-05 | 4.33E-01 | 5.37E-07 | 6.81E-03 | 1.47E-02 | 9.52E-07 | 6.15E-05 | 3.25E-07 | 1.26E-10 | 1.85E-09 | 1.33E-06 | 5.86E-06 | 5.80E-07 |
| Tic-tac-toe | 1.69E-14 | 1.57E-13 | 4.16E-14 | 6.13E-14 | 6.12E-14 | 3.15E-13 | 1.19E-13 | 6.75E-13 | 2.03E-13 | 5.67E-13 | 1.55E-13 | 2.54E-13 | 3.15E-13 | 6.37E-13 | 3.17E-13 |
| Vote | 2.12E-02 | 7.61E-05 | 2.37E-02 | 6.89E-01 | 1.07E-04 | 2.61E-10 | 3.14E-03 | 3.70E-11 | 9.78E-04 | 1.08E-06 | 1.21E-04 | 4.40E-02 | 3.96E-11 | 3.62E-01 | 5.07E-10 |
| WaveformEW | 9.33E-02 | 3.37E-01 | 9.77E-02 | 3.64E-02 | 5.64E-01 | 1.54E-01 | 4.04E-01 | 7.20E-05 | 4.29E-01 | 8.50E-02 | 7.49E-04 | 2.39E-08 | 6.84E-01 | 1.10E-02 | 3.44E-06 |
| WineEW | 6.23E-04 | 1.85E-01 | 2.46E-11 | 2.21E-11 | 2.41E-11 | 2.18E-11 | 2.25E-11 | 1.31E-09 | 2.50E-11 | 6.33E-10 | 3.55E-08 | 2.19E-03 | 7.51E-05 | 9.16E-10 | 2.00E-09 |
| Zoo | 1.29E-11 | 1.60E-11 | 9.91E-12 | 9.64E-12 | 7.52E-05 | 1.47E-11 | 1.16E-11 | 1.59E-11 | 9.30E-08 | 1.29E-11 | 1.29E-11 | 1.62E-11 | 1.57E-11 | 1.49E-11 | 2.56E-01 |
| Clean1 | 3.00E-11 | 6.28E-06 | 3.00E-11 | 3.01E-11 | 2.14E-10 | 3.00E-11 | 3.66E-11 | 4.43E-07 | 2.11E-07 | 6.63E-01 | 3.01E-11 | 3.33E-11 | 3.01E-11 | 1.67E-01 | 4.96E-01 |
| Semeion | 8.11E-09 | 3.01E-11 | 3.14E-10 | 3.02E-11 | 3.47E-10 | 3.01E-11 | 3.67E-11 | 4.21E-05 | 2.43E-09 | 9.90E-11 | 4.98E-09 | 8.77E-02 | 3.01E-11 | 1.96E-01 | 4.21E-04 |
| Colon | 2.97E-11 | 3.01E-11 | 2.99E-11 | 3.00E-11 | 2.99E-11 | 3.00E-11 | 2.99E-11 | 3.00E-11 | 3.01E-11 | 3.01E-11 | 3.01E-11 | 3.00E-11 | 3.00E-11 | 3.01E-11 | 1.44E-03 |
| Leukemia | 3.45E-02 | 3.00E-11 | 2.99E-11 | 3.00E-11 | 2.98E-11 | 4.75E-10 | 4.03E-11 | 3.00E-11 | 3.00E-11 | 3.00E-11 | 3.00E-11 | 3.00E-11 | 3.00E-11 | 4.08E-06 | 3.00E-11 |

From Table 19, the p-values are below 0.05 for majority of cases, while for 39 cases, the they are bigger than 0.05. Therefore, the improvements in the results of the BSSA_S3_CP are statistically superior to those of other versions in dealing with majority of the datasets, which verifies the efficacy of this algorithm.

Due to the importance of the classification accuracy and fitness results in dealing with the feature selection tasks, the BSSA_S3_CP variant is employed to be further compared with other well-regarded algorithms in the next subsection.

### *6.4. Comparison with other metaheuristics*

In this section, efficiency of the BSSA_S3_CP strategy is investigated in comparison with a number of well-established metaheuristics in the field. For this purpose, the binary bGWO [74], BGSA [70], and BBA [75] algorithms are considered here to verify the performance of the proposed BSSA_S3_CP technique. The experiments performed according to a fair and same computing condition for all algorithms. Table 20 presents the detailed parameter settings for utilized methods.

Table 20: Parameter settings

| **Algorithm** | **Parameter** | **Value** |
|---|---|---|
| GWO | $a$ | [2 0] |
| BA | $Q_{min}$ Frequency minimum | 0 |
| | $Q_{max}$ Frequency maximum | 2 |
| | $A$ Loudness | 0.5 |
| | $r$ Pulse rate | 0.5 |
| GSA | $G_0$ | 100 |
| | $\alpha$ | 20 |

Table 21 reflects the average fitness results obtained by the proposed BSSA-based algorithm against other optimizers. Tables 22 and 23 also report the average classification accuracy, and the number of selected features together with the F-test ranking and STD values for all techniques.

From the results in Table 21, it can be recognized that the developed BSSA_S3_CP can surpass other peers on 82% of the datasets. Regarding the overall ranks, after the BSSA_S3_CP, which is the ranked one, the second best approaches are bGWO and BGSA, which each of which outperformed other contestants on two datasets. Based on STD values, the proposed BSSA_S3_CP has attained better fitness results with preferable STD values compared to other competitors in majority of datasets. The reason is that the BSSA_S3_CP still inherits all the advantages of the basic SSA over other optimizers such as its satisfactory LO escaping capacity. In addition, it has an advanced exploration capability due to the used crossover between salps, which boost its exploration tendency over the search when it is required and in the next phase, it can effectively focus on the vicinity of explored food source (leading salp), mainly, during the last iterations. Hence, it has established a more stable balance between the exploration and exploitation tendencies, which its effect can be detected in the improved fitness results of BSSA_S3_CP compared to the bGWO, BGSA, and BBA optimizers.

The results of Table 22 indicate that the proposed BSSA_S3_CP provides the best accuracies compared to the bGWO, BGSA, and BBA on 86% of the datasets. Regarding

