

## An efficient binary social spider algorithm for feature selection problem

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### ABSTRACT

The social spider algorithm (SSA) is a heuristic algorithm created on spider behaviors to solve continuous problems. In this paper, firstly a binary version of the social spider algorithm called binary social spider algorithm (BinSSA) is proposed. Currently, there is insufficient focus on the binary version of SSA in the literature. The main part of the binary version is the transfer function. The transfer function is responsible for mapping continuous search space to binary search space. In this study, eight of the transfer functions divided into two families, S-shaped and V-shaped, are evaluated. BinSSA is obtained from SSA, by transforming constant search space to binary search space with eight different transfer functions (S-Shapes and V-Shaped). Thus, eight different variations of BinSSA are formed as BinSSA1, BinSSA2, BinSSA3, BinSSA4, BinSSA5, BinSSA6, BinSSA7, and BinSSA8. For increasing, exploration and exploitation capacity of BinSSA, a crossover operator is added as BinSSA-CR. In secondly, the performances of BinSSA variations are tested on feature selection task. The optimal subset of features is a challenging problem in the process of feature selection. In this paper, according to different comparison criteria (mean of fitness values, the standard deviation of fitness values, the best of fitness values, the worst of fitness values, accuracy values, the mean number of the selected features, CPU time), the best BinSSA variation is detected. In the feature selection problem, the K-nearest neighbor (K-NN) and support vector machines (SVM) are used as classifiers. A detailed study is performed for the fixed parameter values used in the fitness function. BinSSA is evaluated on low-scaled, middle-scaled and large-scaled twenty-one well-known UCI datasets and obtained results are compared with state-of-art algorithms in the literature. Obtained results have shown that BinSSA and BinSSA-CR show superior performance and offer quality and stable solutions.

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### 1. Introduction

Classification is one of the most common tasks in data mining (Yin & Gai, 2015). Because of the vast growth in the data in the world, a pre-processing procedure like feature selection becomes a challenging and fundamental task in data mining applications (Jensen, 2005). Feature selection means that the performance of the learning algorithm is improved by removing the repeated features and irrelevant features from the data set (Liu & Motoda, 1998; Pal & Maiti, 2010). In feature selection, finding the optimal subset is a decisive issue. Exhaustive search can produce all possible subsets by examining all the entire set of features. This approach is impractical for the large datasets and has an extremely high computational cost because if a dataset holds  $M$  features,

then there are  $2^M$  subsets of features (Guyon & Elisseeff, 2003; Yin, Gai & Wang, 2016). Feature selection is available in many different areas. For example: text categorization (Üğuz, 2011), face recognition (Kanan & Faez, 2008), cancer classification (Yu, Gu, Liu, Shen & Zhao, 2009), gene classification (Tabakhi, Najafi, Ranjbar & Moradi, 2015), finance (Huang & Tsai, 2009), recommender systems (Ramezani, Moradi & Tab, 2013) and customer relationship management (Kuri-Morales & Rodríguez-Erazo, 2009) etc. Many feature selection algorithms include heuristic or random search strategies to find the most appropriate or optimal feature subset to reduce computation time. Feature selection methods can be categorized into filter (Ke, Feng & Ren, 2008; Sun, 2007; Yang & Honavar, 1998), wrapper (Abe, 2005; Chun-Nan, Hung-Ju & Dietrich, 2002; Guan, Liu & Qi, 2004; Qiao, Peng & Peng, 2006), hybrid (Huang, Cai & Xu, 2007; Kabir, Shahjahan & Murase, 2012; Sivagaminathan & Ramakrishnan, 2007) and embedded (Dash & Liu, 1997; Huan & Lei, 2005; Lai, Reinders & Wessels, 2006) approaches. The filter approach is not based on any particular learn-

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ing model and looks for features that maximize a criterion. The wrapper approach uses a learning algorithm to select a candidate property subset. In the wrapper approach, the feature selection process is wrapped around the learning model and requires a high calculation cost for large-dimensional data sets. Filter-based approaches are faster than wrappers. The quality of the final result in filter-based approaches is lower than that of the wrapper approach. Hybrid-based methods combine the computational efficiency of the filter model with the appropriate performance of the wrapper model. However, the hybrid model may be devoid of accuracy because the filter and wrapper models are considered as two separate steps (Moradi & Gholampour, 2016). Finally, the embedded approach seeks to subsume feature selection as part of the model building process and is thus associated with a specific learning model (Moradi & Gholampour, 2016). These approaches have a number of disadvantages, such as stagnation in local optima and high computational cost.

In the previous two decades, metaheuristics have demonstrated their productivity and efficiency in solving challenging and large-scale problems (Dorigo, 1990; Parpinelli & Lopes, 2011; Xue, Zhang, Browne & Yao, 2016). Metaheuristic methods have both local and global search strategies. Global search methods apply randomness to search for strategies to explore most of the solution space. And so they achieve more successful results in feature selection issues. Swarm-based techniques imitative the searching mechanism of natural animals like bat, cuckoo, ant, moth, etc. (Valdez, 2015). Many metaheuristic algorithms have been used for the feature selection task in literature. These algorithms include genetic algorithm (GA) (Oh, Lee & Moon, 2004), particle swarm optimization (PSO) (Zhangn, Gong, Hu & Zhang, 2015; Fan, Weijia & Li, 2013; Kennedy & Eberhart, 1995; Prescilla & Immanuel, 2013; Tawhid & Dsouza, 2019), ant colony optimization (ACO) (Huang, 2009; Rizk-Allah, 2014; Wan, Wang, Ye & Lai, 2016), the grey wolf optimization (GWO) (Emary, Zawbaa & Hassanien, 2016), black hole algorithm (BHA) (Pashaei & Aydin, 2017), coral reefs optimization (CRO) (Yan, Ma, Luo & Patel, 2019), artificial algae algorithm (AAA) (Korkmaz, Babalik & Servet, 2017), bat algorithm (BA) (Mirjalili, Mirjalili & Yang, 2014; Rizk-Allah & Hassanien, 2018b), salp swarm algorithm (SSA) (Rizk et al., 2018a), and ant lion optimizer (ALO) (Zawbaa, Emary & Parv, 2015).

Yu and Li have offered a social spider algorithm (SSA) which is configured according to social spider behaviors (Yu & Li, 2015). Some spider species, which generally live solitary, can live as colonies. Spiders live in colonies can communicate with each other by web structure. The vibration they produce on the web enables this communication. They can make random walks to each other by the vibration information they share (Yu & Li, 2015). El-Bages and Elsayed have solved the static transmission expansion planning problem by using SSA. In the proposed method; the DC power flow sub-problem is solved by developing the SSA based web and adding potential solutions to the result (El-Bages & Elsayed, 2017). Yu and Li have solved an economic load dispatch (ELD) formulation by developing an SSA based new approach. ELD is one of the essential components in power system control and operation (Yu & Li, 2016). Mousa and Bentahar have adapted a QoS-aware web service selection process to the SSA approach (Mousa & Bentahar, 2016) and Elsayed et al. have solved the non-convex economic load dispatch problem with the SSA based approach (Elsayed, Hegazy, Bendary & El-bages, 2016).

Social spider optimization (SSO) is another heuristic algorithm that is very similar to the SSA algorithm but totally different from it. SSO is not covered by the scope of this paper. Cuevas, Cienfuegos, Zaldívar and Pérez-Cisneros (2013) have developed the SSO algorithm by inspiring from spider behaviors. In SSO, there are two different searching agents (spider) in the search space of SSO. These are male and female spiders. Depending upon the gender,

each individual operates a range of different evolutionary operators that imitates various collaboration behaviors that typically exist in colonies. In SSA, there is only one type of spider and no gender discrimination is made. In SSO, the vibration structure is very different. There is three special vibration type in SSO approach. In SSA, there is one special vibration type. The spiders can make random walks to each other by the vibration information in SSA. The vibration calculation method is different in both algorithms. There are also various different studies in the literature with SSO. Shukla and Nanda (2018) have developed a parallel social spider clustering algorithm for high dimensional datasets and a binary social spider optimization algorithm for unsupervised band selection in compressed hyperspectral images. Pereira, Rodrigues, Ribeiro, Papa and Weber (2014) have developed a social spider optimization-based artificial neural networks training and applied its applications for Parkinson's disease identification. Sun, Qi, Sun, Ren & Ruan (2017) have developed the hybrid SSO algorithms and applied it for the estimation of thermophysical properties of phase change material.

SSA (Yu & Li, 2015) is a new heuristic algorithm developed to solve continuous optimization problems. There is no significant study on the binary version of SSA (BinSSA) in the literature. In this paper, we propose a binary version of SSA, a new approach that has not really focused on the literature. The aim of this study is first to develop the binary form of SSA, which has been developed for continuous optimization problems and then test the success of BinSSA as a binary optimization algorithm for feature selection. In binary optimization problems, transfer functions are used to convert continuous search space to binary search space. There are many transfer functions (S-shaped and V-shaped) in the literature. The selection of the transfer function in binary optimization directly affects the success of the algorithm used. Therefore, in this paper, different types of versions of BinSSA are presented according to transfer functions. The original social spider algorithm is modified again according to eight different transfer functions for mapping the continuous search space to the binary search space. Eight binary variations of the BinSSA (i.e., BinSSA1, BinSSA2, BinSSA3, BinSSA4, BinSSA5, BinSSA6, BinSSA7, and BinSSA8) are proposed based on eight transfer functions (S-shaped and V-shaped). BinSSA has been tested on the feature selection problem that is one of the binary optimization problem types. The purpose of feature selection is to move the useless features without sacrificing the predictive accuracy and find a feature subset from an original set of features (Zhangn et al., 2015). It provides the highest accuracy by selecting the least and most accurate features in the feature selection problem. BinSSA is very convenient to apply the feature selection problem to a binary structure. If a feature is selected, the value is "1" in binary structure or If a feature is not selected, the value is "0" in binary structure. Binary structures perform the operation of whether or not to select a feature. BinSSA has provided us with a binary structure, which features can be selected. After deciding which features to select, a classification is performed. There is a need for a classifier in the feature selection problem. K-nearest neighbor (K-NN) or support vector machine (SVM) is used as a classifier in BinSSA. If the dataset contains two classes, we have chosen the SVM classifier. If the dataset contains more than two classes, we have preferred the K-NN classifier. The BinSSA is tested on low-scaled, middle-scaled, and large-scaled twenty-one well-known UCI datasets. In many different comparisons, these versions of BinSSA have been compared. Thus, the most successful version of BinSSA is tried to be determined. In addition to this study, a crossover operator has been added to increase the success of transfer functions. A feature selection method can improve the predictive accuracy of the algorithm and reduce the calculation cost required in data mining. The crossover operator has improved BinSSA's ability to search locally and discover new spots

globally. Local traps are avoided in the search space thanks to the crossover operator. In this paper, the balance between exploration and exploitation of the proposed BinSSA is improved through the crossover operator. The crossover operator is used to produce a different candidate spider than the parent spiders. Thus, BinSSA can randomly search the binary search space at any point. Thanks to the crossover operator, BinSSA can find global optimum or local optimum solutions in the search space. This reduces the time cost of the BinSSA to achieve the optimal solution. Thanks to the crossover operator, BinSSA's exploration and exploitation capability has been increased.

Also, the main contributions of this paper are as follows:

- (a) We proposed a binary social spider algorithm (BinSSA) and then we solved the feature selection task with BinSSA. The original social spider algorithm is transformed according to the binary search space;
- (b) A detailed literature study is done for BinSSA and the feature selection. The proposed BinSSA is designed to be the first to apply BinSSA for feature selection problems;
- (c) In this paper, BinSSA is developed by adding a crossover operator and tested on twenty-one UCI datasets used in the feature selection problem. Both the exploration and exploitation capabilities of BinSSA are enhanced;
- (d) In the previous feature selection studies in the literature, generally low or medium scaled datasets were used for testing. In this study, large-scale datasets are used for testing. The maximum number of features is 856;
- (e) The impact of  $\rho$  and  $\varphi$  values are tested on the CNAE dataset (National classification of economic activities).  $\rho$  and  $\varphi$  values are fixed values that can be changed slightly in the fitness function.  $\rho$  determines the weight of the classification accuracy, while  $\varphi$  corresponds to the weight of the features reduction rate. In the literature, these values are usually determined randomly in feature selection problems. In this paper, according to the accuracy rate, the most appropriate  $\rho$  and  $\varphi$  values are determined;
- (f) Different combinations of population size and number of the maximum iteration are tested on the CNAE dataset. According to the accuracy rate, the most appropriate population size and the number of the maximum iteration are determined;
- (g) Many different criteria (mean of fitness values, standard deviation of fitness values, the best of fitness values, the worst of fitness values, accuracy value, the mean number of the selected features, and CPU time) are evaluated in this study for feature selection task while trying to maximize classification accuracy in previous studies in the literature;
- (h) The best BinSSA variations are determined according to different criteria.

The organization of the paper is as follows. Related works for feature selection are analyzed in [Section 2](#), the original SSA is studied in [Section 3](#), BinSSA is detailed in [Section 4](#). BinSSA is tested on twenty-one well-known UCI datasets in [Section 5](#) and obtained results are compared with well known binary heuristic methods. The results are evaluated.

## 2. Related works

Feature selection plays an important role in the classification. There are many different algorithms proposed for feature selection in literature. Recently, many algorithms based swarm in the literature have been proposed for feature selection. The literature review has focused more on swarm methods since BinSSA is a swarm-based algorithm. [Table 1](#) shows some of the earlier research algorithms for feature selection.

## 3. Original social spider algorithm (SSA)

Social spider algorithm (SSA) is a heuristic algorithm that is created by imitating spiders' behaviors in nature. SSA is created for organizing searching space of optimization problems as a high dimensional spider web. Each position on the web represents a convenient solution for the optimization problem and all convenient solutions to the problem correspond to positions on this web. This web also serves as a transmission medium of vibrations created by spiders. Each spider on the web is held in a position and the conformity value of the solution is calculated with the objective function. Spiders can move randomly on the web. But they can not move out of positions which represent convenient solutions for optimization problems. When a spider moves towards a new position, a vibration is produced and this vibration spreads on the web. Other spiders execute social information sharing via this vibration. Flowchart for the original SSA is shown in [Fig. 1](#).

There are two important terms in SSA: spider and vibration. Spider structure: Spiders are SSA agents that perform optimization. At the beginning of the algorithm, a predetermined number of spiders are placed on the web. The number of spiders cannot be changed afterward. "a" represents a spider and a memory is allocated for each spider a. Spider information is stored here. This information: the position of spider a on the web, the fitness value at the current position of spider a, the target vibration of spider a in the previous iteration, the iteration number where the target vibration last changed, the movement of spider a in the previous iteration and the dimension mask of spider a that guided the movement in the previous iteration. The dimension mask is a {0,1} binary vector of length D, where D is the dimension of the optimization problem ([Yu & Li, 2015](#)). Spider locations are initially set at random. Each spider produces a vibration when it moves from a position to a different location. The severity of the vibration is related to the fitness value that the spider produces in that position. Vibration can spread over the web and other spiders on the web can feel it. Thus, other spiders on the web can obtain the personal information of the spider that produces the vibration, and information sharing takes place. Vibration structure: The vibration in the SSA is a very important term. It is one of the most important characteristics distinguishing SSA from other heuristic algorithms. Two properties are used to define a vibration. a-) The source position b-) The source of vibration severity  $[0, +\infty)$

[Eq. \(1\)](#) ([Yu & Li, 2015](#)) is used to calculate the vibration intensity.

$$I(P_a, P_a, t) = \log\left(\frac{1}{f(P_a) - C}\right) + 1 \quad (1)$$

where a represents a spider and spider a generates vibration at its current position. It defines the position of a spider a at time t as  $P_a(t)$ , or simply as  $P_a$  if the time argument is t. Where  $I(P_a, P_a, t)$  is the vibration value produced by the spider in the source position at time t.  $f(P_a)$  represents the spider of fitness value in its current position. Where C is a confidently small constant such that all possible fitness values are larger than C for minimization problems.  $Dis(P_a, P_b)$  is showing the distance between spider a and spider b. This distance is calculated by [Eq. \(2\)](#) ([Yu & Li, 2015](#)). Manhattan distance structure is used when calculating this distance. The vibration attenuation over distance is calculated by [Eq. \(3\)](#) ([Yu & Li, 2015](#)).

$$Dis(P_a, P_b) = \|P_a - P_b\| \quad (2)$$

$$I(P_a, P_b, t) = I(P_a, P_a, t) \times \exp\left(-\frac{Dis(P_a, P_b)}{\bar{\sigma} \times r_a}\right) \quad (3)$$

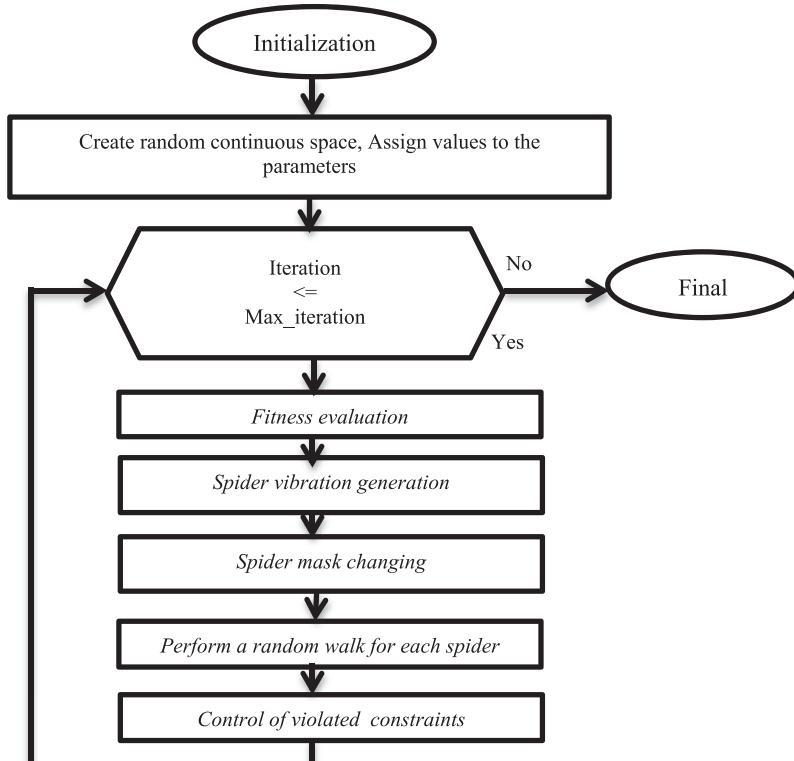
**Table 1**

The earlier research algorithms for feature selection in literature.