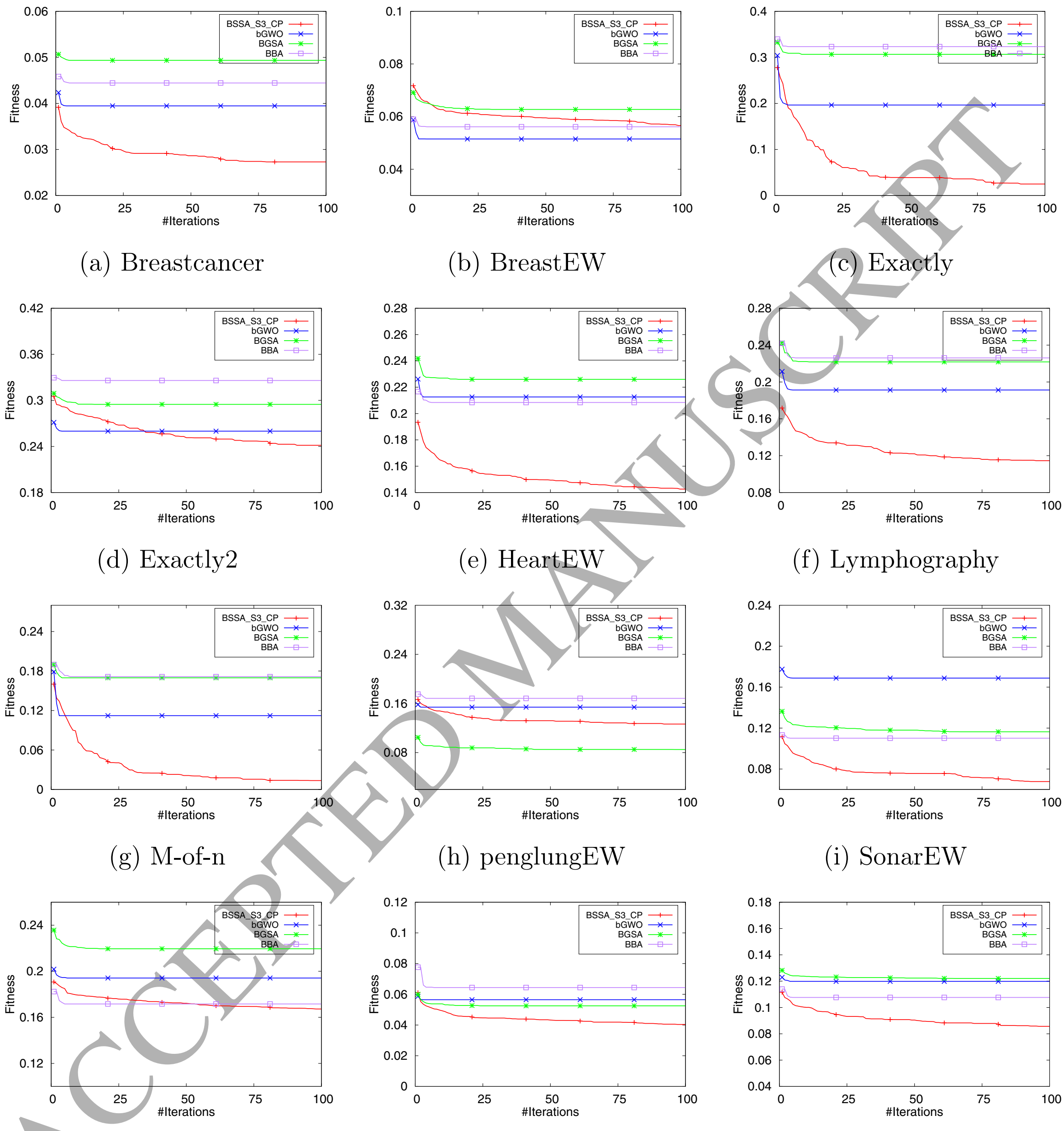
Table 21: Comparison between the BSSA_S3_CP and other metaheuristics based on the average fitness results.

| | BSSA_S3_CP | | bGWO | | BGSA | | BBA | |
|---|---|---|---|---|---|---|---|---|
| Benchmark | AVG | STD | AVG | STD | AVG | STD | AVG | STD |
| Breastcancer | **0.0273** | 0.0006 | 0.0395 | 0.0031 | 0.0494 | 0.0034 | 0.0444 | 0.0047 |
| BreastEW | 0.0566 | 0.0033 | **0.0515** | 0.0069 | 0.0627 | 0.0057 | 0.0561 | 0.0062 |
| Exactly | **0.0251** | 0.0254 | 0.1965 | 0.0766 | 0.3066 | 0.0593 | 0.3233 | 0.0745 |
| Exactly2 | **0.2415** | 0.0197 | 0.2599 | 0.0192 | 0.2949 | 0.0241 | 0.3259 | 0.0167 |
| HeartEW | **0.1426** | 0.0074 | 0.2126 | 0.0170 | 0.2260 | 0.0214 | 0.2084 | 0.0147 |
| Lymphography | **0.1146** | 0.0108 | 0.1912 | 0.0281 | 0.2218 | 0.0215 | 0.2262 | 0.0237 |
| M-of-n | **0.0136** | 0.0136 | 0.1122 | 0.0415 | 0.1697 | 0.0625 | 0.1714 | 0.0562 |
| penglungEW | 0.1266 | 0.0134 | 0.1541 | 0.0130 | **0.0851** | 0.0002 | 0.1683 | 0.0169 |
| SonarEW | **0.0678** | 0.0095 | 0.1688 | 0.0159 | 0.1164 | 0.0148 | 0.1101 | 0.0209 |
| SpectEW | **0.1673** | 0.0044 | 0.1941 | 0.0136 | 0.2196 | 0.0241 | 0.1716 | 0.0119 |
| CongressEW | **0.0404** | 0.0037 | 0.0565 | 0.0109 | 0.0525 | 0.0083 | 0.0644 | 0.0147 |
| IonosphereEW | **0.0857** | 0.0080 | 0.1198 | 0.0089 | 0.1221 | 0.0104 | 0.1076 | 0.0118 |
| KrvskpEW | **0.0410** | 0.0058 | 0.0730 | 0.0150 | 0.0966 | 0.0473 | 0.1174 | 0.0468 |
| Tic-tac-toe | **0.1844** | 0.0000 | 0.2512 | 0.0322 | 0.2514 | 0.0237 | 0.2568 | 0.0237 |
| Vote | **0.0514** | 0.0057 | 0.0603 | 0.0103 | 0.0731 | 0.0109 | 0.0712 | 0.0130 |
| WaveformEW | **0.2695** | 0.0071 | 0.2825 | 0.0073 | 0.3073 | 0.0140 | 0.3037 | 0.0135 |
| WineEW | **0.0115** | 0.0057 | 0.0467 | 0.0117 | 0.0542 | 0.0151 | 0.0365 | 0.0130 |
| Zoo | **0.0042** | 0.0004 | 0.0317 | 0.0085 | 0.0653 | 0.0078 | 0.0415 | 0.0149 |
| clean1 | 0.1248 | 0.0041 | **0.0987** | 0.0062 | 0.1058 | 0.0104 | 0.1559 | 0.0130 |
| semeion | **0.0255** | 0.0014 | 0.0356 | 0.0026 | 0.0337 | 0.0020 | 0.0334 | 0.0026 |
| Colon | 0.3163 | 0.0185 | 0.3405 | 0.0217 | **0.2370** | 0.0143 | 0.2786 | 0.0352 |
| Leukemia | **0.0166** | 0.0247 | 0.1197 | 0.0162 | 0.1599 | 0.0135 | 0.0845 | 0.0229 |
| **Ranking (W\|T\|L)** | **18\|0\|4** | | 2\|0\|20 | | 2\|0\|20 | | 0\|0\|22 | |
| **Overall Ranking (F-Test)** | **1.3636** | | 2.5 | | 3.1818 | | 2.9545 | |

the rates of BBA, the BSSA_S3_CP can obtain superior rates on a11 100% of cases. The maximum and minimum rates have reached by the BSSA_S3_CP are 100% and 69% on Zoo and Colon problems, respectively. For M-of-n dataset, the BSSA_S3_CP have attained accuracy of 100%, while bGWO has not gone higher than the accuracy of 89%, which this fact affirms the improved efficiency of the proposed BSSA-based optimizer. The proposed BSSA_S3_CP has also found satisfactory solutions with acceptable SD values.

From Table 23, it seems that the BBA technique has a better performance on 82% of the datasets. The proposed BSSA_S3_CP can reveal the best efficacy in dealing with 18% of problems: Exactly2, HeartEW, CongressEW, and Vote.

The convergence curve of the proposed algorithm is compared to other competitors in Figs. 5 and 6. Inspecting the figures, it is seen that the BSSA_S3_CP can outperform all algorithms in dealing with 17 datasets. It is detected that the BSSA_S3_CP can reveal an accelerated trend in solving all problems. Premature convergence can be observed in the behaviors of the bGWO, BBA and BGSA algorithms on a number of the datasets such as the Tic-tac-toe, Zoo, Exactly, SpectEW, and Vote datasets. Regarding the above-mentioned observations, it can be concluded that the new crossover-based operator have improved the capabilities of BSSA in maintaining a fine balance between the explorative and exploitative phases. Therefore, the premature convergence and inactivity problems of the algorithm are relieved noticeably compared to bGWO, BGSA, and BBA optimizers.