Algorithm	Instruction
GWO ( <a href="#">Emary et al., 2016</a> )	Proposed a binary version of the Grey wolf optimization (GWO) for the feature selection domain.
BALO ( <a href="#">Zawbaa et al., 2015</a> )	Introduced a feature selection method using a binary ant lion optimizer (BALO).
BBHA ( <a href="#">Pashaei &amp; Aydin, 2017</a> )	Introduced the binary black hole algorithm for feature selection (BBHA). The BBHA is an extension of existing BHA through appropriate binarization.
MBACO ( <a href="#">Wan et al., 2016</a> )	A feature selection approach based on a modified binary-coded ant colony optimization algorithm (MBACO) combined with a genetic algorithm (GA) is introduced.
HBEPSON ( <a href="#">Tawhid &amp; Dsouza, 2019</a> )	Introduced hybrid binary bat enhanced particle swarm optimization algorithm (HBEPSON). It is combined the bat algorithm with its capacity for echolocation helping explore the feature space and enhanced version of the particle swarm optimization with its ability to converge to the best global solution in the search space.
BCROSAT ( <a href="#">Yan et al., 2019</a> )	Introduced a hybrid binary coral reefs optimization algorithm with simulated annealing for feature selection in high-dimensional biomedical datasets.
BBSO ( <a href="#">Papa, Rosa, Souza &amp; Afonso, 2018</a> )	Introduced binary brain storm optimization (BBSO) for feature selection. The variation of the brainstorm optimization for feature selection purposes, where real-valued solutions are mapped onto a boolean hypercube using different transfer functions.
ISSA ( <a href="#">Hegazy et al., 2018</a> )	Introduced improved salp swarm algorithm (ISSA) to enhance solution accuracy, reliability and convergence speed for feature selection. A new control parameter, inertia weight, is added to adjust the present best solution.
BSSA ( <a href="#">Faris et al., 2018</a> )	Introduced a binary salp swarm algorithm (BSSA) for feature selection. Two new wrapper feature selection approaches that use SSA as the search strategy are proposed.
Rc-BBFA ( <a href="#">Zhang, Song &amp; Gong, 2017</a> )	Proposed return-cost-based binary FFA (Rc-BBFA) for feature selection. The proposed method has the capability of preventing premature convergence and is particularly efficient attributed to the following three aspects.

Where  $\bar{\sigma}$  represents the mean of the standard deviation of the positions of all spiders in each dimension.  $r_a$  is represented as a user-controlled parameter  $r_a \in (0, \infty)$ . This parameter controls the attenuation rate of the vibration intensity over the distance. The larger  $r_a$  is, the weaker the attenuation imposed on the vibration ([Yu & Li, 2015](#)). Whenever a spider moves to a new position, it generates vibration at its current position.  $I(P_a, P_b, t)$  is the felt value of the spider's vibration in "a" point, by the spider in the "b" point. The value of  $r_a$  is selected from the set {1/10, 1/5, 1/4, 1/3, 1/2, 1, 2, 3, 4, 5, 10} and the values of  $p_c$  and  $p_m$  are both selected from the set {0.01, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 0.99} ([Yu & Li, 2015](#)). After setting the values, the algorithm creates an ini-

tial population of spiders for optimization. Each spider is assigned a fixed size memory for storing spider information. The positions of spiders are randomly generated in the search space. Fitness values of the spiders calculated and stored. The initial target vibration of each spider in the population is set at its current position, and the vibration intensity is zero. All spiders produce vibration using their position. The algorithm uses vibrations to activate the propagation process.  $V$  represents spider vibrations. Each spider receives the vibrations generated by other spiders. A spider selects the strongest of these vibration values. This value shows as  $V_a^{\text{best}}$ ,  $a$  represents a spider. Spider  $a$  which is stored in the memory of the target vibration shows as  $V_a^{\text{tar}}$ .  $V_a^{\text{best}}$  compares vibration val-

**Fig. 1.** Flowchart for the original SSA.

- Step 1. Parameter setting:** Required constant parameter sets are adjusted. For example, lower and upper limits of variables, number of maximum iteration, etc.
- Step 2. Initialization:** Random starting position locations are determined for each spider in the swarm. Assign memory for them. The target vibration for each spider is started.
- Step 3. Evaluation:** Fitness value is calculated for each spider. The best in the swarm are detected and recorded.
- Step 4.** Vibration value is calculated for each spider calculated by using vibration Equations (1,2, and 3). The best in the swarm are detected and recorded.
- Step 5.** Vibration comparison: The received the best vibration is compared to the target vibration values.
- Step 6.** Update the spider mask.
- Step 7.**  $P_a^{fo}$  value is calculated by Equation 4
- Step 8. Movement:** Each spider moves to a new position by Equation 5 and a new population is obtained.
- Step 9. Repeat:** All criteria beginning from Step 3 are repeated until reaching stopping criteria.
- Step 10. Output:** Optimum outputs are obtained.

**Fig. 2.** The work steps of the original SSA.

ues and if the intensity of the  $V_a^{\text{best}}$  is not greater than the target vibration, the spider's memory is changed to  $V_a^{\text{best}}$ .  $cs$ , the number of iterations since spider  $a$  has last changed its target vibration, is reset to zero; otherwise, the original  $V_a^{\text{tar}}$  is retained and  $cs$  is incremented by one. The dimension mask  $m$  is determined so that a random walk can be performed towards the  $V_a^{\text{tar}}$ . The dimension mask is a {0, 1} binary vector of length  $D$  and  $D$  is the dimension of the optimization problem. The dimension mask is used to perform a random walk. Initially, all the values of this mask are zero. In each iteration, spiders have a probability of  $1 - p_c^{cs}$  to change its mask where  $p_c \in (0, 1)$  is a user-defined attribute that describes the probability of changing mask. If the mask is decided to be changed, each bit of the vector has a probability of  $p_m$  to be assigned with a one, and  $1 - p_m$  to be a zero.  $P_m$  is also a user-controlled parameter defined in (0, 1) (Yu & Li, 2015). Each bit of the mask is changed independently. The new mask does not have any correlation with the previous mask. In case all bits are zeros or ones, one random value of the mask is changed to one or zero. After the dimension mask is determined, a new following position  $P_a^{fo}$  is generated based on the mask for a spider.  $P_a^{fo}$  value is calculated by Eq. (4) (Yu & Li, 2015).

$$P_{a,i}^{fo} = \begin{cases} P_{a,i}^{\text{tar}}, & m_{a,i} = 0 \\ P_r^r, & m_{a,i} = 1 \end{cases} \quad (4)$$

Where  $r$  is a random integer value generated in [1, population\_size] and  $m_{a,i}$  stands for the  $i$ th dimension of the dimension mask  $m$  of spiders. The random walk of each spider is calculated by Eq. (5) (Yu & Li, 2015).

$$P_a(t+1) = P_a + (P_a - P_a(t-1)) \times r + (P_a^{fo} - P_a) \odot R \quad (5)$$

Where  $\odot$  denotes element-wise multiplication.  $R$  is a vector of random float-point numbers generated from zero to one uniformly. Before following  $P_a^{fo}$ , spider  $a$  first moves along its previous direction, which is the direction of movement in the previous iteration. The distance along this direction is a random portion of the previous movement. Then spider  $a$  approaches  $P_a^{fo}$  along each dimension with random factors generated in (0, 1). After each spider performs a random walk, the spiders may move out of the web. It blocks the constraints of the optimization problem to be violated. The work steps of the original SSA is shown in Fig. 2.

#### 4. A binary social spider algorithm (BinSSA) for solving the feature selection

The binary optimization problem (BOP) is shown as a binary-based problem space that represents an important class of the

combinatorial optimization problems (Rizk-Allah, Hassanien, Elhosny & Gunasekaran, 2018a). In continuous optimization, search agents take continuous values in search space, while in binary optimization search agents in the search space take {0, 1} values. "0" represents absence and "1" represents presence. Many problems can be solved in a binary space by using these two values in the search space. Some algorithms are capable of solving problems with continuous search spaces, while some problems have discrete search spaces (Mirjalili & Lewis, 2013). In general, there are many problems with binary search fields, such as feature selection and diminishing dimensionality. They need binary algorithms for their solution. In addition, algorithms with a continuous real search field can solve binary problems by converting variables into binary variables. Regardless of the type of binary problems, binary search space has its own unique structure with some limitations. In the literature, many traditional methods (including relaxation methods, lagrangian techniques, branch-and-bound methods, reduction schemes and integer programming (Rizk-Allah et al., 2018a) have been proposed to solve the binary optimization problem. Although these methods perform well in low-scaled problems, they do not perform well in large-scaled problem solutions. Although there are many methods for the solution of binary optimization problems, the solution with heuristic algorithms has given us many advantages. Especially, it has shortened the solution time of high-scale problems. Due to these limitations in the deterministic methods, more and more are becoming interested in the heuristic algorithms inspired by specific phenomena.

In binary optimization, the solution is restricted to the binary {0, 1} values. In the original social spider algorithm (SSA), spiders change their positions in constant search space randomly. In the BinSSA, the solution pool is represented by {0, 1} binary string values. Positions of spiders are created in binary search space at the beginning of the algorithm. In order to realize this purpose, a random number is produced in [0, 1] for each dimension of the problem. If the produced number is smaller than 0.5, the related bit of the problem is assigned as 0 value, otherwise 1 value. For the feature selection problem, the "1" value shows that the corresponding feature is chosen and the "0" value shows that the corresponding feature is not chosen. Binary search space production schema at the beginning of the algorithm is shown in Equation 6.

$$X_{i,j} = \begin{cases} 0 & \text{if}(r_{i,j} < 0.5) \\ 1 & \text{otherwise} \end{cases} \quad (6)$$

Where  $r_{i,j}$  is a randomly generated number in [0,1] and  $X_{i,j}$  is the  $j$ th dimension of the  $i$ th spider.

The original SSA algorithm performs a random walk in the continuous search space (in Eq. (5)). The positions of a spider are up-

**Table 2**

S-shaped and V-shaped transfer functions ([Beskirli, Koc, Hakli & Kodaz, 2018](#); [Faris et al., 2018](#)).

S-Shaped Family		V-Shaped Family	
Name	Transfer Functions	Name	Transfer Functions
<b>S1</b>	$T(x) = \frac{1}{1+e^{-\alpha x}}$	<b>V1</b>	$T(x) =  \operatorname{erf}(\frac{\sqrt{x}}{2}) $
<b>S2</b>	$T(x) = \frac{1}{1+e^{-x}}$	<b>V2</b>	$T(x) =  \tanh(x) $
<b>S3</b>	$T(x) = \frac{1}{1+e^{(-x)/2}}$	<b>V3</b>	$T(x) =  (x)/\sqrt{1+x^2} $
<b>S4</b>	$T(x) = \frac{1}{1+e^{(-x)/3}}$	<b>V4</b>	$T(x) =  \frac{2}{\pi} \operatorname{arc tan}(\frac{\pi}{2}x)$

dating through a 0–1 flipping operation. This flipping process is performed by a certain threshold value that is related to the transfer function. The transfer function is the most important part of converting to binary form. A transfer function defines the probability of changing a position vector's elements from 0 to 1 and vice versa. As a result, binary values are converted to continuous values. With eight different transfer functions used in BinSSA, continuous values are converted to binary values in each iteration. Transfer functions used in BinSSA are divided into two groups; S-shaped and V-shaped. [Table 2](#) shows the S-shaped and V-shaped transfer functions.

The BinSSA consists of two stages. In the first stage, the continuous search space is converted to binary search space with eight different transfer functions. In the second stage, new candidate solutions are produced with a crossover operator in binary search space.

#### 4.1. The BinSSA with crossover(BinSSA-CR)

In order to improve the quality of the solutions obtained by BinSSA, a new candidate solution set is obtained with the crossover operator. The crossover operator is shown in [Eqs. 7](#) and [8](#).

$$V_i = x_i \Leftrightarrow x_{i+1} \quad (7)$$

$$V_i^n = \begin{cases} x_i^n & , rand \geq 0.5 \\ x_{i+1}^n & , otherwise \end{cases} \quad (8)$$

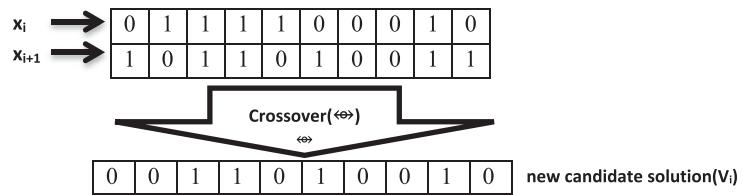
where  $\Leftrightarrow$  is a crossover operator that performs the crossover scheme on two binary solutions.  $V_i$  is  $i$ th new candidate solution after applying the crossover process on  $x_i$  and  $x_{i+1}$ . ( $n=1,2,\dots$ , dimension) ( $i=1,2,\dots$ , population size). [Fig. 3](#) is shown in the crossover process.

#### 4.2. Feature selection with BinSSA

In feature selection problems, the binary solutions set consists of {0, 1} values. Binary solution space in BinSSA is defined as population size (n) x feature number (N). For the feature selection, the "1" value shows that the corresponding feature is chosen and the "0" value shows that the corresponding feature is not chosen. [Fig. 4](#) shows the binary search space in BinSSA.

**Binary Spider Population(5x10)**

0	1	1	1	1	0	0	0	1	0
1	0	1	1	0	1	0	0	1	1
1	0	0	0	0	1	0	1	0	0
0	1	1	0	1	1	0	1	0	1
1	0	0	1	0	0	1	1	0	0

**Fig. 3.** Crossover process.

		Feature number(N)	
Population size(n)			
0	1	...	1 0
1	0	...	0 1
0	1	...	0 0
.	.		.
.	.		.
.	.	...	.
0	0	...	0 1
1	1	...	1 1

**Fig. 4.** Binary search space for BinSSA.

According to Liu and Motoda ([Liu & Motoda, 1998](#)), 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. The feature selection improves the accuracy performance of the classifier and learning time performance of the classifier by removing irrelevant and redundant features. For this purpose, we aim to the most effective minimum number of selected features with BinSSA and maximum classification accuracy.

In order to balance between the number of selected features in each solution (minimum) and the classification accuracy (maximum), [Eq. \(9\)](#) is used in BinSSA. [Eq. \(9\)](#) shows the fitness function.

$$\downarrow \text{Fitness} = \rho \text{Error}(D) + \varphi \frac{|M|}{|N|} \quad (9)$$

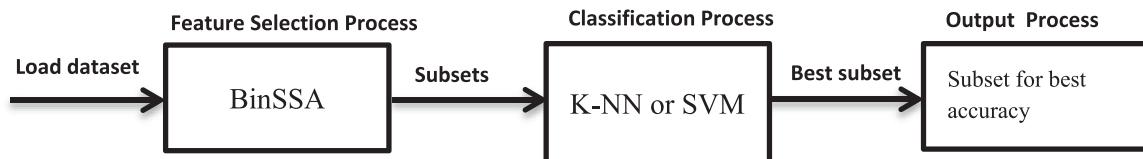
Where  $\text{Error}(D)$  is the classifier error rate.  $\rho$  and  $\varphi$  are constants to control the classification accuracy and feature reduction.  $|M|$  is the size of the selected feature subset.  $|N|$  is the total number of features.  $\rho$  in [0,1] and  $\varphi=(1-\rho)$ .

#### 4.3. K-nearest neighbor classifier (K-NN) and support vector machine classifier (SVM)

K-nearest neighbor classifier (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) ([Pernkopf, 2005](#)). Despite the different distance measurements in the literature for K-NN, the most commonly used is Euclidean distance. [Eq. \(10\)](#) shows the Euclidean distance. K-NN classifier (where  $K=5$ ) is preferred to produce the optimal subset.

$$\text{distance}(x_a - x_b) = \left( \sum_{i=1}^N (x_{ai} - x_{bi}) \right)^{0.5} \quad (10)$$

Support vector machine (SVM) has been invented by [Vapnik \(1995\)](#) and proposed for classification and regression tasks. SVM has been constructed on a strong statistical learning theory including Vapnik-Chervonenkis dimension and structural risk minimization ([Babaoglu, Fındık & Ulker, 2010](#)). Support vector machines have significant successes in classification.

**Fig. 5.** Feature selection processes for BinSSA.

**Step 1. Parameter setting:** Required constant parameter sets are adjusted. For example, lower and upper limits of variables, number of maximum iteration, etc.

**Step 2. Initialization:** Random starting position locations are determined for each spider in the swarm. Assign memory for them. The target vibration for each spider is started.

**Step 3.** Assign each spider to a feature subset.

**Step 4. Evaluation:** Fitness value is calculated for each spider. The best in the swarm are detected and recorded.

**Step 5.** Vibration value is calculated for each spider calculated by using vibration Equations (1, 2, and 3). The best in the swarm are detected and recorded.

**Step 6.** Vibration comparison: The received the best vibration is compared to the target vibration values.

**Step 7.** Update the spider mask.

**Step 8.**  $P_a^{fo}$  value is calculated by Equation 4

**Step 9. Movement:** Each spider moves to a new position by Equation 5 and a new population is obtained.

**Step 10. Transfer Function:** The continuous search space is converted to binary search space by eight different transfer functions.

**Step 11. Crossover operator:** In order to produce new candidate solutions, the crossover operator is applied between two solutions and the new candidate solutions are evaluated.

**Step 12. Repeat:** All criteria beginning from Step 4 are repeated until reaching stopping criteria.

**Step 13. Output:** Optimum best subset is obtained.

**Fig. 6.** The steps of the BinSSA.

K-NN or SVM is used as a classifier in BinSSA. If the dataset contains two classes, we have chosen the SVM classifier. If the dataset contains more than two classes, we have preferred the K-NN classifier. Fig. 5 shows feature selection processes for BinSSA.

For both SVM and K-NN, k-fold (where  $k=10$ ) cross-validation technique is adapted on the dataset to produce training and test set. 80% of the datasets are used for the training set and 20% for the test set. The steps of the BinSSA is shown in Fig. 6. Flowchart for BinSSA is shown in Fig. 7.