(a) Breastcancer (b) BreastEW (c) Exactly

(d) Exactly2 (e) HeartEW (f) Lymphography

(g) M-of-n (h) penglungEW (i) SonarEW

(j) SpectEW (k) CongressEW (l) IonosphereEW

Figure 5: Convergence curves for BSSA_S3_CP and other state-of-art methods for Breastcancer, BreastEW, Exactly, Exactly2, HeartEW, Lymphography, M-of-n, penglungEW, and SonarEW, SpectEW, CongressEW, and IonosphereEW datasets.

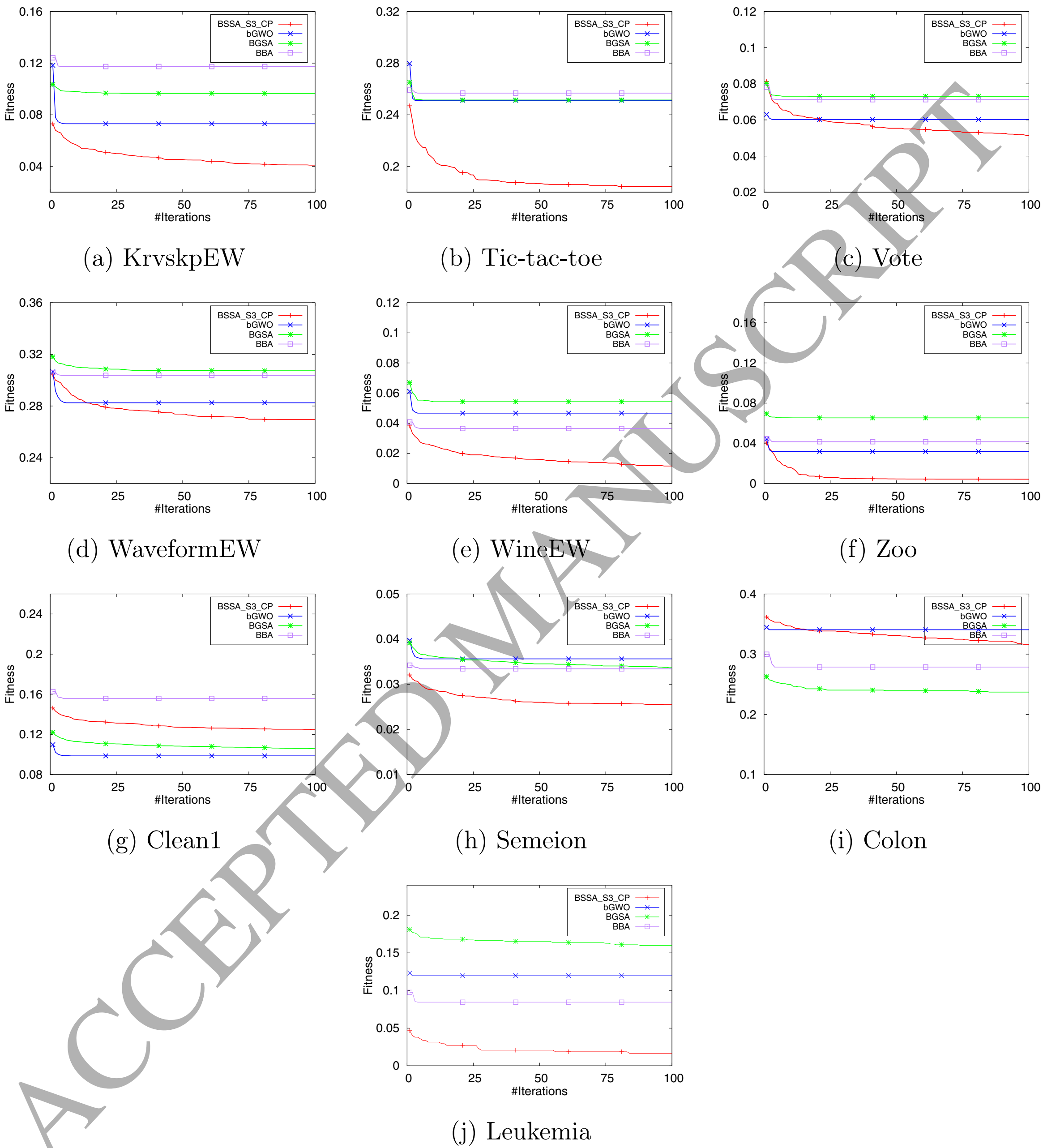



Figure 6: Convergence curves for BSSA_S3_CP and other state-of-art methods for KrvskpEW, Tic-tac-toe, Vote, WaveformEW, WineEW, Zoo, Clean1, Semeion, Colon, and Leukemia datasets.

Table 22: Comparison between the BSSA_S3_CP and other metaheuristics based on the average accuracy results.

| | BSSA_S3_CP | | bGWO | | BGSA | | BBA | |
|---|---|---|---|---|---|---|---|---|
| Benchmark | AVG | STD | AVG | STD | AVG | STD | AVG | STD |
| Breastcancer | **0.9768** | 0.0010 | 0.9681 | 0.0023 | 0.9570 | 0.0039 | 0.9367 | 0.0305 |
| BreastEW | 0.9484 | 0.0035 | **0.9544** | 0.0071 | 0.9422 | 0.0057 | 0.9315 | 0.0144 |
| Exactly | **0.9803** | 0.0253 | 0.8095 | 0.0762 | 0.6971 | 0.0601 | 0.6099 | 0.0647 |
| Exactly2 | **0.7582** | 0.0183 | 0.7431 | 0.0172 | 0.7061 | 0.0235 | 0.6282 | 0.0573 |
| HeartEW | **0.8605** | 0.0070 | 0.7916 | 0.0169 | 0.7770 | 0.0216 | 0.7538 | 0.0326 |
| Lymphography | **0.8900** | 0.0110 | 0.8131 | 0.0284 | 0.7811 | 0.0217 | 0.7014 | 0.0690 |
| M-of-n | **0.9918** | 0.0133 | 0.8941 | 0.0412 | 0.8352 | 0.0632 | 0.7219 | 0.0797 |
| penglungEW | 0.8775 | 0.0137 | 0.8495 | 0.0136 | **0.9189** | 0.0000 | 0.7946 | 0.0289 |
| SonarEW | **0.9372** | 0.0097 | 0.8356 | 0.0160 | 0.8875 | 0.0150 | 0.8439 | 0.0359 |
| SpectEW | **0.8361** | 0.0054 | 0.8097 | 0.0135 | 0.7826 | 0.0241 | 0.7998 | 0.0265 |
| CongressEW | **0.9628** | 0.0035 | 0.9476 | 0.0107 | 0.9512 | 0.0081 | 0.8717 | 0.0753 |
| IonosphereEW | **0.9182** | 0.0081 | 0.8847 | 0.0093 | 0.8813 | 0.0105 | 0.8765 | 0.0190 |
| KrvskpEW | **0.9644** | 0.0059 | 0.9339 | 0.0146 | 0.9081 | 0.0478 | 0.8164 | 0.0807 |
| Tic-tac-toe | **0.8205** | 0.0000 | 0.7538 | 0.0322 | 0.7526 | 0.0244 | 0.6653 | 0.0628 |
| Vote | **0.9511** | 0.0059 | 0.9438 | 0.0099 | 0.9313 | 0.0111 | 0.8511 | 0.0957 |
| WaveformEW | **0.7335** | 0.0069 | 0.7227 | 0.0067 | 0.6946 | 0.0142 | 0.6693 | 0.0326 |
| WineEW | **0.9933** | 0.0056 | 0.9596 | 0.0117 | 0.9509 | 0.0155 | 0.9187 | 0.0519 |
| Zoo | **1.0000** | 0.0000 | 0.9745 | 0.0091 | 0.9392 | 0.0079 | 0.8739 | 0.0949 |
| clean1 | **0.8796** | 0.0042 | 0.9077 | 0.0062 | 0.8982 | 0.0106 | 0.8265 | 0.0208 |
| semeion | **0.9799** | 0.0015 | 0.9716 | 0.0030 | 0.9711 | 0.0021 | 0.9622 | 0.0063 |
| Colon | 0.6860 | 0.0188 | 0.6613 | 0.0220 | **0.7656** | 0.0145 | 0.6817 | 0.0376 |
| Leukemia | **0.9889** | 0.0253 | 0.8843 | 0.0164 | 0.8435 | 0.0136 | 0.8769 | 0.0289 |
| **Ranking (W\|T\|L)** | **19\|0\|3** | | 1\|0\|21 | | 2\|0\|20 | | 0\|0\|22 | |
| **Overall Ranking (F-Test)** | **1.2273** | | 2.1818 | | 2.7727 | | 3.8182 | |