## 5. Experimental results and analysis

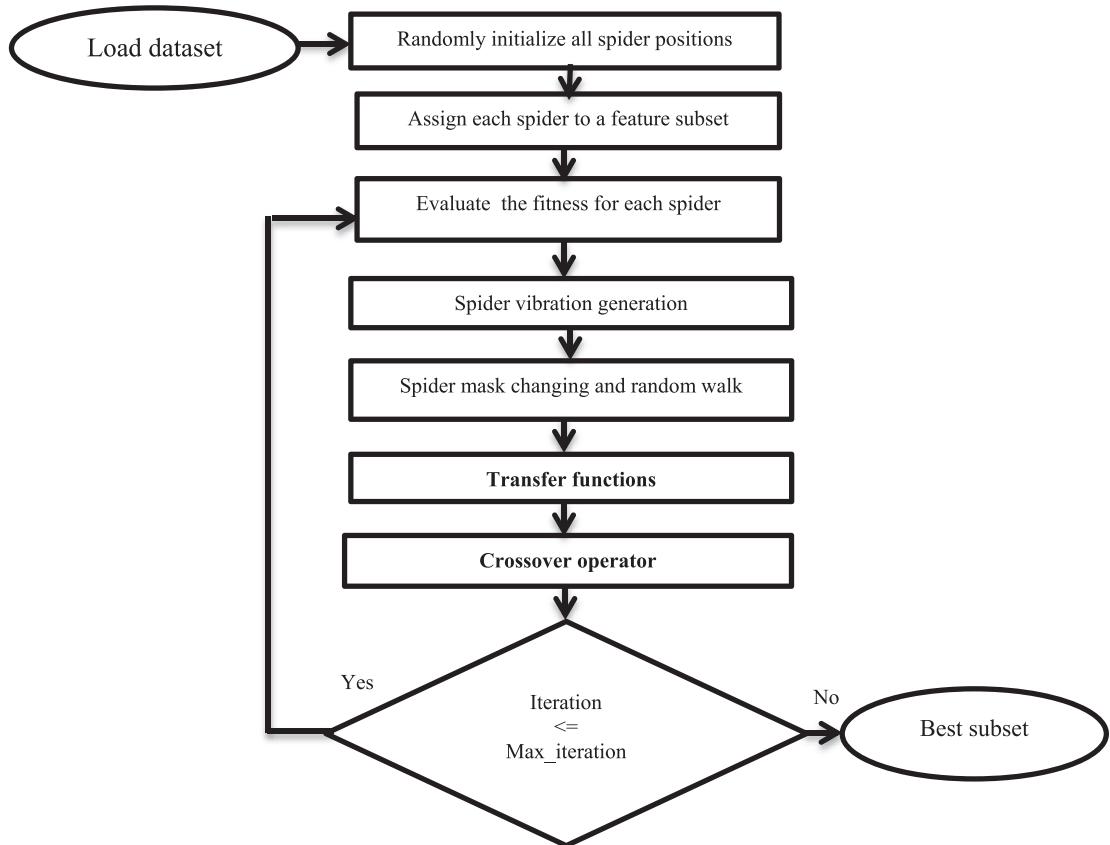
In this paper, the variations of binary social spider algorithm without crossover operator (BinSSA) and the variations of binary social spider algorithm with crossover operator (BinSSA-CR) have been carefully compared and according to different criteria, their performance has been examined on the feature selection problem. The best BinSSA variations detect according to different criteria. The best variations of BinSSA and the best variations of BinSSA-CR are compared with the new and known heuristic algorithms in the literature. The performance of BinSSA is analyzed and discussed.

The variations of BinSSA and the variations of BinSSA-CR are tested on Matlab R2014a that installed over windows 7, 64 bit, the system of 2.30 GHz processor with 4 GB RAM. Low-scaled, middle-scaled, and large-scaled twenty-one UCI benchmark datasets taken from OR-Lib ([UCI Machine Learning Repository](#)) are used to measure BinSSA performance on feature selection problem. The datasets that have various numbers of attributes (from 9 to 856), various numbers of classes (from 2 to 16), and various numbers of instances (from 32 to 5000) are suitable for the feature selection problem. In this study, it is preferred in large dimensional datasets to show the performance of the algorithm. Twenty-one UCI bench-

mark datasets are shown in Table 3. K-NN or SVM has been preferred as a classifier. If the dataset contains two classes, we have chosen the SVM classifier. If the dataset contains more than two classes, we have preferred the K-NN classifier. 80% of the datasets are used for the training set and 20% for the test set. 5-NN classifier (where  $K=5$ ) is preferred to produce the optimal subset. For both SVM and K-NN, k-fold (where  $k=10$ ) cross-validation technique is adapted on the dataset. Each application has 20 independent runs.

**Table 3**  
The UCI benchmark datasets details used for BinSSA.

Type	ID No	Dataset	#Features	#Samples	#Classes
Low-Scaled $\leq 19$	N1	Wine	13	178	3
	N2	Hepatitis	19	155	2
	N3	Vehicle	18	846	4
	N4	Zoo	16	101	7
	N5	Heart	13	270	2
	N6	Breast Cancer	9	699	2
Medium-Scaled [22] 90]	N7	Ionosphere	34	351	2
	N8	Lung Cancer	56	32	3
	N9	Dermatology	34	366	6
	N10	Sonar	60	208	2
	N11	BreastEW	30	569	2
	N12	Soybean Small	35	47	4
	N13	Movementlibras	90	360	15
	N14	Parkinsons	22	195	2
	N15	Spambase	57	4601	2
	N16	Waveform	40	5000	3
	N17	Arrhythmia	279	452	16
	N18	Semeion	256	1593	10
	N19	Clean	166	476	2
	N20	CNAE	856	1080	9
	N21	Hillvalley	101	606	2



**Fig. 7.** Flowchart for BinSSA.

To have fair comparisons, all algorithms have been carefully run in the same programming language, similar platform, and similar parameter values.

The UCI benchmark datasets divide into 3 groups according to their dimension size.

- *Group-I*: Low-scaled dimension (N1-N6).
- *Group-II*: Middle-scaled dimension (N7-N16).
- *Group-III*: Large-scaled dimension (N17-N21).

### 5.1. Determination of population size, the maximum number of iteration, $\varphi$ , and $\rho$ on the fitness function

Different combinations of population size and number of the maximum iteration are tested on the national classification of economic activities (CNAE) dataset (UCI Machine Learning Repository). The reason for selecting the CNAE dataset is that this dataset is more sensitive for evaluation and has more features. The accuracy rate is measured for different combinations of population size ( $n$ )

and the number of maximum iteration on the performance of the basic BinSSA with different transfer functions. For **Table 4**, we have selected maximum iteration = {50, 75, 100}, population size = {10, 25, 50},  $\rho = 0.99$ , and  $\varphi = 0.01$ . The results are shown in **Table 4**. According to the results, the most appropriate values are determined as 50 for the population size and 100 for the number of maximum iteration.

The impact of  $\rho$  and  $\varphi$  values (in Eq. (9)) is tested on the CNAE dataset.  $\rho$  and  $\varphi$  values are fixed values that can be changed slightly in the fitness function.  $\rho$  determines the weight of the classification accuracy, while  $\varphi$  corresponds to the weight of the features reduction rate. In the literature, these values are usually determined randomly in feature selection problems.  $\rho$  is usually determined as high value (i.e.  $\rho \geq 0.9$ ) and  $\varphi$  is usually determined as a small value (i.e.  $\varphi \leq 0.5$ ). The accuracy rate is measured for different combinations of  $\rho$  and  $\varphi$  values on the performance of the basic BinSSA with different transfer functions. For **Table 5**, we have selected population size = 50, maximum iteration = 100,

**Table 4**

Average accuracy results according to different combinations of population size ( $n$ ) and the number of maximum iteration on the CNAE dataset.

Population Size ( $n$ )/ Maximum Iteration	10			25			50		
	50	75	100	50	75	100	50	75	100
<b>BinSSA1</b>	86	88,52	89	88,75	89	90,45	89	90,5	<b>91,75</b>
<b>BinSSA2</b>	80	81	82	83,15	84,56	85	84	85	<b>86,5</b>
<b>BinSSA3</b>	77,45	77,56	78	79	80	81,56	82,5	84,5	<b>85,75</b>
<b>BinSSA4</b>	80	81,5	82	83	83,45	84,15	84,5	85	<b>86,25</b>
<b>BinSSA5</b>	77	77,25	78	77,41	78,25	79	78,5	79	<b>79,25</b>
<b>BinSSA6</b>	77	77,54	78,5	77,55	78,65	79,65	79	79,75	<b>80,25</b>
<b>BinSSA7</b>	76,98	77,25	78	77,27	78,25	79,05	79	79,5	<b>79,75</b>
<b>BinSSA8</b>	78	78,14	78,58	78,35	79,15	79,75	79,5	80	<b>80,25</b>

**Table 5**

According to average accuracy results, the impact of  $\rho$  and  $\varphi$  on the CNAE dataset.

$\rho/\varphi$	0.5/0.5 Mean	0.7/0.3 Mean	0.9/0.1 Mean	0.99/0.01 Mean
BinSSA1	86	86,15	89,25	91,75
BinSSA2	82	84,5	85,5	86,5
BinSSA3	79	82,25	83,5	85,75
BinSSA4	81	83,5	85	86,25
BinSSA5	77	77,5	78,5	79,25
BinSSA6	78	80	80,15	80,25
BinSSA7	78	79,25	79,5	79,75
BinSSA8	79	80	80,15	80,25

**Table 6**

Parameters setup for the variations of BinSSA and BinSSA-CR.

Parameters	Values
Population size (n)	50
Maximum iteration	100
Number of runs	20
Problem dimension (N)	Number of features in the dataset
$\rho$	0,99
$\varphi$	0,01
K	5 (K value in K-NN) (Zawbaa et al., 2015)
k	5 (k value in k-fold)
Other parameters	$r_a = 1; p_c = 0,7; p_m = 0,1$ (Yu & Li, 2015)

**Table 7**

The measurement criteria in the comparison of BinSSA.

The measurement criteria	Explanation
Fitness values	is obtained from fitness function by using the selected features on the benchmark datasets. (The mean, standard deviation, the best, the worst values of the fitness function is calculated)
Classification accuracy	is obtained from the classifier by using the selected features on the benchmark datasets.
Selection feature size	is the mean number of the selected features.
CPU time	is time to produce a candidate in seconds

$\rho = \{0.5, 0.7, 0.9, 0.99\}$ , and  $\varphi = \{0.5, 0.3, 0.1, 0.01\}$ . The results are shown in Table 5. In general, there is an increase in the accuracy rate by decreasing the value of  $\varphi$  and increasing the value of  $\rho$ . Ac-

cording to the results, the most appropriate values are determined as 0.99 for  $\rho$  and 0.01 for  $\varphi$ .

The parameters used in BinSSA and BinSSA-CR are shown in Table 6. Each variation of BinSSA and BinSSA-CR has tested 20 independent runs. The measurement criteria used in the comparison of BinSSA are fitness values, classification accuracy, selection feature size, and CPU time. These criteria are shown in Table 7.

## 5.2. Comparison between different variations of BinSSA

In this section, variations (S-shaped and V-shaped) of BinSSA based on the social spider algorithm is analyzed on the feature selection problem in different criteria (mean of fitness function, standard deviation of fitness function, the best of fitness function, the worst of fitness function, mean of accuracy values, the mean number of the selected features, and mean of CPU time). Twenty-one benchmark datasets are determined for the feature selection problem.

Table 8 shows the mean and the standard deviation of fitness values of the BinSSA variations. The best values are marked with bold. According to the mean of fitness function results, V-shaped BinSSA variations show a higher success than the S-shaped BinSSA variations. BinSSA5 shows high success at roughly 33% of benchmark datasets for 7 datasets out of 21 datasets (N2, N7, N10, N12, N14, N17, and N19). According to the standard deviation of fitness results, BinSSA6, BinSSA7, and BinSSA8 variations show a high success for feature selection problem. BinSSA6, BinSSA7, and BinSSA8 variations show success at roughly 23,81% of benchmark datasets for 5 out of 21 datasets.

Table 9 shows the best and the worst of the fitness values of the BinSSA variations. According to the best of fitness results, BinSSA5, BinSSA6, and BinSSA8 variations show a high success for feature selection problem. BinSSA5 and BinSSA6 variations show success at roughly 38% of benchmark datasets (for 8 out of 21 datasets). The BinSSA8 variation shows superior performance at roughly 42,86% of benchmark datasets for 9 out of 21 datasets (N1, N4, N7, N9, N10, N12, N13, N14, and N21). According to the worst of fitness results, BinSSA5 variation has a minimum value for 7 out of 21 datasets for feature selection problem.

Table 10 shows the mean accuracy values of the BinSSA variations. According to the mean of accuracy values, the variations of BinSSA1, BinSSA4, and BinSSA7 show high performance. BinSSA1,

**Table 8**

According to the mean of fitness values (as Mean) and the standard deviation of fitness values (as S.D.), comparison between different variations of BinSSA.

ID	Benchmark	BinSSA1		BinSSA2		BinSSA3		BinSSA4		BinSSA5		BinSSA6		BinSSA7		BinSSA8	
		Mean	S.D.	Mean	S.D.	Mean	S.D.	Mean	S.D.	Mean	S.D.	Mean	S.D.	Mean	S.D.	Mean	S.D.
N1	Wine	00,138	<b>00,133</b>	00,158	00,141	<b>00,114</b>	00,156	00,145	00,186	00,256	00,225	00,203	00,204	00,177	00,139	00,160	00,142
N2	Hepatitis	00,952	00,317	01,043	00,434	01,056	00,337	00,924	<b>00,302</b>	<b>00,821</b>	00,472	00,887	00,401	00,986	00,376	00,869	00,435
N3	Vehicle	02,336	00,215	02,458	00,236	02,331	00,223	02,322	00,232	02,398	00,227	02,392	00,193	02,361	00,201	02,498	<b>00,153</b>
N4	Zoo	00,263	00,464	<b>00,085</b>	<b>00,151</b>	00,186	00,224	00,210	00,369	00,150	00,272	00,248	00,377	00,276	00,299	00,200	00,333
N5	Heart	01,255	00,307	01,164	00,312	01,170	00,365	01,180	00,380	01,304	00,271	01,262	<b>00,237</b>	01,328	00,259	<b>01,036</b>	00,372
N6	Breast Cancer	00,240	00,095	00,260	00,115	00,227	00,135	00,205	00,109	00,211	00,102	<b>00,186</b>	<b>00,070</b>	00,238	00,084	00,248	00,114
N7	Ionosphere	00,342	00,169	00,317	00,291	00,269	00,190	00,352	00,157	<b>00,171</b>	<b>00,120</b>	00,207	00,123	00,206	00,173	00,268	00,180
N8	Lung Cancer	00,714	00,830	00,544	00,942	00,375	00,677	00,372	00,862	00,252	00,604	00,087	00,369	<b>00,005</b>	<b>00,004</b>	00,087	00,369
N9	Dermatology	<b>00,057</b>	<b>00,005</b>	00,063	00,043	00,081	00,060	00,090	00,080	00,101	00,081	00,100	00,092	00,138	00,105	00,148	00,108
N10	Sonar	00,682	00,306	00,500	00,404	00,544	00,299	00,407	00,283	<b>00,308</b>	00,260	00,359	00,281	00,309	00,284	<b>00,206</b>	
N11	BreastEW	00,423	00,132	00,354	00,210	00,427	00,131	00,364	00,121	00,345	00,106	00,386	00,122	00,318	<b>00,097</b>	<b>00,296</b>	00,126
N12	Soybean Small	00,035	00,004	00,031	00,003	00,026	00,003	00,025	00,003	<b>00,005</b>	<b>00,001</b>	<b>00,005</b>	<b>00,001</b>	<b>00,005</b>	<b>00,001</b>	<b>00,005</b>	<b>00,001</b>
N13	Movementlibras	02,227	00,336	02,071	00,408	02,148	00,448	01,877	00,528	01,689	00,340	<b>01,544</b>	<b>00,333</b>	01,689	00,510	01,742	00,392
N14	Parkinsons	00,034	00,006	00,028	00,004	00,023	00,005	00,022	00,003	<b>00,005</b>	<b>00,002</b>	00,057	00,152	00,057	00,221	00,006	<b>00,002</b>
N15	Spambase	<b>00,666</b>	<b>00,041</b>	00,674	00,071	00,708	00,081	00,731	00,063	00,764	00,094	00,794	00,093	00,872	00,107	00,844	00,110
N16	Waveform	01,606	00,093	<b>01,550</b>	00,106	01,644	00,072	01,690	<b>00,038</b>	01,722	00,080	01,693	00,129	01,770	00,131	01,821	00,083
N17	Arrhythmia	03,138	00,526	03,417	00,429	03,124	00,467	03,198	00,543	<b>02,779</b>	00,353	02,931	00,482	02,975	<b>00,325</b>	03,039	00,331
N18	Semeion	07,966	00,112	07,978	00,167	07,992	00,175	07,970	00,115	07,851	00,124	07,827	00,127	<b>07,825</b>	00,127	07,872	<b>00,073</b>
N19	Clean	00,390	00,164	00,337	00,200	00,371	00,197	00,344	00,137	<b>00,268</b>	<b>00,109</b>	00,288	00,161	00,301	00,134	00,369	00,144
N20	CNAE	<b>01,088</b>	00,175	01,385	00,176	01,419	00,185	01,570	00,221	02,084	00,237	02,181	<b>00,138</b>	02,182	00,231	02,097	00,180
N21	Hillvalley	04,428	00,330	04,473	00,306	04,370	00,490	04,310	00,445	03,914	00,332	03,822	00,417	04,019	<b>00,262</b>	<b>03,801</b>	00,315

**Table 9**

According to the best and the worst of fitness values, comparison between different variations of BinSSA.