### *6.5. Comparison with other algorithms reported in previous literature*

In this part, the classification efficacy of the proposed BSSA_S3_CP is compared to the reported results for these datasets. Table 24 reveals the comparative classification rates of different approaches. The average classification rates of the BSSA_S3_CP is compared here to the reported performances of the GA and PSO algorithms in [27]. In addition, the results of the BSSA_S3_CP approach is also compared to the results of the bGWO1, bGWO2, GA, and PSO techniques reported in [46]. Note that the accuracies of the first and second GA and PSO optimizers are reported from [27], whereas the results of the rest of methods for the matching datasets are reported based on [46].

By comparing the results in Table 24, it can be seen that the accuracies of the BSSA_S3_CP proposed in this study is superior to those obtained from the past works on 86% of the datasets. It shows a substantial advantage over the binary GWO, PSO, and GA algorithms on the Lymphography, SonarEW, Tic-tac-toe, and Zoo datasets. The results of the BSSA_S3_CP are better than those of bGWO1, GA and PSO in [46] for all matching datasets. The BSSA_S3_CP technique can realize enhanced classification rates compared to the bGWO2 on around 94% of the matching datasets. It also surpasses the rates of GA and PSO from [27] on 100% and 90% of the problems, respectively.

The extensive experiments vividly demonstrated the merits of the proposed binary SSA algorithm combined with crossover scheme for dealing with feature selection tasks. The proposed algorithm outperformed various state-of-the-art approaches on majority of the selected datasets with different scales ranging from low-dimensional datasets like Breast

Table 23: Comparison between the BSSA_S3_CP and other metaheuristics based on average number of features.

| | BSSA_S3_CP | | bGWO | | BGSA | | BBA | |
|---|---|---|---|---|---|---|---|---|
| Benchmark | AVG | STD | AVG | STD | AVG | STD | AVG | STD |
| Breastcancer | 3.8667 | 0.3457 | 7.1000 | 1.4468 | 6.0667 | 1.1427 | **3.6667** | 1.3730 |
| BreastEW | 16.7000 | 2.3364 | 19.0000 | 4.3072 | 16.5667 | 2.9790 | **12.4000** | 2.7618 |
| Exactly | 7.2000 | 0.6644 | 10.2333 | 1.6543 | 8.7333 | 1.0483 | **5.7333** | 1.8925 |
| Exactly2 | **2.7333** | 2.3916 | 7.3333 | 4.1550 | 5.1000 | 2.1066 | 6.0667 | 2.3332 |
| HeartEW | **5.8000** | 1.4239 | 8.1667 | 2.0014 | 6.8333 | 1.3153 | 5.9000 | 1.6474 |
| Lymphography | 10.2667 | 1.9286 | 11.1000 | 1.9713 | 9.1667 | 1.8952 | **7.8000** | 2.2034 |
| M-of-n | 7.1000 | 0.6618 | 9.6333 | 0.9643 | 8.4667 | 1.4320 | **6.1667** | 2.0858 |
| penglungEW | 171.6000 | 9.9329 | 166.3333 | 28.2322 | 157.1667 | 7.7285 | **126.1667** | 15.6008 |
| SonarEW | 33.3667 | 2.8585 | 36.2333 | 8.6131 | 30.0333 | 3.6998 | **24.7000** | 5.3765 |
| SpectEW | 10.9333 | 3.5809 | 12.6333 | 2.4422 | 9.5333 | 2.3004 | **7.9667** | 2.2816 |
| CongressEW | **5.7333** | 1.3629 | 7.3000 | 2.1359 | 6.7667 | 2.4023 | 6.2333 | 2.0625 |
| IonosphereEW | 15.8667 | 2.5829 | 19.2333 | 5.0150 | 15.4000 | 2.5134 | **13.4000** | 2.5944 |
| KrvskpEW | 20.4667 | 2.5560 | 27.3667 | 3.3885 | 19.9667 | 2.1251 | **15.0000** | 2.8527 |
| Tic-tac-toe | 6.0000 | 0.0000 | 6.7000 | 1.3429 | 5.8667 | 1.1366 | **4.7000** | 1.4890 |
| Vote | **4.8333** | 1.4875 | 7.4000 | 2.2221 | 8.1667 | 1.8210 | 6.1333 | 2.1772 |
| WaveformEW | 22.9000 | 3.3255 | 31.9667 | 4.6125 | 19.9000 | 2.9167 | **16.6667** | 3.3045 |
| WineEW | 6.3333 | 0.9589 | 8.6000 | 1.7538 | 7.3667 | 1.0981 | **6.0667** | 1.7407 |
| Zoo | 6.7000 | 0.7022 | 10.3667 | 2.4842 | 8.1667 | 1.1769 | **6.5667** | 2.5008 |
| clean1 | 92.1667 | 6.2427 | 121.2667 | 20.6914 | 83.7000 | 5.4212 | **64.7667** | 10.0161 |
| semeion | 147.5000 | 8.7168 | 200.1000 | 31.0221 | 133.5333 | 7.4219 | **107.0333** | 10.9465 |
| Colon | 1097.4333 | 44.7165 | 1042.1000 | 126.7211 | 995.8333 | 20.0208 | **827.5000** | 55.3707 |
| Leukemia | 3959.9333 | 530.6809 | 3663.7667 | 294.8722 | 3555.1333 | 39.7125 | **2860.0000** | 247.6421 |
| **Ranking (W\|T\|L)** | 4\|0\|18 | | 0\|0\|22 | | 0\|0\|22 | | 18\|0\|4 | |
| **Overall Ranking (F-Test)** | 2.5455 | | 3.8182 | | 2.4091 | | 1.2273 | |

Table 24: Comparison between the BSSA_S3_CP and other approaches from previous works based on the average accuracy results.

| | BSSA_S3_CP | GA [27] | PSO [27] | bGWO1[46] | bGWO2 [46] | GA [46] | PSO [46] |
|---|---|---|---|---|---|---|---|
| Breastcancer | **0.9768** | 0.957 | 0.949 | 0.976 | 0.975 | 0.968 | 0.967 |
| BreastEW | **0.9484** | 0.923 | 0.933 | 0.924 | 0.935 | 0.939 | 0.933 |
| Exactly | **0.9803** | 0.822 | 0.973 | 0.708 | 0.776 | 0.674 | 0.688 |
| Exactly2 | **0.7582** | 0.677 | 0.666 | 0.745 | 0.750 | 0.746 | 0.730 |
| HeartEW | **0.8605** | 0.732 | 0.745 | 0.776 | 0.776 | 0.780 | 0.787 |
| Lymphography | **0.89** | 0.758 | 0.759 | 0.744 | 0.700 | 0.696 | 0.744 |
| M-of-n | 0.9918 | 0.916 | **0.996** | 0.908 | 0.963 | 0.861 | 0.921 |
| penglungEW | 0.8775 | 0.672 | **0.879** | 0.600 | 0.584 | 0.584 | 0.584 |
| SonarEW | **0.9372** | 0.833 | 0.804 | 0.731 | 0.729 | 0.754 | 0.737 |
| SpectEW | **0.8361** | 0.756 | 0.738 | 0.820 | 0.822 | 0.793 | 0.822 |
| CongressEW | **0.9628** | 0.898 | 0.937 | 0.935 | 0.938 | 0.932 | 0.928 |
| IonosphereEW | **0.9182** | 0.863 | 0.876 | 0.807 | 0.834 | 0.814 | 0.819 |
| KrvskpEW | **0.9644** | 0.940 | 0.949 | 0.944 | 0.956 | 0.920 | 0.941 |
| Tic-tac-toe | **0.8205** | 0.764 | 0.750 | 0.728 | 0.727 | 0.719 | 0.735 |
| Vote | **0.9511** | 0.808 | 0.888 | 0.912 | 0.920 | 0.904 | 0.904 |
| WaveformEW | 0.7335 | 0.712 | 0.732 | 0.786 | **0.789** | 0.773 | 0.762 |
| WineEW | **0.9933** | 0.947 | 0.937 | 0.930 | 0.920 | 0.937 | 0.933 |
| Zoo | **1** | 0.946 | 0.963 | 0.879 | 0.879 | 0.855 | 0.861 |
| clean1 | **0.8796** | 0.862 | 0.845 | - | - | - | - |
| semeion | **0.9799** | 0.963 | 0.967 | - | - | - | - |
| Colon | **0.686** | 0.682 | 0.624 | - | - | - | - |
| Leukemia | **0.9889** | 0.705 | 0.862 | - | - | - | - |
| **Ranking (W\|T\|L)** | **19\|0\|3** | 0\|0\|22 | 2\|0\|20 | 0\|0\|18 | 1\|0\|17 | 0\|0\|18 | 0\|0\|18 |

cancer and Vote datasets, up to high-dimensional datasets like Leukemia. The main reason that this algorithm can perform well is behind the operators integrated in the algorithm. For one, the crossover operator can significantly change the position and behaviors of the leader salp. This results in driving the salp chain to different regions and promoting the exploratory tendencies. For another, the utilized S-shaped and V-shaped TFs can effectively map the continuous values to binary ones. Note that this does not mean that the proposed binary SSA algorithms are and will be the best option to tackle all classes of the optimization problems. According to NFL theorem [66], all algorithms perform equal when considering all types of optimization problems. Since the binary SSA approaches performed well on most of the FS problems, we suggest them to researchers in different fields particularly feature selection. The proposed algorithms have a high potential to provide very promising and/or superior results.

## 7. Conclusions and future directions

In this paper, an enhanced binary SSA-based optimizer with transfer functions and crossover scheme was proposed to tackle FS problems. The proposed techniques were tested on 22 well-regarded benchmark datasets. To detect the best TF for binary versions, the classification accuracy, features, and fitness measures was studied and statistical tests were also provided in detail. After the comparisons between the proposed versions, it was observed that the BSSA with S3-shaped TF and crossover outperform other hybrid variants. The efficacy of the BSSA_S3_CP method was compared to three state-of-the-art methods and several algorithms reported in previous works. The comparative evaluations of the BSSA_S3_CP against bGWO, BGSA, BBA, showed the superior efficiency of the proposed technique in terms of accuracy and fitness values for different FS problems.

For future research, interested researchers can investigate the efficacy of the proposed binary SSA in dealing with other datasets or machine learning tasks. The future work can also investigate the impact of other new S-shaped and V-shaped family of TFs on BSSA or other studied binary algorithms. Furthermore, the implementation of of slopes and saturations as new TFs for new metaheuristics, BSSA and other algorithms can be investigated in future researches.

## 8. Acknowledgements

We want to gratefully acknowledge the anonymous reviewers for providing their constructive comments.

## Appendix A

Table 25: Comparison between the BSSA with TFs approaches and the proposed method (with CP) based on the Best and Worst accuracy.