ID	Benchmark	BinSSA1		BinSSA2		BinSSA3		BinSSA4		BinSSA5		BinSSA6		BinSSA7		BinSSA8	
		Best	Worst														
N1	<i>Wine</i>	00,023	00,329	00,023	00,321	<b>00,015</b>	00,581	00,023	00,588	<b>00,015</b>	00,848	<b>00,015</b>	00,573	<b>00,015</b>	<b>00,306</b>	<b>00,015</b>	<b>00,306</b>
N2	<i>Hepatitis</i>	00,393	01,687	00,367	02,017	00,372	01,692	00,367	<b>01,357</b>	<b>00,011</b>	01,666	<b>00,011</b>	01,655	00,346	01,661	00,335	01,991
N3	<i>Vehicle</i>	01,894	02,809	02,042	02,803	01,919	<b>02,681</b>	<b>01,777</b>	02,792	02,042	02,951	02,078	02,775	01,978	02,893	02,248	02,893
N4	<i>Zoo</i>	00,031	02,011	00,025	<b>00,533</b>	00,031	<b>00,533</b>	00,025	01,523	00,019	01,015	<b>00,013</b>	01,510	00,019	01,021	<b>00,013</b>	01,021
N5	<i>Heart</i>	00,640	01,828	00,815	01,813	00,581	01,688	<b>00,405</b>	01,872	00,756	<b>01,681</b>	00,924	<b>01,681</b>	00,756	01,688	00,573	02,040
N6	<i>Breast Cancer</i>	00,105	00,403	00,044	00,536	00,033	00,536	<b>00,022</b>	00,475	00,044	00,464	00,056	<b>00,320</b>	00,105	00,392	00,056	00,453
N7	<i>Ionosphere</i>	00,053	00,760	00,038	01,167	00,038	00,751	00,174	00,616	<b>00,009</b>	<b>00,436</b>	00,012	<b>00,436</b>	<b>00,009</b>	00,577	<b>00,009</b>	00,580
N8	<i>Lung Cancer</i>	00,039	01,711	00,038	03,339	00,038	01,702	00,034	03,336	<b>00,002</b>	01,654	<b>00,002</b>	01,655	00,004	<b>00,021</b>	00,004	01,654
N9	<i>Dermatology</i>	00,047	<b>00,068</b>	00,041	01,192	00,041	01,186	00,038	00,324	<b>00,015</b>	00,292	<b>00,015</b>	00,301	00,021	00,445	<b>00,015</b>	00,307
N10	<i>Sonar</i>	00,053	01,291	00,048	01,291	00,053	01,038	00,047	01,042	00,010	<b>00,753</b>	00,010	00,997	<b>00,008</b>	01,000	<b>00,008</b>	00,758
N11	<i>BreastEW</i>	00,248	00,651	<b>00,050</b>	00,644	00,228	00,641	00,228	00,545	00,205	00,505	00,228	00,601	00,228	00,505	00,109	<b>00,502</b>
N12	<i>Soybean Small</i>	00,023	00,043	00,026	00,034	00,017	00,031	00,017	00,029	<b>00,003</b>	<b>00,006</b>	<b>00,003</b>	<b>00,006</b>	<b>00,003</b>	<b>00,006</b>	<b>00,003</b>	<b>00,006</b>
N13	<i>Movementlibras</i>	01,309	02,824	01,298	02,941	01,298	03,079	01,147	03,204	00,974	02,209	00,973	<b>01,935</b>	01,108	02,621	<b>00,971</b>	02,759
N14	<i>Parkinsons</i>	00,023	00,041	00,018	00,036	00,014	00,032	00,018	00,027	<b>00,005</b>	<b>00,009</b>	<b>00,005</b>	00,500	<b>00,005</b>	00,995	<b>00,005</b>	<b>00,009</b>
N15	<i>Spambase</i>	00,581	<b>00,719</b>	00,581	00,822	<b>00,569</b>	00,820	00,654	00,841	00,622	00,910	00,601	00,935	00,719	01,013	00,659	01,061
N16	<i>Waveform</i>	01,501	<b>01,721</b>	01,726	01,562	01,758	01,639	01,726	01,607	01,810	01,527	01,822	01,627	01,894	01,743	01,958	
N17	<i>Arrhythmia</i>	02,169	04,144	02,813	04,242	02,143	04,125	02,249	04,339	01,990	<b>03,319</b>	<b>01,983</b>	03,961	02,313	03,745	02,426	03,631
N18	<i>Semeion</i>	07,770	08,193	<b>07,486</b>	08,249	07,580	08,237	07,711	08,143	07,640	08,069	07,539	08,064	07,545	<b>08,059</b>	07,737	08,062
N19	<i>Clean</i>	00,073	00,694	00,057	00,893	00,060	00,882	00,155	00,573	<b>00,014</b>	<b>00,533</b>	00,020	00,534	00,120	00,645	00,219	00,737
N20	<i>CNAE</i>	<b>00,822</b>	<b>01,267</b>	01,104	01,651	01,097	01,739	00,995	01,788	01,676	02,552	01,916	02,315	01,915	02,647	01,881	02,506
N21	<i>Hillvalley</i>	03,788	05,110	03,768	05,088	03,429	04,996	03,506	05,242	03,307	04,456	03,220	04,543	03,632	04,456	<b>03,054</b>	<b>04,292</b>

BinSSA4, and BinSSA7 variations show success at roughly 33,33% of benchmark datasets for 7 out of 21 datasets.

**Table 11** shows the mean number of the selected features of the BinSSA variations. According to the mean number of the selected features, the variations of BinSSA (BinSSA4, BinSSA6, and BinSSA8) have selected fewer features than the other variations of BinSSA. BinSSA4 variation has chosen minimum features for 16 out of 21 datasets (N1, N3, N4, N5, N6, N7, N8, N10, N11, N12, N13, N14, N16, N18, N20, and N21). The variation of BinSSA8 shows a high success for 9 out of 21 datasets.

**Table 12** shows the mean of CPU time (in seconds) of the BinSSA variations. The CPU time is time to produce a candidate (in seconds). The number of candidates produced in each iteration is fixed. So we have calculated the CPU time as a comparison criterion in BinSSA. According to the mean of CPU time results, BinSSA3 variation has obtained results as soon as a possible time for 6 out of 21 datasets (N7, N8, N9, N11, N14, and N15).

**Fig. 8** shows convergence graphics for comparison between different variations of BinSSA.

### 5.3. Comparison between different variations of BinSSA-CR

In this section, the variations of S-shaped and V-shaped BinSSA-CR based on social spider algorithm is assessed on the feature selection problem in different criteria (mean of fitness values, standard deviation of fitness values, the best of fitness values, the worst of fitness values, mean of accuracy values, the mean number of the selected features, and mean of CPU time).

**Table 13** shows the mean and standard deviation of fitness results of the variations of BinSSA-CR. The best results are marked with bold. According to the mean of fitness results, S-shaped BinSSA4-CR variation shows a higher success than the other BinSSA-CR variations (S-shaped and V-shaped). The BinSSA4-CR variation shows high success at roughly 42,86% of benchmark datasets for 9 datasets out of 21 datasets (N1, N2, N4, N6, N11, N15, N17, N18, and N21). The reason is that both exploration and exploitation capabilities of BinSSA-CR are enhanced with the crossover operator in the binary space. In general, according to the mean fitness results, the variations (BinSSA5, BinSSA6, BinSSA7,

**Table 10**  
According to the mean of accuracy values, comparison between different variations of BinSSA.

ID	Benchmark	BinSSA1	BinSSA2	BinSSA3	BinSSA4	BinSSA5	BinSSA6	BinSSA7	BinSSA8
N1	<i>Wine</i>	99,44	98,33	99,44	<b>100</b>	99,44	98,33	98,33	99,44
N2	<i>Hepatitis</i>	92,67	94	89,33	<b>94,63</b>	88,67	90	90,67	86,67
N3	<i>Vehicle</i>	75,26	76,09	<b>77,75</b>	75,6	76,9	74,56	75,86	73,01
N4	<i>Zoo</i>	<b>95</b>	85	82	84	59	85	74	76
N5	<i>Heart</i>	85,93	88,52	<b>90</b>	87,41	87,04	87,41	86,30	88,15
N6	<i>Breast Cancer</i>	97,38	98,55	97,12	97,39	98,84	98,41	<b>99,13</b>	98,12
N7	<i>Ionosphere</i>	<b>99,14</b>	98,57	98,28	98	98,86	<b>99,14</b>	<b>99,14</b>	98,57
N8	<i>Lung Cancer</i>	93,33	86,67	96,67	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>
N9	<i>Dermatology</i>	99,73	99,73	99,45	<b>100</b>	98,63	98,90	99,18	99,18
N10	<i>Sonar</i>	95,5	95,5	93	95	<b>97</b>	95,5	96,5	96,5
N11	<i>BreastEW</i>	97,2	96,6	<b>97,6</b>	95,8	97,4	96,8	97	96,6
N12	<i>Soybean Small</i>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>
N13	<i>Movementlibras</i>	80	78,61	78,61	80,83	82,78	84,72	<b>86,11</b>	82,5
N14	<i>Parkinsons</i>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>
N15	<i>Spambase</i>	<b>94,38</b>	94,08	93,71	92,58	91,83	93,17	92,38	92,13
N16	<i>Waveform</i>	84,03	84,43	83,23	<b>84,67</b>	81,77	81,83	82,4	82,93
N17	<i>Arrhythmia</i>	69,56	68,22	67,33	70,11	<b>73,33</b>	72,22	71,33	70,44
N18	<i>Semeion</i>	19,27	20,6	19,8	19,73	21,4	20,67	<b>22,4</b>	20,53
N19	<i>Clean</i>	<b>97,5</b>	<b>97,5</b>	95,75	96,5	96,5	95,75	95,75	96,25
N20	<i>CNAE</i>	<b>91,75</b>	86,5	85,75	86,25	79,25	80,25	79,75	80,25
N21	<i>Hillvalley</i>	57,5	53,17	56,83	61,67	60	<b>61,5</b>	58,67	57,33

**Table 11**

According to the mean number of the selected features, comparison between different variations of BinSSA.

ID	Benchmark	BinSSA1	BinSSA2	BinSSA3	BinSSA4	BinSSA5	BinSSA6	BinSSA7	BinSSA8
N1	<i>Wine</i>	7	6	6	<b>5</b>	<b>5</b>	6	6	<b>5</b>
N2	<i>Hepatitis</i>	10	9	9	9	8	8	8	<b>7</b>
N3	<i>Vehicle</i>	12	10	9	<b>8</b>	9	<b>8</b>	<b>8</b>	<b>8</b>
N4	<i>Zoo</i>	8	7	7	<b>6</b>	<b>6</b>	<b>6</b>	<b>6</b>	<b>6</b>
N5	<i>Heart</i>	9	8	8	<b>5</b>	7	<b>5</b>	8	7
N6	<i>Breast Cancer</i>	<b>4</b>	<b>4</b>	<b>4</b>	<b>4</b>	<b>4</b>	<b>4</b>	<b>4</b>	<b>4</b>
N7	<i>Ionosphere</i>	18	17	16	<b>14</b>	15	15	17	<b>14</b>
N8	<i>Lung Cancer</i>	31	28	29	<b>24</b>	29	30	26	25
N9	<i>Dermatology</i>	20	17	<b>16</b>	17	19	19	20	19
N10	<i>Sonar</i>	39	33	30	<b>28</b>	30	29	30	<b>28</b>
N11	<i>BreastEW</i>	17	15	13	<b>12</b>	13	13	14	13
N12	<i>Soybean Small</i>	15	17	16	<b>14</b>	<b>14</b>	<b>14</b>	15	<b>14</b>
N13	<i>Movementlibras</i>	62	52	46	<b>40</b>	41	41	41	49
N14	<i>Parkinsons</i>	12	11	9	<b>8</b>	<b>8</b>	<b>8</b>	9	
N15	<i>Spambase</i>	45	38	34	33	32	32	<b>30</b>	31
N16	<i>Waveform</i>	30	27	25	<b>23</b>	24	24	25	24
N17	<i>Arrhythmia</i>	209	173	155	147	140	144	143	<b>138</b>
N18	<i>Semeion</i>	185	162	142	<b>137</b>	144	<b>137</b>	141	142
N19	<i>Clean</i>	112	102	88	87	85	<b>84</b>	86	87
N20	<i>CNAE</i>	671	547	492	<b>421</b>	436	425	448	427
N21	<i>Hillvalley</i>	68	59	51	<b>49</b>	54	53	52	52

**Table 12**

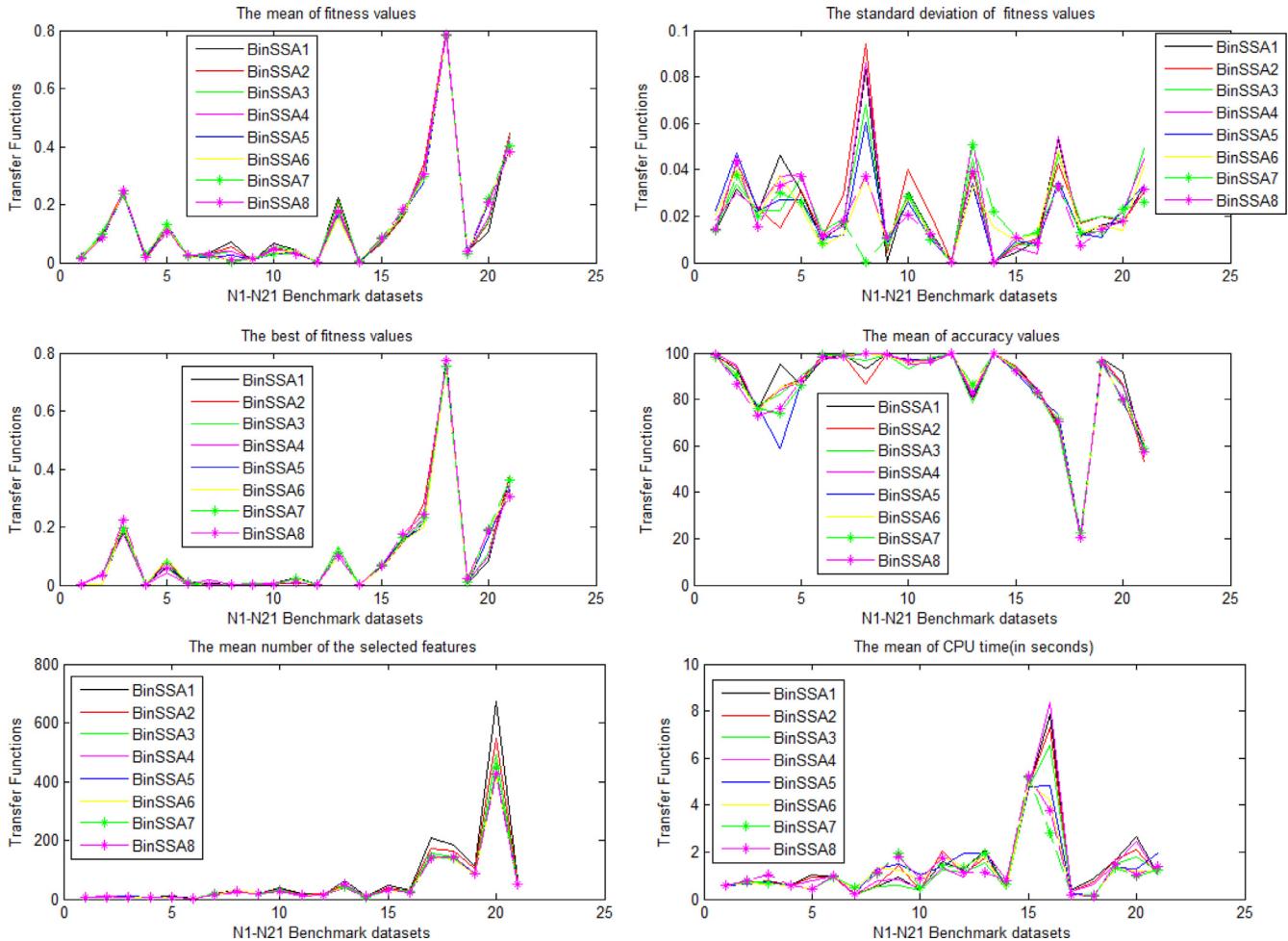
According to the mean of CPU time (in seconds), comparison between different variations of BinSSA.

ID	Benchmark	BinSSA1	BinSSA2	BinSSA3	BinSSA4	BinSSA5	BinSSA6	BinSSA7	BinSSA8
N1	<i>Wine</i>	0,012,951	0,011,959	0,011,802	0,011,927	0,011,794	0,011,943	0,011,871	<b>0,011,654</b>
N2	<i>Hepatitis</i>	0,013,486	0,013,938	0,013,944	0,013,696	<b>0,012,519</b>	0,013,955	0,014,354	0,015,966
N3	<i>Vehicle</i>	0,014,397	0,015,873	0,014,239	0,013,733	0,015,081	<b>0,012,790</b>	0,013,727	0,020,219
N4	<i>Zoo</i>	0,011,560	<b>0,011,367</b>	0,011,411	0,011,524	0,011,624	0,011,500	0,011,513	0,011,556
N5	<i>Heart</i>	0,020,210	0,018,348	0,016,082	0,015,992	0,008,635	<b>0,008,167</b>	0,008,462	0,008,222
N6	<i>Breast Cancer</i>	<b>0,018,628</b>	0,018,768	0,020,056	0,020,041	0,019,629	0,019,809	0,018,795	0,019,938
N7	<i>Ionosphere</i>	0,003,323	0,003,321	<b>0,003,307</b>	0,003,402	0,004,909	0,007,584	0,009,888	0,004,521
N8	<i>Lung Cancer</i>	0,010,889	0,011,145	<b>0,010,635</b>	0,015,652	0,025,774	0,026,552	0,021,707	0,022,269
N9	<i>Dermatology</i>	0,019,162	0,028,312	<b>0,011,538</b>	0,016,282	0,029,356	0,024,762	0,039,027	0,035,915
N10	<i>Sonar</i>	0,007,885	<b>0,007,858</b>	0,007,999	0,008,934	0,021,084	0,015,992	0,009,510	0,017,647
N11	<i>BreastEW</i>	0,031,945	0,041,322	<b>0,025,036</b>	0,026,352	0,027,515	0,035,685	0,029,197	0,034,884
N12	<i>Soybean Small</i>	0,025,202	0,022,008	0,022,684	<b>0,018,920</b>	0,038,578	0,027,287	0,027,012	0,022,864
N13	<i>Movementlibras</i>	0,042,026	0,034,521	0,030,830	0,040,801	0,038,578	0,036,183	0,039,311	<b>0,022,449</b>
N14	<i>Parkinsons</i>	0,010,770	0,012,701	<b>0,008,113</b>	0,016,344	0,010,589	0,008,134	0,012,414	0,016,158
N15	<i>Spambase</i>	0,094,527	0,096,210	<b>0,094,008</b>	0,094,553	0,095,587	0,098,474	0,103,117	0,104,591
N16	<i>Waveform</i>	0,156,636	0,146,358	0,130,794	0,166,894	0,096,887	0,084,169	<b>0,055,741</b>	0,075,010
N17	<i>Arrhythmia</i>	0,007,596	0,006,798	0,006,439	0,006,368	0,004,633	<b>0,003,834</b>	0,003,857	0,003,869
N18	<i>Semeion</i>	0,017,521	0,014,371	0,012,710	0,012,195	0,004,030	0,003,837	0,003,375	<b>0,002,895</b>
N19	<i>Clean</i>	0,033,037	0,032,540	0,030,222	0,029,595	0,027,146	<b>0,025,755</b>	0,026,431	0,030,037
N20	<i>CNAE</i>	0,053,236	0,041,479	0,035,407	0,048,600	0,025,650	0,023,499	<b>0,020,041</b>	0,020,384
N21	<i>Hillvalley</i>	0,022,073	0,021,074	0,023,293	<b>0,020,265</b>	0,039,391	0,024,058	0,025,112	0,027,707

**Table 13**

According to the mean of fitness values (as Mean) and the standard deviation of fitness values (as S.D.), comparison between different variations of BinSSA-CR.

ID	Benchmark	BinSSA1-CR		BinSSA2-CR		BinSSA3-CR		BinSSA4-CR		BinSSA5-CR		BinSSA6-CR		BinSSA7-CR		BinSSA8-CR	
		Mean	S.D.	Mean	S.D.	Mean	S.D.	Mean	S.D.	Mean	S.D.	Mean	S.D.	Mean	S.D.	Mean	S.D.
N1	<i>Wine</i>	0,0151	0,135	0,0173	0,190	0,0160	0,184	<b>0,072</b>	<b>0,102</b>	0,0135	0,166	0,0122	0,135	0,0137	0,166	0,0166	0,213
N2	<i>Hepatitis</i>	0,0153	0,525	0,0143	0,519	0,0889	0,591	<b>0,625</b>	<b>0,175</b>	0,0840	0,348	0,0694	0,294	0,0709	0,464	0,692	0,363
N3	<i>Vehicle</i>	0,2402	0,228	0,2380	0,187	0,2464	0,232	0,295	<b>0,046</b>	<b>0,164</b>	0,216	0,2187	0,193	0,206	0,198	0,236	0,216
N4	<i>Zoo</i>	0,0194	0,458	0,0211	0,366	0,0236	0,404	<b>0,080</b>	<b>0,157</b>	0,0100	0,183	0,0153	0,217	0,0275	0,493	0,125	0,343
N5	<i>Heart</i>	0,0119	0,229	0,1228	0,388	0,140	0,242	0,099	<b>0,172</b>	0,111	0,335	0,105	0,390	<b>0,083</b>	0,264	0,128	0,308
N6	<i>Breast Cancer</i>	0,0217	0,094	0,0226	0,107	0,0202	0,095	<b>0,200</b>	0,0104	0,222	<b>0,084</b>	0,241	0,148	0,211	0,116	0,207	0,037
N7	<i>Ionosphere</i>	0,0303	0,089	0,0228	0,126	0,0276	0,197	0,0299	0,0150	0,143	0,113	<b>0,086</b>	<b>0,087</b>	0,112	0,114	0,156	0,129
N8	<i>Lung Cancer</i>	0,0125	0,427	0,0544	0,777	0,0455	0,907	0,029	0,680	0,006	0,002	0,005	0,002	<b>0,004</b>	0,002	0,004	<b>0,001</b>
N9	<i>Dermatology</i>	0,0066	<b>0,031</b>	0,0071	0,066	0,073	0,056	0,072	0,059	0,040	0,041	<b>0,036</b>	0,032	0,050	0,056	0,058	0,075
N10	<i>Sonar</i>	0,0645	0,371	0,0587	0,302	0,0372	0,254	0,0394	<b>0,118</b>	<b>0,105</b>	0,0122	<b>0,105</b>	0,0122	0,139	0,0150	0,250	0,203
N11	<i>BreastEW</i>	0,0363	0,166	0,0324	0,133	0,0396	0,140	<b>0,295</b>	<b>0,083</b>	0,323	0,176	0,0406	0,185	0,0376	0,154	0,369	0,149
N12	<i>Soybean Small</i>	0,0035	0,004	0,0030	0,003	0,027	0,003	0,025	0,003	<b>0,005</b>	<b>0,001</b>	<b>0,005</b>	<b>0,001</b>	<b>0,005</b>	<b>0,001</b>	<b>0,005</b>	<b>0,001</b>
N13	<i>Movementlibras</i>	0,2151	0,462	0,2086	0,357	0,2065	0,496	0,1584	0,355	<b>0,1458</b>	0,463	0,1587	0,362	0,1543	0,305	0,1561	<b>0,269</b>
N14	<i>Parkinsons</i>	0,0082	0,157	0,0077	0,153	0,0025	0,004	0,020	0,003	0,007	<b>0,002</b>	0,032	0,111	0,032	0,111	<b>0,006</b>	<b>0,002</b>
N15	<i>Spambase</i>	0,0644	0,078	0,0685	0,060	0,0707	0,056	<b>0,630</b>	<b>0,026</b>	0,0679	0,073	0,0721	0,103	0,0734	0,070	0,702	0,073
N16	<i>Waveform</i>	0,1615	0,044	<b>0,1572</b>	0,051	0,1676	0,080	0,1604	<b>0,014</b>	0,1580	0,039	0,1593	0,043	0,1594	0,089	0,633	0,127
N17	<i>Arrhythmia</i>	0,3,302	0,0482	0,3,174	0,0414	0,3,333	0,0329	<b>0,2,520</b>	<b>0,0289</b>	0,2,780	0,0403	0,2,777	0,0391	0,2,756	0,0319	0,2,581	0,388
N18	<i>Semeion</i>	0,7,987	0,0127	0,7,938	0,0162	0,7,903	0,0151	<b>0,7,574</b>	<b>0,086</b>	0,7,803	0,0137	0,7,819	0,0100	0,7,783	0,0094	0,7,837	0,0118
N19	<i>Clean</i>	0,0,342	0,0,176	0,0,359	0,0,211	0,0,360	0,0,171	0,0,164	0,0,134	0,0,123	<b>0,0,121</b>	<b>0,0,105</b>	0,0,160	0,0,119	0,0,208	0,0,163	
N20	<i>CNAE</i>	<b>0,0,995</b>	0,0,188	0,1,336	0,0,178	0,0,1429	0,0,247	0,0,129	0,0,174	0,1,566	<b>0,0,143</b>	0,1,413	0,0,184	0,1,789	0,0,145	0,1,823	0,0,237
N21	<i>Hillvalley</i>	0,0,474	0,0,377	0,0,4509	0,0,355	0,0,423	0,0,261	<b>0,0,3677</b>	<b>0,0,055</b>	0,0,4212	0,0,373	0,0,4217	0,0,484	0,0,204	0,0,427	0,0,3898	0,0,377



**Fig. 8.** Convergence graphics for comparison between different variations of BinSSA.

and BinSSA8) of V-shaped BinSSA-CR are more successful except for the variation of S-shaped BinSSA4-CR. According to the standard deviation of fitness results, BinSSA4-CR, BinSSA5-CR, and BinSSA8-CR variations show a high success for feature selection problem. BinSSA5-CR and BinSSA8-CR variations show success at roughly 19,05% of benchmark datasets for 4 out of 21 datasets. BinSSA4-CR variation significantly shows a high success at roughly 57,14% of benchmark datasets for 12 out of 21 datasets. The reason is that BinSSA4-CR variation jumps out of suboptimal solutions more efficiently, whereas the other variations are still disposed to stagnation to local solutions.

Table 14 shows the best and the worst of fitness values of variations of the BinSSA-CR. According to the best fitness results, BinSSA4-CR, BinSSA5-CR, BinSSA7-CR, and BinSSA8-CR variations show a high success for feature selection problem. BinSSA4-CR and BinSSA5-CR variations show success at roughly 38,1% of benchmark datasets for 8 out of 21 datasets. The BinSSA7-CR variation shows superior performance at roughly 47,62% of benchmark datasets for 10 out of 21 datasets (N1, N2, N4, N7, N8, N9, N10, N12, N14, and N19). The BinSSA8-CR variation shows high performance at roughly 42,86% of benchmark datasets for 9 out of 21 datasets (N1, N4, N8, N9, N10, N12, N14, N16, and N17). According to the worst of fitness results, BinSSA6 variation has a minimum value for 9 out of 21 datasets for feature selection problem.

Table 15 shows the mean accuracy values of the variations of BinSSA-CR. According to the mean of accuracy values, the variations of BinSSA4-CR, and BinSSA5-CR show high performance. The BinSSA5-CR variation shows success at roughly 38,10% of bench-

mark datasets for 8 out of 21 datasets (N1, N7, N8, N10, N11, N12, N13, and N14). The BinSSA4-CR variation shows success at roughly 61,90% of benchmark datasets for 13 out of 21 datasets (N1, N3, N4, N6, N8, N9, N12, N14, N15, N16, N19, N20, and N21). The reason for this success is due to a more balanced diversification between the candidate solutions with the crossover operator.

Table 16 shows the mean number of the selected features of the variations of the BinSSA-CR. According to the mean number of the selected features, the variations of BinSSA-CR (BinSSA4-CR, BinSSA6-CR, BinSSA7-CR, and BinSSA8-CR) have selected fewer features. BinSSA4-CR variation has chosen minimum features for 15 out of 21 datasets (N1, N3, N4, N5, N6, N7, N8, N9, N10, N11, N12, N13, N14, N18, and N21). BinSSA8-CR has chosen minimum features for 11 out of 21 datasets and BinSSA6-CR and BinSSA7-CR have chosen minimum features for 6 out of 21 datasets.

We can notice that the BinSSA4-CR and BinSSA8-CR variations have obtained the best place among other variations. The reason is that the crossover operator has improved the searching competences of the BinSSA-CR on the majority of benchmark datasets.

Table 17 shows the mean of CPU time of the variations of BinSSA-CR. According to the mean of CPU time results, BinSSA8-CR variation has obtained results as soon as a possible time for 7 out of 21 datasets (N2, N6, N9, N17, N18, N19, and N20). BinSSA8-CR variation performs the exploration and exploitation phases quicker than other variations of BinSSA-CR.

Fig. 9 shows convergence graphics for comparison between different variations of BinSSA-CR.

**Table 14**

According to the best and the worst of fitness values, comparison between different variations of BinSSA-CR.

ID	Benchmark	BinSSA1-CR		BinSSA2-CR		BinSSA3-CR		BinSSA4-CR		BinSSA5-CR		BinSSA6-CR		BinSSA7-CR		BinSSA8-CR	
		Best	Worst	Best	Worst	Best	Worst	Best	Worst	Best	Worst	Best	Worst	Best	Worst	Best	Worst
N1	<i>Wine</i>	00,031	00,321	00,031	00,588	00,023	00,581	<b>00,015</b>	<b>00,313</b>	<b>00,015</b>	00,588	<b>00,015</b>	<b>00,313</b>	<b>00,015</b>	00,565	<b>00,015</b>	00,856
N2	<i>Hepatitis</i>	00,058	02,357	00,351	02,033	00,032	02,666	00,021	01,676	00,346	01,676	00,341	<b>01,346</b>	<b>00,005</b>	01,661	00,021	01,666
N3	<i>Vehicle</i>	01,936	02,880	01,936	02,756	01,989	02,873	<b>01,719</b>	02,745	01,796	02,664	01,807	<b>02,521</b>	01,855	02,628	01,796	02,616
N4	<i>Zoo</i>	00,025	01,548	00,019	01,504	00,025	01,510	<b>00,013</b>	01,028	<b>00,013</b>	00,526	00,019	<b>00,526</b>	<b>00,013</b>	01,999	<b>00,013</b>	01,504
N5	<i>Heart</i>	00,772	01,688	00,756	02,055	00,764	01,513	00,596	01,856	00,581	01,688	<b>00,222</b>	01,856	00,756	<b>01,490</b>	00,573	01,856
N6	<i>Breast Cancer</i>	00,044	00,414	00,044	00,464	00,022	<b>00,381</b>	<b>00,021</b>	00,547	00,094	00,392	00,094	00,618	00,033	00,464	00,022	00,547
N7	<i>Ionosphere</i>	00,180	00,477	00,035	00,480	00,032	00,742	00,032	00,613	00,009	00,309	00,009	<b>00,295</b>	<b>00,006</b>	00,436	00,009	00,436
N8	<i>Lung Cancer</i>	00,043	05,018	00,041	01,711	00,034	03,336	00,029	01,695	00,004	00,011	<b>00,002</b>	00,004	<b>00,002</b>	00,009	<b>00,002</b>	00,007
N9	<i>Dermatology</i>	00,053	00,197	00,038	00,321	00,038	00,200	00,029	00,194	<b>00,015</b>	00,165	<b>00,015</b>	<b>00,165</b>	<b>00,015</b>	00,168	<b>00,015</b>	00,295
N10	<i>Sonar</i>	00,052	01,548	00,058	01,283	00,045	00,796	00,058	00,791	<b>00,010</b>	00,276	<b>00,010</b>	00,276	<b>00,010</b>	00,507	<b>00,010</b>	00,754
N11	<i>BreastEW</i>	00,166	00,746	00,132	00,548	00,047	<b>00,532</b>	00,235	00,637	<b>00,106</b>	00,706	00,205	00,703	00,116	00,604	00,112	00,611
N12	<i>Soybean Small</i>	00,029	00,043	00,023	00,034	00,023	00,031	00,020	00,029	<b>00,003</b>	00,006	<b>00,003</b>	<b>00,003</b>	<b>00,003</b>	<b>00,003</b>	<b>00,003</b>	<b>00,003</b>
N13	<i>Movementlibras</i>	01,036	02,962	01,568	02,807	01,285	03,215	01,290	02,799	<b>00,570</b>	02,354	00,994	02,635	01,114	02,219	00,973	<b>02,075</b>
N14	<i>Parkinsons</i>	00,023	00,540	00,018	00,527	00,018	00,036	00,018	00,032	<b>00,005</b>	<b>00,009</b>	00,504	<b>00,005</b>	00,504	<b>00,005</b>	<b>00,005</b>	<b>00,009</b>
N15	<i>Spambase</i>	00,523	<b>00,761</b>	00,585	00,792	00,622	00,834	<b>00,515</b>	00,884	00,569	00,808	00,613	00,917	00,656	00,859	00,560	00,781
N16	<i>Waveform</i>	01,550	01,674	01,498	01,634	01,592	01,765	01,595	01,681	01,545	01,639	01,518	<b>01,624</b>	01,503	01,703	<b>01,414</b>	01,716
N17	<i>Arrhythmia</i>	02,606	04,253	02,591	03,904	02,697	04,009	01,919	04,010	02,222	03,536	02,109	03,533	02,318	03,530	<b>01,544</b>	<b>03,087</b>
N18	<i>Semeion</i>	07,664	08,192	07,589	08,178	07,676	08,179	<b>07,474</b>	08,101	07,483	08,056	07,645	08,009	07,614	<b>08,002</b>	07,668	08,028
N19	<i>Clean</i>	00,069	00,595	00,056	00,892	00,052	00,683	00,048	00,578	00,017	<b>00,339</b>	00,016	00,346	<b>00,014</b>	00,428	00,015	00,538
N20	<i>CNAE</i>	00,577	<b>01,218</b>	00,954	01,600	01,048	01,840	<b>00,575</b>	01,738	01,270	01,667	01,118	01,706	01,559	02,007	01,406	02,255
N21	<i>Hillvalley</i>	03,944	05,098	04,017	05,340	04,008	04,921	<b>03,207</b>	05,495	03,645	04,887	03,397	05,225	03,226	<b>04,707</b>	03,304	04,786

**Table 15**

According to the mean of accuracy values, comparison between different variations of BinSSA-CR.

ID	Benchmark	BinSSA1-CR	BinSSA2-CR	BinSSA3-CR	BinSSA4-CR	BinSSA5-CR	BinSSA6-CR	BinSSA7-CR	BinSSA8-CR
N1	<i>Wine</i>	98,33	97,78	<b>100</b>	<b>100</b>	<b>100</b>	99,44	98,89	98,89
N2	<i>Hepatitis</i>	92,67	90	93,33	94,65	94,67	94,67	89,33	<b>95,33</b>
N3	<i>Vehicle</i>	77,75	76,57	75,27	<b>78,34</b>	77,51	76,80	77,16	76,45
N4	<i>Zoo</i>	85	88	81	<b>95</b>	89	87	80	72
N5	<i>Heart</i>	87,04	87,04	89,26	89,26	89,63	<b>91,11</b>	89,26	87,78
N6	<i>Breast Cancer</i>	97,48	97,54	97,12	<b>98,55</b>	98,26	98,12	97,83	98,12
N7	<i>Ionosphere</i>	97,14	98	96,86	98,29	<b>99,71</b>	99,14	98,86	98,86
N8	<i>Lung Cancer</i>	90	96,67	93,33	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>
N9	<i>Dermatology</i>	<b>100</b>	99,73	99,45	<b>100</b>	99,45	<b>100</b>	99,73	99,73
N10	<i>Sonar</i>	93,5	95,5	94	96	<b>99,5</b>	98	97	99
N11	<i>BreastEW</i>	97,4	96,6	96,6	97	<b>97,6</b>	97,2	97,4	97,2
N12	<i>Soybean Small</i>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>
N13	<i>Movementlibras</i>	78,06	79,17	79,17	85,33	<b>87,78</b>	86,39	85	84,72
N14	<i>Parkinsons</i>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>
N15	<i>Spambase</i>	94,18	94,53	93,38	<b>95,18</b>	93,75	94,08	92,75	93,04
N16	<i>Waveform</i>	84,82	83,9	84,1	<b>85,20</b>	85	85,13	84,87	83,93
N17	<i>Arrhythmia</i>	67,11	71,22	70,11	74,11	74,67	70,67	<b>74,89</b>	72,44
N18	<i>Semeion</i>	19	19,6	19,4	20,2	21,87	<b>22</b>	21,2	20,87
N19	<i>Clean</i>	95,25	96,5	95,25	<b>97,75</b>	96,25	96,25	96,25	96,5
N20	<i>CNAE</i>	89,5	87,5	84,75	<b>91,50</b>	85,75	86,5	83,5	82,5
N21	<i>Hillvalley</i>	55,83	55,5	60,5	<b>68,17</b>	56,33	56,5	57,83	59,67

**Table 16**

According to the mean number of the selected features, comparison between different variations of BinSSA-CR.

ID	Benchmark	BinSSA1-CR	BinSSA2-CR	BinSSA3-CR	BinSSA4-CR	BinSSA5-CR	BinSSA6-CR	BinSSA7-CR	BinSSA8-CR
N1	<i>Wine</i>	6	5	5	4	5	6	6	<b>4</b>
N2	<i>Hepatitis</i>	9	8	8	7	7	7	7	<b>6</b>
N3	<i>Vehicle</i>	11	9	9	7	8	8	8	8
N4	<i>Zoo</i>	6	<b>5</b>						
N5	<i>Heart</i>	6	5	6	<b>4</b>	5	<b>4</b>	5	5
N6	<i>Breast Cancer</i>	<b>4</b>							
N7	<i>Ionosphere</i>	17	15	15	<b>13</b>	14	14	15	14
N8	<i>Lung Cancer</i>	30	28	24	<b>23</b>	24	24	23	<b>23</b>
N9	<i>Dermatology</i>	19	16	16	<b>15</b>	17	17	17	17
N10	<i>Sonar</i>	38	32	29	<b>27</b>	29	29	28	<b>27</b>
N11	<i>BreastEW</i>	17	14	12	<b>11</b>	12	12	13	12
N12	<i>Soybean Small</i>	14	16	15	<b>13</b>	<b>13</b>	<b>13</b>	14	<b>13</b>
N13	<i>Movementlibras</i>	60	51	45	<b>39</b>	40	40	40	<b>39</b>
N14	<i>Parkinsons</i>	11	10	8	<b>7</b>	<b>7</b>	<b>7</b>	<b>7</b>	<b>7</b>
N15	<i>Spambase</i>	44	36	33	32	31	31	<b>29</b>	30
N16	<i>Waveform</i>	27	25	24	22	23	22	<b>21</b>	22
N17	<i>Arrhythmia</i>	205	170	150	140	137	138	139	<b>135</b>
N18	<i>Semeion</i>	183	160	140	<b>130</b>	140	<b>130</b>	135	136
N19	<i>Clean</i>	110	94	86	84	81	77	83	86
N20	<i>CNAE</i>	576	530	450	422	430	422	437	<b>420</b>
N21	<i>Hillvalley</i>	60	55	48	<b>45</b>	48	50	49	48

**Table 17**

According to the mean of CPU time (in seconds), comparison between different variations of BinSSA-CR.