| Benchmark | Stat.Measure | BSSA_S1 | BSSA_S1_CP | BSSA_S2 | BSSA_S2_CP | BSSA_S3 | BSSA_S3_CP | BSSA_S4 | BSSA_S4_CP | BSSA_V1 | BSSA_V1_CP | BSSA_V2 | BSSA_V2_CP | BSSA_V3 | BSSA_V3_CP | BSSA_V4 | BSSA_V4_CP |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Breastcancer | Best | 0.9771 | 0.9629 | 0.9571 | 0.9743 | 0.9743 | 0.9771 | 0.9686 | 0.9829 | 0.9686 | 0.9714 | 0.9714 | 0.9771 | 0.9686 | 0.9743 | 0.9686 | 0.9714 |
| | Worst | 0.9771 | 0.9571 | 0.9571 | 0.9629 | 0.9743 | 0.9743 | 0.9686 | 0.9829 | 0.9629 | 0.9686 | 0.9657 | 0.9686 | 0.9629 | 0.9714 | 0.9657 | 0.9629 |
| BreastEW | Best | 0.9544 | 0.9684 | 0.9649 | 0.9649 | 0.9719 | 0.9544 | 0.9614 | 0.9649 | 0.9649 | 0.9684 | 0.9719 | 0.9790 | 0.9684 | 0.9579 | 0.9614 | 0.9719 |
| | Worst | 0.9404 | 0.9544 | 0.9474 | 0.9404 | 0.9509 | 0.9404 | 0.9474 | 0.9544 | 0.9474 | 0.9544 | 0.9474 | 0.9579 | 0.9474 | 0.9298 | 0.9439 | 0.9544 |
| Exactly | Best | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 |
| | Worst | 0.9600 | 0.9520 | 0.9420 | 0.9820 | 0.8600 | 0.9260 | 0.9260 | 0.9440 | 0.7760 | 0.8340 | 0.8280 | 0.7780 | 0.8100 | 0.8580 | 0.7720 | 0.8720 |
| Exactly2 | Best | 0.7620 | 0.7700 | 0.7460 | 0.7700 | 0.7560 | 0.7680 | 0.7620 | 0.7380 | 0.7720 | 0.7400 | 0.7520 | 0.7540 | 0.7660 | 0.7400 | 0.7620 | 0.7540 |
| | Worst | 0.7120 | 0.7200 | 0.7200 | 0.7340 | 0.7560 | 0.7180 | 0.7360 | 0.7080 | 0.6920 | 0.7080 | 0.7080 | 0.7540 | 0.7500 | 0.7060 | 0.7060 | 0.7100 |
| HeartEW | Best | 0.8593 | 0.8370 | 0.8444 | 0.8444 | 0.8222 | 0.8667 | 0.8519 | 0.8519 | 0.8370 | 0.8370 | 0.8222 | 0.8444 | 0.8370 | 0.8444 | 0.8444 | 0.8370 |
| | Worst | 0.8370 | 0.8222 | 0.8074 | 0.8222 | 0.7926 | 0.8370 | 0.8222 | 0.8296 | 0.8000 | 0.8000 | 0.7852 | 0.8222 | 0.8148 | 0.8074 | 0.8000 | 0.8000 |
| Lymphography | Best | 0.8784 | 0.8514 | 0.8243 | 0.8649 | 0.8784 | 0.9054 | 0.8784 | 0.8919 | 0.8919 | 0.8649 | 0.8784 | 0.8919 | 0.8514 | 0.8378 | 0.8243 | 0.8784 |
| | Worst | 0.8514 | 0.8243 | 0.7973 | 0.8108 | 0.8243 | 0.8767 | 0.8243 | 0.8649 | 0.8378 | 0.8108 | 0.8243 | 0.8243 | 0.7973 | 0.7838 | 0.7703 | 0.8243 |
| M-of-n | Best | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 |
| | Worst | 0.9760 | 0.9760 | 0.9860 | 0.9820 | 0.9360 | 0.9600 | 0.9640 | 0.9760 | 0.8520 | 0.9460 | 0.8840 | 0.9240 | 0.8880 | 0.8620 | 0.9320 | 0.9300 |
| PenglungEW | Best | 0.8649 | 0.9460 | 0.9189 | 0.8108 | 0.8649 | 0.8919 | 0.8649 | 0.9460 | 0.9460 | 0.8649 | 0.8919 | 0.9189 | 0.9189 | 0.9189 | 0.9189 | 0.8919 |
| | Worst | 0.8378 | 0.8919 | 0.8649 | 0.7838 | 0.7838 | 0.8649 | 0.8108 | 0.9189 | 0.9189 | 0.8108 | 0.8378 | 0.9189 | 0.8919 | 0.8649 | 0.8649 | 0.8649 |
| SonarEW | Best | 0.8846 | 0.9423 | 0.8942 | 0.9231 | 0.9231 | 0.9615 | 0.8942 | 0.9135 | 0.9231 | 0.9231 | 0.9519 | 0.9135 | 0.9231 | 0.9231 | 0.8750 | 0.9231 |
| | Worst | 0.8462 | 0.9135 | 0.8558 | 0.8846 | 0.8654 | 0.9231 | 0.8558 | 0.8750 | 0.8846 | 0.8750 | 0.9231 | 0.8942 | 0.8750 | 0.8846 | 0.8173 | 0.8846 |
| SpectEW | Best | 0.8358 | 0.8657 | 0.8806 | 0.8508 | 0.8881 | 0.8433 | 0.8582 | 0.8582 | 0.8433 | 0.8358 | 0.8657 | 0.8508 | 0.8657 | 0.8881 | 0.8433 | 0.8508 |
| | Worst | 0.8060 | 0.8508 | 0.8433 | 0.8284 | 0.8582 | 0.8209 | 0.8358 | 0.8209 | 0.8209 | 0.7836 | 0.8209 | 0.8060 | 0.8358 | 0.8582 | 0.8134 | 0.8134 |
| CongressEW | Best | 0.9679 | 0.9771 | 0.9725 | 0.9771 | 0.9725 | 0.9679 | 0.9771 | 0.9725 | 0.9633 | 0.9817 | 0.9908 | 0.9725 | 0.9771 | 0.9679 | 0.9817 | 0.9817 |
| | Worst | 0.9495 | 0.9587 | 0.9587 | 0.9633 | 0.9495 | 0.9541 | 0.9633 | 0.9541 | 0.9450 | 0.9633 | 0.9679 | 0.9495 | 0.9541 | 0.9495 | 0.9633 | 0.9541 |
| IonosphereEW | Best | 0.9148 | 0.8807 | 0.9318 | 0.9375 | 0.9432 | 0.9375 | 0.9091 | 0.9205 | 0.9489 | 0.9205 | 0.9602 | 0.9205 | 0.9602 | 0.9318 | 0.9261 | 0.9205 |
| | Worst | 0.8977 | 0.8523 | 0.9148 | 0.9205 | 0.9148 | 0.9034 | 0.8750 | 0.8921 | 0.9205 | 0.8977 | 0.9148 | 0.8807 | 0.9375 | 0.8977 | 0.8864 | 0.8977 |
| KrvskpEW | Best | 0.9718 | 0.9731 | 0.9775 | 0.9743 | 0.9637 | 0.9737 | 0.9700 | 0.9769 | 0.9687 | 0.9743 | 0.9675 | 0.9568 | 0.9668 | 0.9731 | 0.9693 | 0.9681 |
| | Worst | 0.9543 | 0.9612 | 0.9625 | 0.9537 | 0.9481 | 0.9493 | 0.9499 | 0.9481 | 0.9368 | 0.9337 | 0.9312 | 0.9293 | 0.9318 | 0.9343 | 0.9387 | 0.9399 |
| Tic-tac-toe | Best | 0.7871 | 0.7933 | 0.7933 | 0.7829 | 0.8100 | 0.8205 | 0.7808 | 0.7954 | 0.8121 | 0.7871 | 0.7912 | 0.7891 | 0.7954 | 0.8079 | 0.7975 | 0.7829 |
| | Worst | 0.7871 | 0.7724 | 0.7829 | 0.7662 | 0.7954 | 0.8205 | 0.7745 | 0.7850 | 0.7954 | 0.7829 | 0.7871 | 0.7808 | 0.7829 | 0.7871 | 0.7724 | 0.7599 |
| Vote | Best | 0.9667 | 0.9800 | 0.9600 | 0.9600 | 0.9667 | 0.9667 | 0.9800 | 0.9533 | 0.9467 | 0.9667 | 0.9533 | 0.9667 | 0.9600 | 0.9800 | 0.9667 | 0.9800 |
| | Worst | 0.9467 | 0.9467 | 0.9400 | 0.9467 | 0.9533 | 0.9400 | 0.9533 | 0.9400 | 0.9267 | 0.9467 | 0.9333 | 0.9467 | 0.9400 | 0.9600 | 0.9400 | 0.9600 |
| WaveformEW | Best | 0.7452 | 0.7440 | 0.7464 | 0.7540 | 0.7468 | 0.7520 | 0.7444 | 0.7496 | 0.7428 | 0.7432 | 0.7440 | 0.7424 | 0.7384 | 0.7436 | 0.7392 | 0.7392 |
| | Worst | 0.7304 | 0.7284 | 0.7200 | 0.7284 | 0.7204 | 0.7168 | 0.7220 | 0.7192 | 0.7128 | 0.7212 | 0.7156 | 0.7124 | 0.7044 | 0.7224 | 0.7116 | 0.7036 |
| WineEW | Best | 1.0000 | 1.0000 | 0.9663 | 0.9775 | 0.9775 | 1.0000 | 0.9888 | 0.9775 | 0.9888 | 0.9663 | 0.9888 | 0.9888 | 1.0000 | 1.0000 | 0.9888 | 0.9888 |
| | Worst | 0.9888 | 0.9888 | 0.9551 | 0.9663 | 0.9663 | 0.9888 | 0.9775 | 0.9663 | 0.9663 | 0.9551 | 0.9663 | 0.9775 | 0.9663 | 0.9663 | 0.9663 | 0.9663 |
| Zoo | Best | 0.9412 | 0.9216 | 0.9608 | 0.9608 | 1.0000 | 1.0000 | 0.9608 | 0.9804 | 0.9608 | 1.0000 | 0.9608 | 0.9608 | 0.9804 | 0.9608 | 0.9608 | 1.0000 |
| | Worst | 0.9216 | 0.8824 | 0.9608 | 0.9608 | 1.0000 | 1.0000 | 0.9412 | 0.9608 | 0.9412 | 0.9608 | 0.9608 | 0.9412 | 0.9412 | 0.9412 | 0.9608 | 1.0000 |
| Clean1 | Best | 0.8571 | 0.9076 | 0.9076 | 0.9118 | 0.9034 | 0.8866 | 0.9160 | 0.9118 | 0.8824 | 0.9076 | 0.8992 | 0.9160 | 0.9034 | 0.9244 | 0.9034 | 0.8950 |
| | Worst | 0.8361 | 0.8782 | 0.8908 | 0.8908 | 0.8824 | 0.8740 | 0.8908 | 0.8866 | 0.8613 | 0.8782 | 0.8698 | 0.8866 | 0.8866 | 0.8908 | 0.8698 | 0.8698 |
| Semeion | Best | 0.9824 | 0.9787 | 0.9812 | 0.9762 | 0.9799 | 0.9824 | 0.9724 | 0.9774 | 0.9799 | 0.9799 | 0.9774 | 0.9812 | 0.9849 | 0.9749 | 0.9837 | 0.9849 |
| | Worst | 0.9762 | 0.9724 | 0.9724 | 0.9674 | 0.9749 | 0.9774 | 0.9649 | 0.9711 | 0.9737 | 0.9724 | 0.9699 | 0.9711 | 0.9774 | 0.9686 | 0.9762 | 0.9774 |
| Colon | Best | 0.8710 | 0.7742 | 0.7419 | 0.8710 | 0.8065 | 0.7097 | 0.7419 | 0.9032 | 0.8387 | 0.9032 | 0.9355 | 0.9032 | 0.8710 | 0.9355 | 0.8710 | 0.9355 |
| | Worst | 0.8387 | 0.7419 | 0.7097 | 0.8387 | 0.7742 | 0.6452 | 0.7097 | 0.8710 | 0.7419 | 0.7097 | 0.8065 | 0.7742 | 0.7742 | 0.8387 | 0.8065 | 0.5807 |
| Leukemia | Best | 0.9333 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 0.9333 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 |
| | Worst | 0.8667 | 0.9333 | 0.9333 | 1.0000 | 1.0000 | 0.9333 | 1.0000 | 0.8667 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 0.9333 | 0.9333 |

## References


[1] L. Yu, H. Liu, Feature selection for high-dimensional data: A fast correlation-based filter solution, in: Proceedings of the 20th international conference on machine learning (ICML-03), pp. 856–863.

[2] H. Liu, H. Motoda, Feature Selection for Knowledge Discovery and Data Mining, Kluwer Academic Publishers, Boston, 1998.

[3] H. Liu, R. Setiono, Chi2: Feature selection and discretization of numeric attributes, 1995.

[4] J. Quinlan, Induction of decision trees, Machine learning 1 (1986) 81–106.

[5] J. Quinlan, C4. 5: programs for machine learning, Morgan kaufmann, 1993.

[6] M. Robnik-Łikonja, I. Kononenko, Theoretical and empirical analysis of relieff and rrelieff, Machine learning 53 (2003) 23–69.

[7] R. Kohavi, G. H. John, Wrappers for feature subset selection, Artificial intelligence 97 (1997) 273–324.

[8] E. Pashaei, N. Aydin, Binary black hole algorithm for feature selection and classification on biological data, Applied Soft Computing 56 (2017) 94–106.

[9] U. Fayyad, G. Piatetsky-Shapiro, P. Smyth, From data mining to knowledge discovery in databases, AI magazine 17 (1996) 37.

[10] I. Guyon, A. Elisseeff, An introduction to variable and feature selection, Journal of machine learning research 3 (2003) 1157–1182.

[11] D. Rodrigues, X.-S. Yang, A. N. De Souza, J. P. Papa, Binary flower pollination algorithm and its application to feature selection, in: Recent Advances in Swarm Intelligence and Evolutionary Computation, Springer, 2015, pp. 85–100.

[12] J. Kennedy, Swarm intelligence, in: Handbook of nature-inspired and innovative computing, Springer, 2006, pp. 187–219.

[13] J. Kennedy, R. Eberhart, A new optimizer using particle swarm theory, in: Micro Machine and Human Science, 1995. MHS '95., Proceedings of the Sixth International Symposium on, pp. 39–43.

[14] M. Dorigo, M. Birattari, T. Stutzle, Ant colony optimization, IEEE computational intelligence magazine 1 (2006) 28–39.

[15] S. Mirjalili, Dragonfly algorithm: a new meta-heuristic optimization technique for solving single-objective, discrete, and multi-objective problems, Neural Computing and Applications 27 (2016) 1053–1073.

[16] S. Mirjalili, A. Lewis, The whale optimization algorithm, Advances in Engineering Software 95 (2016) 51–67.

[17] A. A. Heidari, R. A. Abbaspour, A. R. Jordehi, An efficient chaotic water cycle algorithm for optimization tasks, Neural Computing and Applications 28 (2017) 57–85.

[18] A. A. Heidari, R. A. Abbaspour, A. R. Jordehi, Gaussian bare-bones water cycle algorithm for optimal reactive power dispatch in electrical power systems, Applied Soft Computing 57 (2017) 657–671.

[19] A. H. Gandomi, A. H. Alavi, Krill herd: A new bio-inspired optimization algorithm, Communications in Nonlinear Science and Numerical Simulation 17 (2012) 4831–4845.

[20] W.-T. Pan, A new fruit fly optimization algorithm: Taking the financial distress model as an example, Knowledge-Based Systems 26 (2012) 69–74.

[21] S. Mirjalili, S. M. Mirjalili, A. Lewis, Grey wolf optimizer, Advances in Engineering Software 69 (2014) 46–61.

[22] X.-S. Yang, Firefly Algorithms for Multimodal Optimization, Springer Berlin Heidelberg, Berlin, Heidelberg, pp. 169–178.

[23] E. Zorarpacı, S. A. Özel, A hybrid approach of differential evolution and artificial bee colony for feature selection, Expert Systems with Applications 62 (2016) 91–103.

[24] K. Sorensen, M. Sevaux, F. Glover, A history of metaheuristics, arXiv preprint arXiv:1704.00853 (2017).

[25] S. Mirjalili, A. H. Gandomi, S. Z. Mirjalili, S. Saremi, H. Faris, S. M. Mirjalili, Salp swarm algorithm: A bio-inspired optimizer for engineering design problems, Advances in Engineering Software (2017).

[26] S. Kashef, H. Nezamabadi-pour, A new feature selection algorithm based on binary ant colony optimization, in: Information and Knowledge Technology (IKT), 2013 5th Conference on, IEEE, pp. 50–54.

[27] S. Kashef, H. Nezamabadi-pour, An advanced aco algorithm for feature subset selection, Neurocomputing 147 (2015) 271–279.

[28] P. Shunmugapriya, S. Kanmani, A hybrid algorithm using ant and bee colony optimization for feature selection and classification (ac-abc hybrid), Swarm and Evolutionary Computation (2017).

[29] Y. Wan, M. Wang, Z. Ye, X. Lai, A feature selection method based on modified binary coded ant colony optimization algorithm, Applied Soft Computing 49 (2016) 248–258.

[30] P. Moradi, M. Gholampour, A hybrid particle swarm optimization for feature subset selection by integrating a novel local search strategy, Applied Soft Computing 43 (2016) 117–130.

[31] S. Gunasundari, S. Janakiraman, S. Meenambal, Velocity bounded boolean particle swarm optimization for improved feature selection in liver and kidney disease diagnosis, Expert Systems with Applications 56 (2016) 28–47.

[32] K. K. Bharti, P. K. Singh, Opposition chaotic fitness mutation based adaptive inertia weight bpso for feature selection in text clustering, Applied Soft Computing 43 (2016) 20–34.

[33] L. M. Abualigah, A. T. Khader, E. S. Hanandeh, A new feature selection method to improve the document clustering using particle swarm optimization algorithm, Journal of Computational Science (2017).

[34] Y. Lu, M. Liang, Z. Ye, L. Cao, Improved particle swarm optimization algorithm and its application in text feature selection, Applied Soft Computing 35 (2015) 629–636.

[35] R. Sheikhpour, M. A. Sarram, R. Sheikhpour, Particle swarm optimization for bandwidth determination and feature selection of kernel density estimation based classifiers in diagnosis of breast cancer, Applied Soft Computing 40 (2016) 113–131.

[36] F. G. Mohammadi, M. S. Abadeh, Image steganalysis using a bee colony based feature selection algorithm, Engineering Applications of Artificial Intelligence 31 (2014) 35–43.

[37] A. Moayedikia, R. Jensen, U. K. Wiil, R. Forsati, Weighted bee colony algorithm for discrete optimization problems with application to feature selection, Engineering Applications of Artificial Intelligence 44 (2015) 153–167.

[38] E. Zorarpacı, S. A. Özel, A hybrid approach of differential evolution and artificial bee colony for feature selection, Expert Systems with Applications 62 (2016) 91–103.

[39] S. Mirjalili, The ant lion optimizer, Advances in Engineering Software 83 (2015) 80–98.

[40] H. M. Zawbaa, E. Emary, B. Parv, Feature selection based on antlion optimization algorithm, in: Complex Systems (WCCS), 2015 Third World Conference on, IEEE, pp. 1–7.

[41] E. Emary, H. M. Zawbaa, A. E. Hassanien, Binary ant lion approaches for feature selection, Neurocomputing 213 (2016) 54–65.

[42] H. M. Zawbaa, E. Emary, B. Parv, M. Sharawi, Feature selection approach based on moth-flame optimization algorithm, in: Evolutionary Computation (CEC), 2016 IEEE Congress on, IEEE, pp. 4612–4617.