ID	Benchmark	BinSSA1-CR	BinSSA2- CR	BinSSA3- CR	BinSSA4- CR	BinSSA5- CR	BinSSA6- CR	BinSSA7- CR	BinSSA8- CR
N1	<i>Wine</i>	<b>0,011,602</b>	0,011,716	0,011,806	0,011,804	0,011,808	0,011,714	0,012,050	0,011,692
N2	<i>Hepatitis</i>	0,014,179	0,015,428	0,014,860	0,018,260	0,016,259	0,015,844	0,012,913	<b>0,012,747</b>
N3	<i>Vehicle</i>	0,018,238	0,014,570	0,013,647	0,022,235	0,021,161	<b>0,012,900</b>	0,015,515	0,017,351
N4	<i>Zoo</i>	0,011,140	0,011,292	<b>0,010,200</b>	0,011,426	0,011,610	0,011,504	0,012,204	0,011,478
N5	<i>Heart</i>	0,016,190	0,016,242	0,017,380	0,016,180	<b>0,007,951</b>	0,008,584	0,008,767	0,008,210
N6	<i>Breast Cancer</i>	0,019,958	0,019,660	0,019,291	0,019,138	0,019,752	0,020,111	0,019,407	<b>0,011,219</b>
N7	<i>Ionosphere</i>	0,008,177	0,008,198	0,008,066	<b>0,007,897</b>	0,017,871	0,018,158	0,022,813	0,025,535
N8	<i>Lung Cancer</i>	0,026,990	<b>0,016,945</b>	0,024,442	0,017,774	0,018,998	0,017,382	0,019,486	0,017,804
N9	<i>Dermatology</i>	0,034,272	0,036,433	0,033,375	0,033,385	0,037,107	0,031,614	0,035,545	<b>0,029,326</b>
N10	<i>Sonar</i>	0,008,076	<b>0,008,014</b>	0,008,289	0,008,618	0,024,495	0,024,495	0,016,801	0,021,846
N11	<i>BreastEW</i>	<b>0,024,312</b>	0,024,334	0,026,152	0,027,412	0,027,581	0,025,193	0,033,507	0,058,727
N12	<i>Soybean Small</i>	0,032,701	0,027,046	0,028,220	<b>0,023,690</b>	0,027,761	0,033,327	0,026,914	0,030,128
N13	<i>Movementlibras</i>	0,034,533	0,041,715	0,033,860	0,014,222	0,013,286	<b>0,012,845</b>	0,018,696	0,014,420
N14	<i>Parkinsons</i>	<b>0,006,888</b>	0,012,586	0,013,013	0,016,594	0,011,420	0,007,275	0,007,275	0,006,963
N15	<i>Spambase</i>	0,087,170	0,091,826	0,095,716	0,094,780	<b>0,075,102</b>	0,079,525	0,082,395	0,127,663
N16	<i>Waveform</i>	0,383,870	0,310,974	0,361,996	0,352,527	0,142,839	<b>0,093,220</b>	0,137,592	0,097,726
N17	<i>Arrhythmia</i>	0,007,773	0,006,876	0,006,430	0,006,303	0,004,765	0,004,230	0,004,042	<b>0,003,859</b>
N18	<i>Semeion</i>	0,017,747	0,014,372	0,013,194	0,014,157	0,006,503	0,005,809	0,005,092	<b>0,004,766</b>
N19	<i>Clean</i>	0,032,730	0,031,078	0,029,976	0,029,683	0,029,299	0,026,824	0,026,491	<b>0,026,139</b>
N20	<i>CNAE</i>	0,069,952	0,057,169	0,050,671	0,048,691	0,033,521	0,030,129	0,025,259	<b>0,023,302</b>
N21	<i>Hillvalley</i>	0,021,509	0,020,991	0,031,427	0,020,511	<b>0,019,524</b>	0,023,883	0,021,334	0,035,074

**Table 18**

According to the mean of fitness values, comparison between variations of the BinSSA and BinSSA-CR based S-shaped transfer functions.

ID	Benchmark	BinSSA1	BinSSA2	BinSSA3	BinSSA4	BinSSA1- CR	BinSSA2- CR	BinSSA3- CR	BinSSA4- CR
N1	<i>Wine</i>	00,138	00,158	00,114	00,145	00,151	00,173	00,160	<b>00,072</b>
N2	<i>Hepatitis</i>	00,952	01,043	01,056	00,924	01,053	01,043	00,889	<b>00,625</b>
N3	<i>Vehicle</i>	02,336	02,458	02,331	02,322	02,402	02,38	02,464	<b>02,295</b>
N4	<i>Zoo</i>	00,263	00,085	00,186	00,210	00,194	00,211	00,236	<b>00,080</b>
N5	<i>Heart</i>	01,255	01,164	01,170	01,180	01,119	01,228	01,140	<b>01,099</b>
N6	<i>Breast Cancer</i>	00,240	00,260	00,227	00,205	00,218	00,226	00,202	<b>00,200</b>
N7	<i>Ionosphere</i>	00,342	00,317	00,269	00,352	00,303	<b>00,228</b>	00,276	00,299
N8	<i>Lung Cancer</i>	00,714	00,544	00,375	00,372	01,215	00,544	00,455	<b>00,029</b>
N9	<i>Dermatology</i>	<b>00,057</b>	00,063	00,081	00,090	00,066	00,071	00,073	00,072
N10	<i>Sonar</i>	00,682	00,499	00,544	00,407	00,645	00,587	<b>00,372</b>	00,394
N11	<i>BreastEW</i>	00,423	00,354	00,427	00,364	00,363	00,324	00,396	<b>00,295</b>
N12	<i>Soybean Small</i>	00,035	00,031	00,026	<b>00,025</b>	00,035	00,003	00,027	<b>00,025</b>
N13	<i>Movementlibras</i>	02,227	02,071	02,148	01,877	02,151	02,086	02,065	<b>01,584</b>
N14	<i>Parkinsons</i>	00,034	00,028	00,023	00,022	00,082	00,077	00,025	<b>00,020</b>
N15	<i>Spambase</i>	00,666	00,674	00,708	00,731	00,644	00,685	00,707	<b>00,630</b>
N16	<i>Waveform</i>	01,606	<b>01,550</b>	01,644	01,690	01,615	01,572	01,676	01,604
N17	<i>Arrhythmia</i>	03,138	03,417	03,124	03,198	03,302	03,174	03,333	<b>02,520</b>
N18	<i>Semeion</i>	07,966	07,978	07,992	07,970	07,987	07,938	07,903	<b>07,574</b>
N19	<i>Clean</i>	00,390	00,337	00,371	00,344	00,342	00,359	00,360	<b>00,164</b>
N20	<i>CNAE</i>	01,088	01,385	01,419	01,570	<b>00,995</b>	01,336	01,429	01,239
N21	<i>Hillvalley</i>	04,428	04,473	04,370	04,310	04,474	04,509	04,423	<b>03,677</b>

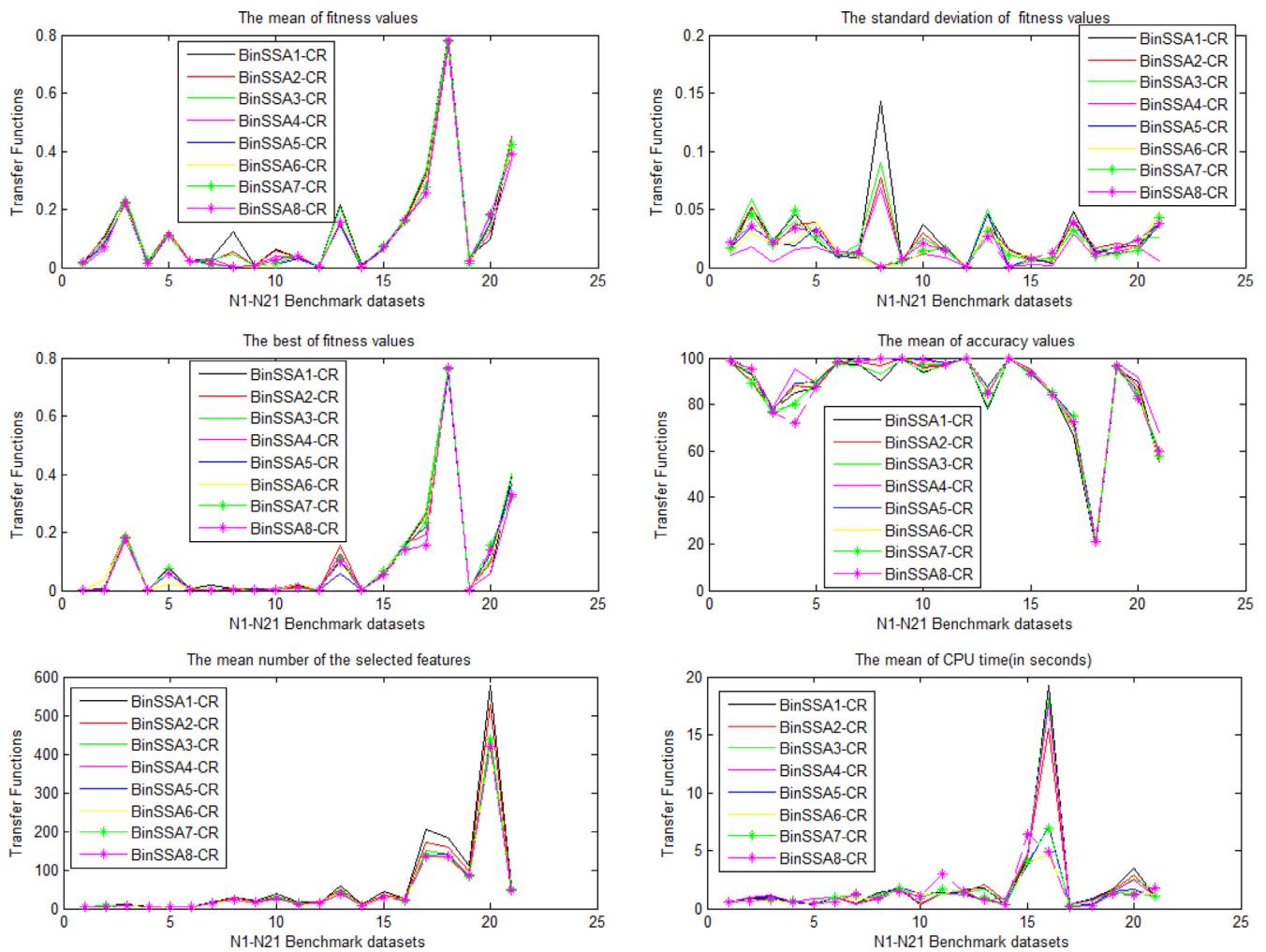
#### 5.4. Comparison between different variations of BinSSA and BinSSA-CR

In this section, the variations of S-shaped and V-shaped BinSSA and BinSSA-CR based on the social spider algorithm is examined on the feature selection problem in different criteria (mean of fitness value, standard deviation of fitness value, the best of fitness value, the worst of fitness value, mean of accuracy values, the mean number of the selected features, and mean of CPU time). **Table 18** shows the mean of fitness results of S-shaped variations of the BinSSA and BinSSA-CR. **Table 19** shows the mean of fitness results of V-shaped variations of the BinSSA and BinSSA-CR. The best results are marked with bold in **Tables 18** and **19**. **Fig. 10** shows convergence graphics for comparison between different variations of the BinSSA-CR and BinSSA.

According to the mean of fitness results, S-shaped BinSSA4-CR variation shows a higher success than the other S-shaped variations of BinSSA and another BinSSA-CR. The BinSSA4-CR variation shows high success at roughly 76,19% of benchmark datasets for 16 datasets out of 21 datasets (N1, N2, N3, N4, N5, N6, N8,

N11, N12, N13, N14, N15, N17, N18, N19, and N21). According to **Table 19**, V-shaped BinSSA5-CR and BinSSA6-CR variations show a higher success than the other V-shaped variations of BinSSA and BinSSA-CR. BinSSA5-CR and BinSSA6-CR variations show high success at roughly 33,33% of benchmark datasets for 7 datasets out of 21 datasets. The results show that the crossover operator has improved the search capability of BinSSA globally and locally. The new candidate solution set produced by the crossover operator has provided a stable solution. Both the exploration and exploitation capabilities of BinSSA are enhanced with the crossover operator in the binary space.

According to the standard deviation of fitness results, BinSSA4-CR, and BinSSA6-CR variations show a high success for feature selection problem. The BinSSA4-CR variation shows success at roughly 71,43% of benchmark datasets for 15 out of 21 datasets. The BinSSA6-CR variation shows a high success at roughly 33,33% of benchmark datasets for 7 out of 21 datasets. The reason is that BinSSA-CR can make a more stable balance between the diversification and intensification leanings between the candidate spiders.



**Fig. 9.** Convergence graphics for comparison between different variations of BinSSA-CR.

According to the mean of accuracy values, the variations of BinSSA4-CR, and BinSSA5-CR show high performance. The BinSSA5-CR variation shows success at roughly 47,62% of benchmark datasets for 10 out of 21 datasets (N1, N3, N4, N7, N8, N10, N11, N12, N13, and N14). The BinSSA4-CR variation shows success at roughly 76,19% of benchmark datasets for 16 out of 21 datasets (N1, N2, N3, N4, N6, N8, N9, N10, N12, N13, N14, N15, N16, N17, N19, and N21). The reason for this success is due to a more balanced diversification between the candidate solutions with the crossover operator.

According to the mean number of the selected features, S-shaped BinSSA4-CR variation has selected fewer features. BinSSA4-CR variation has chosen minimum features for 21 out of 21 datasets. V-shaped BinSSA8-CR variation has chosen minimum features for 15 out of 21 datasets. The results show that the variations of BinSSA-CR have chosen fewer features and have chosen the most optimal features.

According to the mean of CPU time results, BinSSA3 and BinSSA4 variations have obtained results as soon as a possible time for 5 out of 21 datasets. BinSSA8 and BinSSA8-CR variations have obtained results as soon as a possible time for 4 out of 21 datasets.

### 5.5. Wilcoxon signed-rank test and evaluation of BinSSA variations

Wilcoxon signed-rank test is a pairwise test that aims to detect significant differences between the behavior of two algorithms

(Acilar, 2013). In this paper, variations of BinSSA and BinSSA-CR are run with 20 times on various low, middle, and large dimension benchmark datasets with population size = 50 and maximum iteration = 100 equal parameter and 20 trials are done in each variation for each benchmark datasets. The means of fitness results are shown in Tables 8–17. In the Wilcoxon signed-rank test, alpha is selected as 0.05 (Acilar, 2013). p is the probability of the null hypothesis is true. p values of the hypothesis are calculated by using Matlab R2014a a software.

The most performance BinSSA and BinSSA-CR variation is selected based on 5 comparison criteria ((1) the mean of fitness results, (2) the standard deviation of fitness results, (3) the mean of accuracy values, (4) the mean number of the selected features, and (5) the mean of CPU time). The results indicate that the variations of BinSSA-CR are a more successful balance between exploration and exploitation than variations of BinSSA. The crossover operator has enhanced BinSSA's exploration and exploitation capabilities. Among the BinSSA-CR variants, BinSSA4-CR is the most efficient one. According to Tables 13–17, BinSSA4-CR variation shows superior performance for the mean of fitness values, the standard deviation of fitness values, mean of accuracy results, and the mean number of the selected features. BinSSA4-CR shows high performance for 4 of 5 comparison criteria.

Therefore, the Wilcoxon signed-rank test is applied to other variations of BinSSA and BinSSA-CR with BinSSA4-CR variation. Tables 20 and 21 show p-values of the Wilcoxon signed-rank test of BinSSA4-CR fitness results. According to the obtained results, the

**Table 19**

According to the mean of fitness values, comparison between variations of the BinSSA and BinSSA-CR based V-shaped transfer functions.

ID	Benchmark	BinSSA5	BinSSA6	BinSSA7	BinSSA8	BinSSA5- CR	BinSSA6- CR	BinSSA7- CR	BinSSA8- CR
N1	<i>Wine</i>	00,256	00,203	00,177	00,160	00,135	<b>00,122</b>	00,137	00,166
N2	<i>Hepatitis</i>	00,821	00,887	00,986	00,869	00,840	00,694	00,709	<b>00,692</b>
N3	<i>Vehicle</i>	02,398	02,392	02,361	02,498	<b>02,164</b>	02,187	02,206	02,236
N4	<i>Zoo</i>	00,150	00,248	00,276	00,200	<b>00,100</b>	00,153	00,275	00,125
N5	<i>Heart</i>	01,304	01,262	01,328	<b>01,036</b>	01,111	01,105	01,083	01,129
N6	<i>Breast Cancer</i>	00,211	<b>00,186</b>	00,238	00,248	00,222	00,241	00,211	00,207
N7	<i>Ionosphere</i>	00,171	00,207	00,206	00,268	00,143	<b>00,086</b>	00,112	00,156
N8	<i>Lung Cancer</i>	00,252	00,087	00,005	00,087	00,006	00,005	<b>00,004</b>	<b>00,004</b>
N9	<i>Dermatology</i>	00,101	00,100	00,138	00,148	00,040	<b>00,036</b>	00,005	00,058
N10	<i>Sonar</i>	00,308	00,359	00,309	00,458	<b>00,105</b>	<b>00,105</b>	00,139	00,250
N11	<i>BreastEW</i>	00,345	00,386	00,318	<b>00,296</b>	00,323	00,406	00,376	00,369
N12	<i>Soybean Small</i>	<b>00,005</b>							
N13	<i>Movementlibras</i>	01,689	01,544	01,689	01,742	<b>01,458</b>	01,587	01,543	01,561
N14	<i>Parkinsons</i>	<b>00,005</b>	00,057	00,057	00,006	00,007	00,032	00,032	00,006
N15	<i>Spambase</i>	00,764	00,794	00,872	00,844	<b>00,679</b>	00,721	00,734	00,702
N16	<i>Waveform</i>	01,722	01,693	01,770	01,821	<b>01,580</b>	01,593	01,594	01,633
N17	<i>Arrhythmia</i>	02,779	02,931	02,975	03,039	02,780	02,777	02,756	<b>02,581</b>
N18	<i>Semeion</i>	07,851	07,827	07,825	07,872	07,803	07,819	<b>07,783</b>	07,837
N19	<i>Clean</i>	00,268	00,288	00,301	00,369	00,134	<b>00,121</b>	00,160	00,208
N20	<i>CNAE</i>	02,084	02,181	02,182	02,097	01,566	<b>01,413</b>	01,789	01,823
N21	<i>Hillvalley</i>	03,914	03,822	04,019	03,801	04,212	04,217	04,204	03,898

**Table 20**

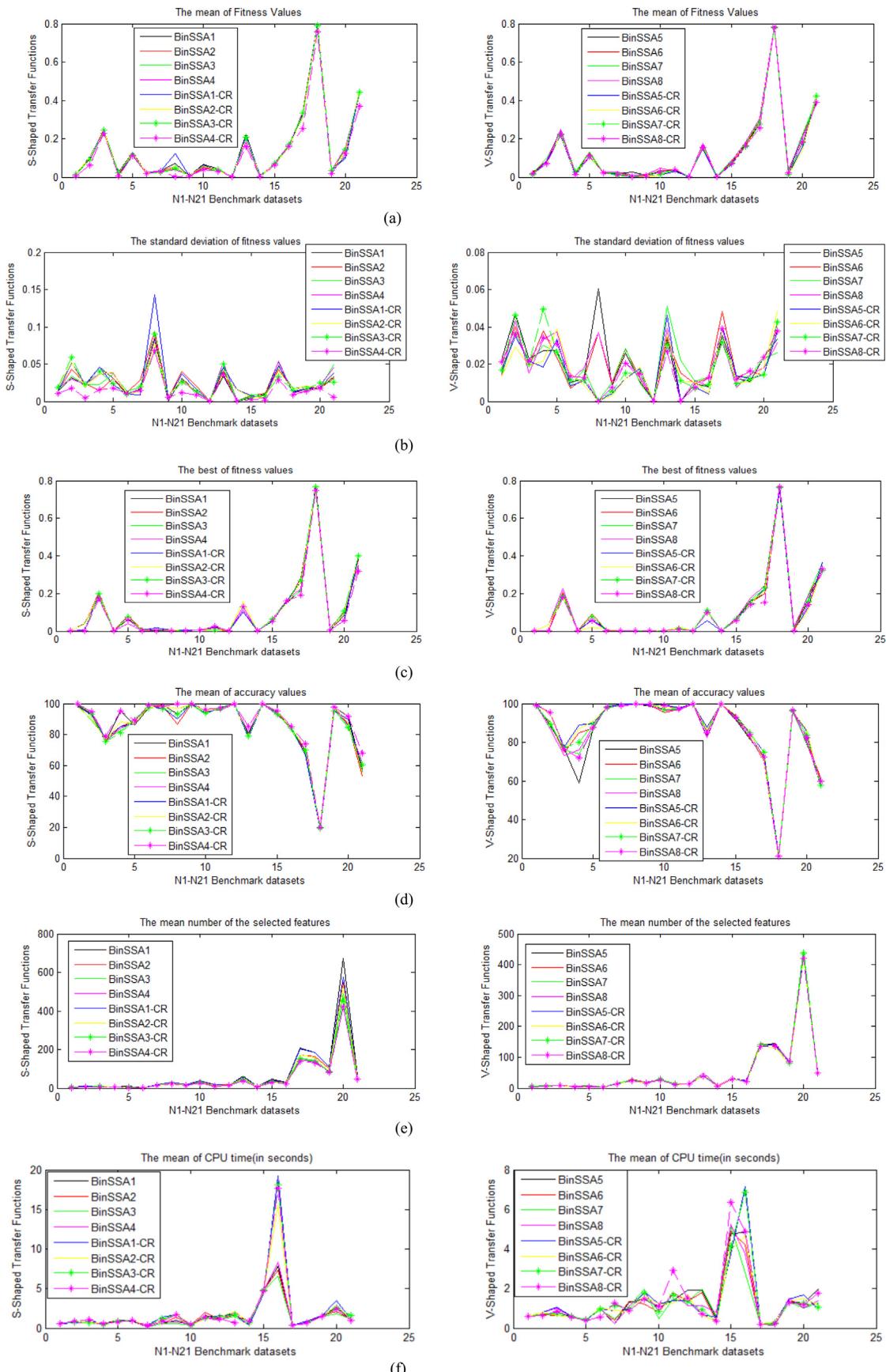
The *p*-values of Wilcoxon signed-rank test of BinSSA4-CR fitness results with variations of BinSSA ( $p \leq 0.05$  are underlined).

ID	Benchmark	BinSSA1	BinSSA2	BinSSA3	BinSSA4	BinSSA5	BinSSA6	BinSSA7	BinSSA8
N1	<i>Wine</i>	<u>00,026</u>	<u>00,235</u>	01,984	01,150	01,511	02,610	01,946	07,213
N2	<i>Hepatitis</i>	<u>00,001</u>	<u>00,002</u>	<u>4,22e-05</u>	<u>000,080</u>	1	01,756	00,369	03,193
N3	<i>Vehicle</i>	<u>6,91e-07</u>	<u>4,60e-08</u>	<u>7,94e-07</u>	<u>7,63e-06</u>	<u>4,56e-08</u>	<u>3,91e-08</u>	<u>1,30e-07</u>	<u>2,43e-08</u>
N4	<i>Zoo</i>	<u>000,075</u>	00,762	<u>00,025</u>	<u>001,469</u>	06,694	09,016	01,458	07,937
N5	<i>Heart</i>	<u>1,21e-06</u>	<u>1,65e-05</u>	<u>000,064</u>	<u>7,74e-05</u>	<u>1,68e-06</u>	<u>1,19e-06</u>	<u>7,20e-07</u>	0,013
N6	<i>Breast Cancer</i>	<u>001,878</u>	<u>00,080</u>	01,343	01,649	00,969	02,140	<u>00,172</u>	<u>00,200</u>
N7	<i>Ionosphere</i>	<u>00,172</u>	03,230	05,329	<u>00,164</u>	<u>00,045</u>	<u>00,370</u>	<u>00,496</u>	06,452
N8	<i>Lung Cancer</i>	<u>7,95e-09</u>	<u>7,95e-09</u>	<u>7,77e-09</u>	<u>7,88e-09</u>	<u>5,08e-05</u>	<u>1,34e-07</u>	<u>4,35e-09</u>	<u>1,16e-07</u>
N9	<i>Dermatology</i>	<u>00,010</u>	<u>00,022</u>	01,127	01,386	04,522	04,316	04,162	04,475
N10	<i>Sonar</i>	<u>00,013</u>	<u>1,85e-05</u>	<u>00,228</u>	04,504	01,577	06,706	<u>00,015</u>	<u>00,003</u>
N11	<i>BreastEW</i>	<u>00,086</u>	05,421	<u>00,299</u>	04,429	04,686	01,373	1	04,690
N12	<i>Soybean Small</i>	<u>4,74e-07</u>	<u>8,54e-07</u>	01,192	09,327	<u>3,09e-08</u>	<u>2,00e-08</u>	<u>2,40e-08</u>	<u>1,61e-08</u>
N13	<i>Movementlibras</i>	<u>2,11e-06</u>	<u>3,88e-05</u>	<u>6,96e-05</u>	00,592	00,826	08,590	08,375	00,611
N14	<i>Parkinsons</i>	<u>1,10e-07</u>	<u>1,70e-06</u>	<u>00,204</u>	<u>00,108</u>	<u>7,38e-09</u>	<u>6,59e-06</u>	<u>3,44e-07</u>	<u>1,06e-08</u>
N15	<i>Spambase</i>	<u>00,423</u>	01,163	<u>00,423</u>	<u>00,006</u>	<u>00,009</u>	<u>00,025</u>	<u>00,001</u>	<u>00,003</u>
N16	<i>Waveform</i>	1	01,429	02,063	<u>00,079</u>	<u>00,317</u>	03,175	<u>00,159</u>	00,079
N17	<i>Arrhythmia</i>	<u>8,89e-08</u>	<u>1,78e-08</u>	<u>5,54e-08</u>	<u>8,90e-08</u>	<u>7,40e-07</u>	<u>1,66e-07</u>	<u>1,21e-07</u>	<u>1,22e-07</u>
N18	<i>Semeion</i>	<u>6,00e-08</u>	<u>7,81e-07</u>	<u>8,21e-08</u>	<u>3,73e-08</u>	<u>5,84e-07</u>	<u>9,26e-06</u>	<u>1,37e-05</u>	<u>2791e-07</u>
N19	<i>Clean</i>	<u>6,72e-06</u>	<u>00,005</u>	<u>00,002</u>	<u>00,004</u>	<u>00,427</u>	<u>00,094</u>	<u>00,231</u>	<u>00,004</u>
N20	<i>CNAE</i>	01,352	<u>00,195</u>	<u>00,351</u>	<u>00,025</u>	<u>00,001</u>	<u>00,001</u>	<u>00,001</u>	<u>00,001</u>
N21	<i>Hillvalley</i>	<u>2,29e-08</u>	<u>2,30e-08</u>	<u>7,65e-05</u>	<u>5,83e-07</u>	<u>00,008</u>	05,638	<u>8,85e-07</u>	<u>00,015</u>

**Table 21**

The *p*-values of Wilcoxon signed-rank test of BinSSA4-CR fitness results with variations of BinSSA-CR ( $p \leq 0.05$  are underlined).

ID	Benchmark	BinSSA1-CR	BinSSA2-CR	BinSSA3-CR	BinSSA5-CR	BinSSA6-CR	BinSSA7-CR	BinSSA8-CR
N1	<i>Wine</i>	<u>00,014</u>	<u>00,131</u>	<u>00,294</u>	09,786	09,895	08,421	06,798
N2	<i>Hepatitis</i>	<u>6,65e-06</u>	<u>000,020</u>	<u>00,368</u>	08,485	01,989	01,723	00,277
N3	<i>Vehicle</i>	<u>4,48e-07</u>	<u>3,87e-07</u>	<u>3,34e-08</u>	<u>00,023</u>	<u>000,092</u>	<u>5,34e-05</u>	<u>3,29e-05</u>
N4	<i>Zoo</i>	<u>000,028</u>	0,017	0,008	02,405	02,590	05,189	03,488
N5	<i>Heart</i>	<u>1,33e-06</u>	<u>3,23e-05</u>	<u>9,28e-06</u>	<u>00,030</u>	<u>00,011</u>	<u>8,13e-05</u>	<u>9,63e-05</u>
N6	<i>Breast Cancer</i>	<u>00,504</u>	<u>00,462</u>	01,574	<u>00,397</u>	005,996	01,380	04,229
N7	<i>Ionosphere</i>	<u>00,228</u>	06,744	04,981	<u>00,010</u>	<u>5,62e-06</u>	<u>3,19e-05</u>	00,034
N8	<i>Lung Cancer</i>	<u>7,96e-09</u>	<u>7,92e-09</u>	<u>7,68e-09</u>	<u>6,47e-09</u>	<u>5,16e-09</u>	<u>6,11e-09</u>	<u>5,28e-09</u>
N9	<i>Dermatology</i>	<u>00,008</u>	<u>00,410</u>	05,568	1	<u>7,46e-05</u>	<u>1,71e-05</u>	<u>00,003</u>
N10	<i>Sonar</i>	<u>8,41e-07</u>	<u>1,45e-06</u>	<u>00,120</u>	<u>00,015</u>	<u>00,219</u>	1	<u>1,38e-06</u>
N11	<i>BreastEW</i>	02,374	03,603	<u>00,245</u>	07,898	04,693	02,374	03,036
N12	<i>Soybean Small</i>	<u>1,43e-07</u>	<u>3,76e-05</u>	<u>00,267</u>	<u>3,09e-08</u>	<u>2,00e-08</u>	<u>1,61e-08</u>	<u>2,77e-08</u>
N13	<i>Movementlibras</i>	<u>8,75e-05</u>	<u>1,88e-05</u>	<u>00,017</u>	05,030	05,385	06,918	<u>08,375</u>
N14	<i>Parkinsons</i>	<u>1,89e-07</u>	<u>6,49e-06</u>	<u>6,96e-05</u>	<u>1,38e-08</u>	<u>3,85e-07</u>	<u>3,85e-07</u>	<u>1,20e-08</u>
N15	<i>Spambase</i>	04,212	<u>00,195</u>	<u>00,010</u>	00,995	<u>00,238</u>	<u>00,003</u>	<u>00,238</u>
N16	<i>Waveform</i>	04,048	01,429	02,063	04,206	08,413	1	01,508
N17	<i>Arrhythmia</i>	<u>7617e-08</u>	<u>5,54e-08</u>	<u>2,92e-08</u>	<u>1,52e-06</u>	<u>5,52e-07</u>	<u>1,51e-06</u>	<u>1,72e-05</u>
N18	<i>Semeion</i>	<u>6,00e-08</u>	<u>1,12e-07</u>	<u>2,40e-07</u>	<u>9,67e-05</u>	<u>1,38e-06</u>	<u>3,18e-06</u>	<u>5,84e-07</u>
N19	<i>Clean</i>	<u>00,002</u>	<u>00,003</u>	<u>00,001</u>	01,694	01,455	07,338	07,960
N20	<i>CNAE</i>	00,508	02,351	01,352	<u>00,015</u>	00,508	<u>00,001</u>	<u>00,005</u>
N21	<i>Hillvalley</i>	<u>1,96e-08</u>	<u>1,95e-08</u>	<u>1,96e-08</u>	<u>5,84e-07</u>	<u>7,66e-05</u>	<u>8,60e-05</u>	00,834



**Fig. 10.** Convergence graphics for comparison between different variations of the BinSSA and BinSSA-CR. (a) the mean of fitness values, (b) the standard deviation of fitness values, (c) the best of fitness values, (d) the mean of accuracy, (e) the mean number of the selected features, and (f) the mean of CPU time.

**Table 22**

Parameters of BinSSA and comparison algorithms.

Algorithms	Parameters	Values
BA ( <a href="#">Mirjalili et al., 2014</a> )	Qmin	0
	Qmax	2
	A (Loudness)	0,5
	r (Pulse rate)	0,5
PSO ( <a href="#">Chuang et al., 2008</a> )	w (Inertia weight)	2
	W <sub>max</sub>	0,9
	W <sub>min</sub>	0,4
	c <sub>1</sub>	2
GWO ( <a href="#">Emary et al., 2016</a> )	c <sub>2</sub>	2
	α	[2 0]
	BinSSA4 ( <a href="#">Yu &amp; Li, 2015</a> )	1
	and	0,7
BinSSA4-CR	p <sub>m</sub>	0,1

p-values are below 0.05 for the majority of cases. Therefore, the improvements in the results of the BinSSA4-CR are statistically superior to those of other variations in dealing with the majority of the datasets, which verifies the efficacy of this algorithm.

### 5.6. Comparison of BinSSA with other metaheuristics algorithms

**Case Study 1:** The performance of the BinSSA4-CR variation is also compared with the well-known heuristic algorithms of the literature. These algorithms are Particle Swarm Optimization ([Chuang, Chang, Tu & Yang, 2008](#)), Bat Algorithm ([Mirjalili et al., 2014](#)), Grey Wolf Optimization ([Emary et al., 2016](#)), BinSSA, and BinSSA-CR. All experiments are performed according to the same parameters and conditions for a fair comparison. Parameters of BinSSA and comparison algorithms are shown in [Table 22](#).

[Table 23](#) shows comparing the mean of the fitness values between BinSSA4-CR with comparison algorithms. According to the mean of fitness results, BinSSA4-CR variation shows superior performance at roughly 80,95% of benchmark datasets for 17 out of 21 datasets except for N8, N12, N16, and N20. BBA is the second-best performing algorithm after BinSSA4-CR. BBA shows performance for 4 out of 21 datasets (N8, N12, N16, and N20). The most important factor in the high performance of BinSSA4-CR is the crossover operator. Thus BinSSA4-CR has had superiority compared to other comparison algorithms. BinSSA4-CR variation has estab-

**Table 24**

According to the mean of accuracy values, comparison of BinSSA4-CR with comparison algorithms.

ID	Benchmark	BinSSA4-CR	BinSSA4	BBA	BGWO	BPSO
N1	<i>Wine</i>	<b>100</b>	<b>100</b>	98,19	98,61	98,47
N2	<i>Hepatitis</i>	<b>94,65</b>	94,63	93,33	91,67	93,83
N3	<i>Vehicle</i>	<b>78,34</b>	75,6	23,25	21,39	22,84
N4	<i>Zoo</i>	95	84	<b>98,25</b>	97,75	94,25
N5	<i>Heart</i>	<b>89,26</b>	87,41	11,57	9,63	11,39
N6	<i>Breast Cancer</i>	<b>98,55</b>	97,39	31,74	31,63	32,28
N7	<i>Ionosphere</i>	<b>98,29</b>	98	97,14	93,86	95,43
N8	<i>Lung Cancer</i>	<b>100</b>	<b>100</b>	<b>100</b>	92,50	95,83
N9	<i>Dermatology</i>	<b>100</b>	<b>100</b>	71,64	66,37	70,07
N10	<i>Sonar</i>	<b>96</b>	95	4,17	2143	2,74
N11	<i>BreastEW</i>	<b>97</b>	95,8	96,15	95,65	96,25
N12	<i>Soybean Small</i>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>
N13	<i>Movementlibras</i>	<b>85,33</b>	80,83	84,10	81,11	81,46
N14	<i>Parkinsons</i>	<b>100</b>	100	94,74	94,10	96,03
N15	<i>Spambase</i>	<b>95,18</b>	92,58	94,50	93,80	92,95
N16	<i>Waveform</i>	85,20	84,67	<b>85,91</b>	84,76	84,10
N17	<i>Arrhythmia</i>	<b>74,11</b>	70,11	73,94	68,89	68,39
N18	<i>Semeion</i>	20,2	19,73	24,11	<b>24,98</b>	21,82
N19	<i>Clean</i>	<b>97,75</b>	96,5	97,58	96,11	93,58
N20	<i>CNAE</i>	91,50	86,25	<b>93,96</b>	92,99	87,13
N21	<i>Hillvalley</i>	<b>68,17</b>	61,67	68,14	61,57	60,58

lished a more stable balance between exploration and exploitation. According to the standard deviation of fitness results, BinSSA4-CR variation shows superior performance at roughly 85,71% of benchmark datasets for 18 out of 21 datasets except for N8, N12, and N20. BBA is the second-best performing algorithm after BinSSA4-CR. BBA shows performance for 2 out of 21 datasets (N8 and N12). BPSO and BinSSA4 show performance for 1 out of 21 datasets. The results show that BinSSA4-CR finds superior solutions with satisfactory standard deviation values. According to the best of fitness value, BinSSA4-CR variation shows performance at roughly 29% of benchmark datasets for 6 out of 21 datasets and BBA shows performance at roughly 52% of benchmark datasets for 11 out of 21 datasets.