[43] A. A. Heidari, P. Pahlavani, An efficient modified grey wolf optimizer with lévy flight for optimization tasks, Applied Soft Computing 60 (2017) 115–134.

[44] A. A. Heidari, R. A. Abbaspour, Enhanced chaotic grey wolf optimizer for real-world optimization problems: A comparative study, in: Handbook of Research on Emergent Applications of Optimization Algorithms, IGI Global, 2018, pp. 693–727.

[45] H. Faris, I. Aljarah, M. A. Al-Betar, S. Mirjalili, Grey wolf optimizer: a review of recent variants and applications, Neural Computing and Applications (2017) 1–23.

[46] E. Emary, H. M. Zawbaa, A. E. Hassanien, Binary grey wolf optimization approaches for feature selection, Neurocomputing 172 (2016) 371–381.

[47] E. Emary, H. M. Zawbaa, C. Grosan, A. E. Hassenian, Feature subset selection approach by gray-wolf optimization, in: Afro-European Conference for Industrial Advancement, Springer, pp. 1–13.

[48] S. Mirjalili, Moth-flame optimization algorithm: A novel nature-inspired heuristic paradigm, Knowledge-Based Systems 89 (2015) 228–249.

[49] M. M. Mafarja, S. Mirjalili, Hybrid whale optimization algorithm with simulated annealing for feature selection, Neurocomputing (2017).

[50] A. K. Das, S. Das, A. Ghosh, Ensemble feature selection using bi-objective genetic algorithm, Knowledge-Based Systems 123 (2017) 116–127.

[51] L. Lu, J. Yan, C. W. de Silva, Feature selection for ecg signal processing using improved genetic algorithm and empirical mode decomposition, Measurement 94 (2016) 372–381.

[52] L. Lu, J. Yan, Y. Meng, Dynamic genetic algorithm-based feature selection scheme for machine health prognostics, Procedia CIRP 56 (2016) 316–320.

[53] S. Sarafrazi, H. Nezamabadi-pour, Facing the classification of binary problems with a gsa-svm hybrid system, Mathematical and Computer Modelling 57 (2013) 270–278.

[54] E. Rashedi, H. Nezamabadi-pour, Feature subset selection using improved binary gravitational search algorithm, Journal of Intelligent & Fuzzy Systems 26 (2014) 1211–1221.

[55] U. Mlakar, I. Fister, J. Brest, B. Potočnik, Multi-objective differential evolution for feature selection in facial expression recognition systems, Expert Systems with Applications 89 (2017) 129–137.

[56] M. Z. Baig, N. Aslam, H. P. Shum, L. Zhang, Differential evolution algorithm as a tool for optimal feature subset selection in motor imagery eeg, Expert Systems with Applications 90 (2017) 184–195.

[57] Z. Zainuddin, K. H. Lai, P. Ong, An enhanced harmony search based algorithm for feature selection: Applications in epileptic seizure detection and prediction, Computers & Electrical Engineering 53 (2016) 143–162.

[58] D. Rodrigues, L. A. Pereira, R. Y. Nakamura, K. A. Costa, X.-S. Yang, A. N. Souza, J. P. Papa, A wrapper approach for feature selection based on bat algorithm and optimum-path forest, Expert Systems with Applications 41 (2014) 2250–2258.

[59] M. Mafarja, I. Aljarah, A. A. Heidari, A. I. Hammouri, H. Faris, A. Al-Zoubi, S. Mirjalili, Evolutionary population dynamics and grasshopper optimization approaches for feature selection problems, Knowledge-Based Systems 145 (2018) 25 – 45.

[60] R. Falcon, M. Almeida, A. Nayak, Fault identification with binary adaptive fireflies in parallel and distributed systems, in: Evolutionary Computation (CEC), 2011 IEEE Congress on, IEEE, pp. 1359–1366.

[61] C. C. Ramos, A. N. Souza, G. Chiachia, A. X. Falcão, J. P. Papa, A novel algorithm for feature selection using harmony search and its application for non-technical losses detection, Computers & Electrical Engineering 37 (2011) 886–894.

[62] D. Rodrigues, L. A. Pereira, T. Almeida, J. P. Papa, A. Souza, C. C. Ramos, X.-S. Yang, Bcs: A binary cuckoo search algorithm for feature selection, in: Circuits and Systems (ISCAS), 2013 IEEE International Symposium on, IEEE, pp. 465–468.

[63] D. Rodrigues, L. A. Pereira, J. P. Papa, C. C. Ramos, A. N. Souza, L. P. Papa, Optimizing feature selection through binary charged system search, in: International Conference on Computer Analysis of Images and Patterns, Springer, pp. 377–384.

[64] M. Dash, H. Liu, Feature selection for classification, Intelligent data analysis 1 (1997) 131–156.

[65] H. Liu, L. Yu, Toward integrating feature selection algorithms for classification and clustering, IEEE Transactions on knowledge and data engineering 17 (2005) 491–502.

[66] D. H. Wolpert, W. G. Macready, No free lunch theorems for optimization, IEEE transactions on evolutionary computation 1 (1997) 67–82.

[67] F. Pernkopf, Bayesian network classifiers versus selective k-nn classifier, Pattern Recognition 38 (2005) 1–10.

[68] S. Mirjalili, A. Lewis, S-shaped versus v-shaped transfer functions for binary particle swarm optimization, Swarm and Evolutionary Computation 9 (2013) 1–14.

[69] J. Kennedy, R. C. Eberhart, A discrete binary version of the particle swarm algorithm, in: Systems, Man, and Cybernetics, 1997. Computational Cybernetics and Simulation., 1997 IEEE International Conference on, volume 5, IEEE, pp. 4104–4108.

[70] E. Rashedi, H. Nezamabadi-Pour, S. Saryazdi, Bgsa: binary gravitational search algorithm, Natural Computing 9 (2010) 727–745.

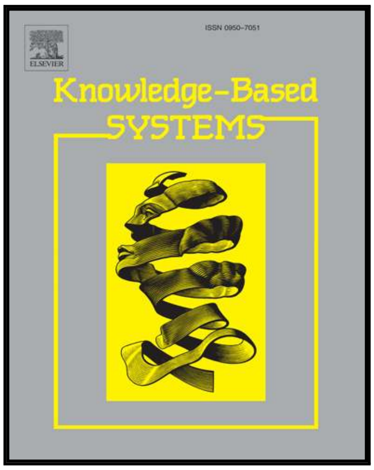
[71] M. Lichman, UCI machine learning repository, 2013.

[72] A. Moayedikia, K.-L. Ong, Y. L. Boo, W. G. Yeoh, R. Jensen, Feature selection for high dimensional imbalanced class data using harmony search, Engineering Applications of Artificial Intelligence 57 (2017) 38–49.

[73] E. Emary, H. M. Zawbaa, C. Grosan, Experienced gray wolf optimization through reinforcement learning and neural networks, IEEE transactions on neural networks and learning systems 29 (2018) 681–694.

[74] E. Emary, H. M. Zawbaa, A. E. Hassanien, Binary grey wolf optimization approaches for feature selection, Neurocomputing 172 (2016) 371–381.

[75] S. Mirjalili, S. M. Mirjalili, X.-S. Yang, Binary bat algorithm, Neural Computing and Applications 25 (2014) 663–681.




An Efficient Binary Salp Swarm Algorithm with Crossover Scheme for Feature Selection Problems

Hossam Faris, Majdi M. Mafarja, Ali Asghar Heidari, Ibrahim Aljarah, Ala' M. Al-Zoubi, Seyedali Mirjalili, Hamido Fujita

PII: S0950-7051(18)30213-2
DOI: 10.1016/j.knosys.2018.05.009
Reference: KNOSYS 4329

To appear in: *Knowledge-Based Systems*

Received date: 17 January 2018
Revised date: 31 March 2018
Accepted date: 3 May 2018