[Table 24](#) shows the mean of the accuracy of the classification for comparison algorithms. According to the accuracy of the classification results, BinSSA4-CR variation shows superior performance at roughly 80,95% of benchmark datasets for 17 out of 21 datasets

**Table 23**

According to the mean of fitness results (as Fitness), the standard deviation of fitness results (as S.D.), and the best fitness values (as Best) comparison of BinSSA4-CR with comparison algorithms.

ID	Benchmark	BinSSA4-CR			BinSSA4			BBA			BGWO			BPSO		
		Fitness	S.D.	Best	Fitness	S.D.	Best	Fitness	S.D.	Best	Fitness	S.D.	Best	Fitness	S.D.	Best
N1	<i>Wine</i>	<b>00,072</b>	<b>00,102</b>	<b>00,015</b>	00,145	00,186	00,023	00,208	00,184	00,023	00,178	00,224	<b>00,015</b>	00,179	00,206	00,023
N2	<i>Hepatitis</i>	<b>00,625</b>	<b>00,175</b>	<b>00,021</b>	00,924	00,302	00,367	00,680	00,451	<b>00,021</b>	00,861	00,392	00,042	00,638	00,357	00,032
N3	<i>Vehicle</i>	<b>02,295</b>	<b>00,046</b>	<b>01,719</b>	02,322	00,232	01,777	07,638	00,283	06,940	07,843	00,155	07,635	07,682	00,211	07,314
N4	<i>Zoo</i>	<b>00,080</b>	<b>00,157</b>	00,013	00,210	00,369	00,025	00,187	00,333	<b>00,006</b>	00,244	00,407	<b>00,006</b>	00,090	00,242	<b>00,006</b>
N5	<i>Heart</i>	<b>01,099</b>	<b>00,172</b>	00,596	01,180	00,380	<b>00,405</b>	08,784	00,229	08,296	08,987	00,191	08,655	08,799	00,244	08,273
N6	<i>Breast Cancer</i>	<b>00,200</b>	<b>00,104</b>	<b>00,021</b>	00,205	00,109	00,022	06,802	00,236	06,335	06,817	00,282	06,203	06,748	00,267	06,357
N7	<i>Ionosphere</i>	<b>00,299</b>	<b>00,150</b>	00,032	00,352	00,157	00,174	00,302	00,217	<b>00,006</b>	00,652	00,325	00,180	00,484	00,208	00,029
N8	<i>Lung Cancer</i>	00,029	00,680	00,029	00,372	00,862	00,034	<b>00,014</b>	<b>00,006</b>	<b>00,004</b>	00,788	00,842	00,036	00,445	00,733	00,025
N9	<i>Dermatology</i>	<b>00,072</b>	<b>00,059</b>	<b>00,029</b>	00,090	00,080	00,038	02,841	00,447	02,199	03,388	00,420	02,638	03,006	00,320	02,347
N10	<i>Sonar</i>	<b>00,394</b>	<b>00,118</b>	00,058	00,407	00,283	<b>00,047</b>	09,497	00,148	09,203	09,723	00,147	09,467	09,657	00,135	09,459
N11	<i>BreastEW</i>	<b>00,295</b>	<b>00,083</b>	00,235	00,364	00,121	00,228	00,392	00,162	<b>00,106</b>	00,465	00,172	00,235	00,395	00,160	00,119
N12	<i>Soybean Small</i>	00,025	00,003	00,020	00,025	00,003	00,017	<b>00,006</b>	<b>00,001</b>	<b>00,003</b>	00,024	00,006	00,011	00,016	00,003	00,011
N13	<i>Movementlibras</i>	<b>01,584</b>	<b>00,355</b>	01,290	01,877	00,528	01,147	01,609	00,539	<b>00,586</b>	01,930	00,359	01,294	01,877	00,487	01,279
N14	<i>Parkinsons</i>	<b>00,020</b>	<b>00,003</b>	00,018	00,022	<b>00,003</b>	00,018	00,533	00,224	00,267	00,617	00,299	00,027	00,414	00,300	<b>00,014</b>
N15	<i>Spambase</i>	<b>00,630</b>	<b>00,026</b>	00,515	00,731	00,063	00,654	00,639	00,062	<b>00,490</b>	00,688	00,083	00,617	00,750	00,049	00,682
N16	<i>Waveform</i>	01,604	<b>00,014</b>	01,595	01,690	00,038	01,639	<b>01,451</b>	00,090	<b>01,258</b>	01,584	00,083	01,461	01,632	00,066	01,488
N17	<i>Arrhythmia</i>	<b>02,520</b>	<b>00,289</b>	<b>01,919</b>	03,198	00,543	02,249	02,621	00,297	02,126	03,146	00,386	02,595	03,177	00,586	02,244
N18	<i>Semeion</i>	<b>07,574</b>	<b>00,086</b>	07,474	07,970	00,115	07,711	07,575	00,167	07,188	07,584	00,167	<b>07,156</b>	07,789	00,154	07,466
N19	<i>Clean</i>	<b>00,164</b>	<b>00,134</b>	00,048	00,344	00,137	00,155	00,280	00,212	<b>00,036</b>	00,452	00,270	00,070	00,682	00,226	00,360
N20	<i>CNAE</i>	01,239	00,174	00,575	01,570	00,220	00,995	<b>00,648</b>	00,144	00,414	00,774	00,178	<b>00,399</b>	01,325	<b>00,142</b>	01,060
N21	<i>Hillvalley</i>	<b>03,677</b>	<b>00,055</b>	03,207	04,310	00,445	03,506	03,680	00,399	<b>02,405</b>	03,870	00,389	03,180	03,947	00,240	03,639

**Table 25**

According to the mean number of the selected features, comparison of BinSSA4-CR with comparison algorithms.

ID	Benchmark	BinSSA4-CR	BinSSA4	BBA	BGWO	BPSO
N1	Wine	<b>4</b>	5	5	6	5
N2	Hepatitis	<b>7</b>	9	7	8	7
N3	Vehicle	<b>7</b>	8	9	11	8
N4	Zoo	<b>5</b>	6	6	6	7
N5	Heart	<b>4</b>	5	6	6	5
N6	Breast Cancer	<b>4</b>	<b>4</b>	<b>4</b>	<b>4</b>	<b>4</b>
N7	Ionosphere	<b>13</b>	14	17	15	14
N8	Lung Cancer	<b>23</b>	24	28	25	28
N9	Dermatology	<b>15</b>	17	17	20	16
N10	Sonar	<b>27</b>	28	<b>27</b>	28	29
N11	BreastEW	<b>11</b>	12	13	20	17
N12	Soybean Small	<b>13</b>	14	14	18	16
N13	Movementlibras	<b>39</b>	40	<b>39</b>	54	40
N14	Parkinsons	<b>7</b>	8	8	9	8
N15	Spambase	<b>32</b>	33	37	43	39
N16	Waveform	<b>22</b>	23	<b>22</b>	30	23
N17	Arrhythmia	<b>140</b>	147	146	144	142
N18	Semeion	<b>130</b>	137	133	152	134
N19	Clean	<b>84</b>	87	87	111	86
N20	CNAE	422	<b>421</b>	428	482	433
N21	Hillvalley	<b>45</b>	49	49	65	51

except for N4, N16, N18, and N20. The maximum mean of the accuracy value of BinSSA4-CR is 100 and the minimum mean of the accuracy value of BinSSA4-CR is 20. BBA has the second-best mean of accuracy after BinSSA4-CR. BBA shows performance for 5 out of 21 datasets. Then, respectively, BinSSA4, BGWO, and BPSO show performance. BinSSA4-CR variation has also achieved accuracy at 100% for N1, N8, N9, N12, and N14 benchmark datasets.

The mean number of the selected features is shown in Table 25. According to the mean number of the selected features, BinSSA4-CR has selected fewer features at roughly 95,24% of benchmark datasets for 20 out of 21. The mean of the CPU time is shown in Table 26. According to the mean of CPU time results, BBA has the shortest CPU time at roughly 76,19% of benchmark datasets for 16 out of 21 datasets except for N14, N16, N17, N18, and N20.

From the results in Tables 23–26, BinSSA4-CR shows high performance for feature selection problem. The second best comparison algorithm after BinSSA4-CR is BBA. BinSSA4-CR has achieved this success thanks to its crossover operator. Thus, the exploration

and exploitation capability of BinSSA4-CR in the binary search space has been improved. Thus, it is more advantages than other comparison algorithms.

Figs. 11–13, respectively, show convergence graphics for BinSSA4-CR, BinSSA4, BBA, BGWO, and BPSO for low-scale, middle-scale, and large-scale datasets. According to convergence graphics, BinSSA4-CR shows outperform all algorithms at roughly 81% of benchmark datasets for 17 out of 21 datasets except N12, N16, N18, and N19. The BinSSA4-CR has an accelerated trend in solving all problems.

#### 5.6.1. Wilcoxon signed-rank test of BinSSA4-CR with BBA, BGWO, and BPSO

The Wilcoxon signed-rank test is applied to BinSSA4-CR variation with BBA, BGWO, and BPSO. Table 27 shows the obtained results through implementing the Wilcoxon test for comparisons between BinSSA4-CR and BBA, BGWO, and BPSO. According to the obtained results, the *p*-values are below 0.05 for the majority of cases. Therefore, the improvements in the results of the BinSSA4-CR are statistically superior to those of other algorithms in dealing with the majority of the datasets, which verifies the efficacy of BinSSA. From these results, we can conclude that the BinSSA4-CR has a superior performance over the other state-of-the-art algorithms.

*Case Study 2:* The performance of the variations of BinSSA-CR and BinSSA is compared with the well-known heuristic algorithms of the literature. These algorithms are the Genetic Algorithm (GA), Particle Swarm Optimization (PSO), Ant Lion Optimization (ALO), Grey Wolf Optimization (GWO), BinSSA-CR, and BinSSA. All experiments are performed according to the same parameters and conditions for a fair comparison. Parameters of BinSSA-CR and comparison algorithms are shown in Table 28. The means of fitness values and the mean accuracy results are taken directly from Hegazy, Makhlof and El-Tawel Gh (2018) for GA, PSO, ALO, and GWO.

In Table 29, BinSSA-CR and comparison algorithms compare according to the mean of the fitness values and accuracy. According to the mean of fitness results, BinSSA-CR shows superior performance at roughly 80,95% of benchmark datasets for 17 out of 21 datasets except for N12, N17, N19, and N21. From the results in Table 29, it can be recognized that the developed BinSSA-CR can surpass other peers on 80,95% of the datasets. The results show

**Table 26**

According to the mean of CPU time (in seconds), comparison of BinSSA4-CR with comparison algorithms.

ID	Benchmark	BinSSA4-CR	BinSSA4	BBA	BGWO	BPSO
N1	Wine	0,011,804	0,011,928	<b>0,006,232</b>	0,025,878	0,006,468
N2	Hepatitis	0,018,260	0,013,696	<b>0,006,174</b>	0,022,520	0,006,726
N3	Vehicle	0,022,236	0,013,732	<b>0,009,508</b>	0,015,736	0,010,780
N4	Zoo	0,011,426	0,011,524	<b>0,006,056</b>	0,011,288	0,006,804
N5	Heart	0,016,180	0,015,992	<b>0,007,698</b>	0,013,500	0,008,720
N6	Breast Cancer	0,019,138	0,020,042	<b>0,007,352</b>	0,013,072	0,008,340
N7	Ionosphere	0,007,896	0,003,402	<b>0,006,600</b>	0,011,516	0,007,030
N8	Lung Cancer	0,017,774	0,015,652	<b>0,005,918</b>	0,011,016	0,006,568
N9	Dermatology	0,033,384	0,016,282	<b>0,006,332</b>	0,011,754	0,006,686
N10	Sonar	0,008,618	0,008,934	<b>0,008,548</b>	0,013,046	0,008,872
N11	BreastEW	0,027,412	0,026,352	<b>0,006,556</b>	0,039,102	0,006,986
N12	Soybean Small	0,023,690	0,018,920	<b>0,006,048</b>	0,036,562	0,006,230
N13	Movementlibras	0,014,222	0,040,802	<b>0,006,962</b>	0,024,082	0,007,550
N14	Parkinsons	0,016,594	0,016,344	0,006,214	0,011,330	<b>0,006,160</b>
N15	Spambase	0,094,780	0,094,552	<b>0,094,048</b>	0,177,964	0,095,612
N16	Waveform	0,352,526	0,166,894	0,084,970	0,182,684	<b>0,080,888</b>
N17	Arrhythmia	0,006,302	0,006,368	0,011,364	0,024,350	0,013,270
N18	Semeion	0,014,158	0,012,196	0,060,226	0,157,566	0,061,514
N19	Clean	0,029,682	0,029,596	<b>0,008,800</b>	0,021,510	0,009,132
N20	CNAE	0,048,692	0,048,600	0,106,238	0,351,940	0,102,870
N21	Hillvalley	0,020,512	0,020,264	<b>0,008,550</b>	0,028,580	0,008,680

**Table 27**

The  $p$ -values of Wilcoxon signed-rank test of BinSSA4-CR fitness results with BBA, BGWO, and BPSO ( $p \leq 0.05$  are underlined).

ID	Benchmark	BinSSA4-CR & BBA	BinSSA4-CR & BGWO	BinSSA4-CR & BPSO
N1	Wine	<u>46245E-04</u>	<u>00,110</u>	06,405
N2	Hepatitis	<u>29114e-06</u>	05,940	<u>01,092</u>
N3	Vehicle	<u>24387E-07</u>	<u>23998E-08</u>	<u>23387E-08</u>
N4	Zoo	02,598	01,498	04,191
N5	Heart	<u>49294E-08</u>	<u>48004E-08</u>	<u>45784E-08</u>
N6	Breast Cancer	<u>63671E-08</u>	<u>62771E-08</u>	<u>62059E-08</u>
N7	Ionosphere	06,947	28352E-05	00,176
N8	Lung Cancer	<u>78321E-09</u>	<u>77461E-09</u>	10664E-06
N9	Dermatology	<u>64673E-08</u>	<u>63761E-08</u>	63761E-08
N10	Sonar	<u>44377E-08</u>	<u>43524E-08</u>	<u>43007E-08</u>
N11	BreastEW	05,948	<u>00,227</u>	01,167
N12	Soybean Small	<u>53345E-08</u>	01,556	10408E-07
N13	Movementlibras	07,326	<u>36081E-04</u>	<u>00,308</u>
N14	Parkinsons	<u>24192E-08</u>	<u>23577E-08</u>	10394E-06
N15	Spambase	00,724	<u>41425E-08</u>	<u>81257E-08</u>
N16	Waveform	<u>43459E-08</u>	<u>26568E-07</u>	00,563
N17	Arrhythmia	<u>20140E-06</u>	<u>10394E-07</u>	14197E-07
N18	Semeion	01,635	03,315	<u>56388E-04</u>
N19	Clean	<u>45562E-06</u>	<u>84982E-06</u>	<u>14084E-07</u>
N20	CNAE	<u>44179E-08</u>	<u>44642E-08</u>	01,148
N21	Hillvalley	<u>11902E-05</u>	<u>00,291</u>	69355E-04

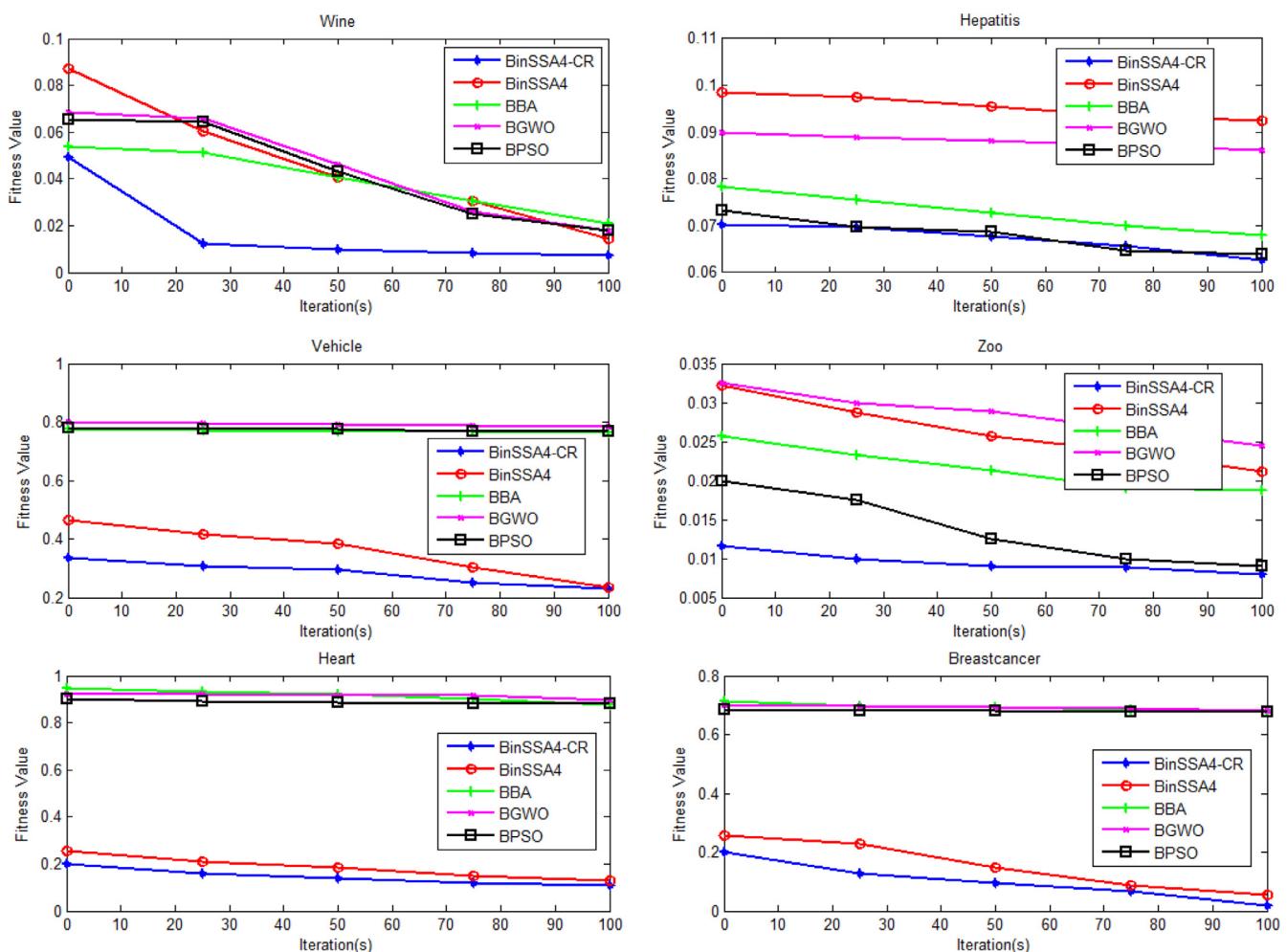
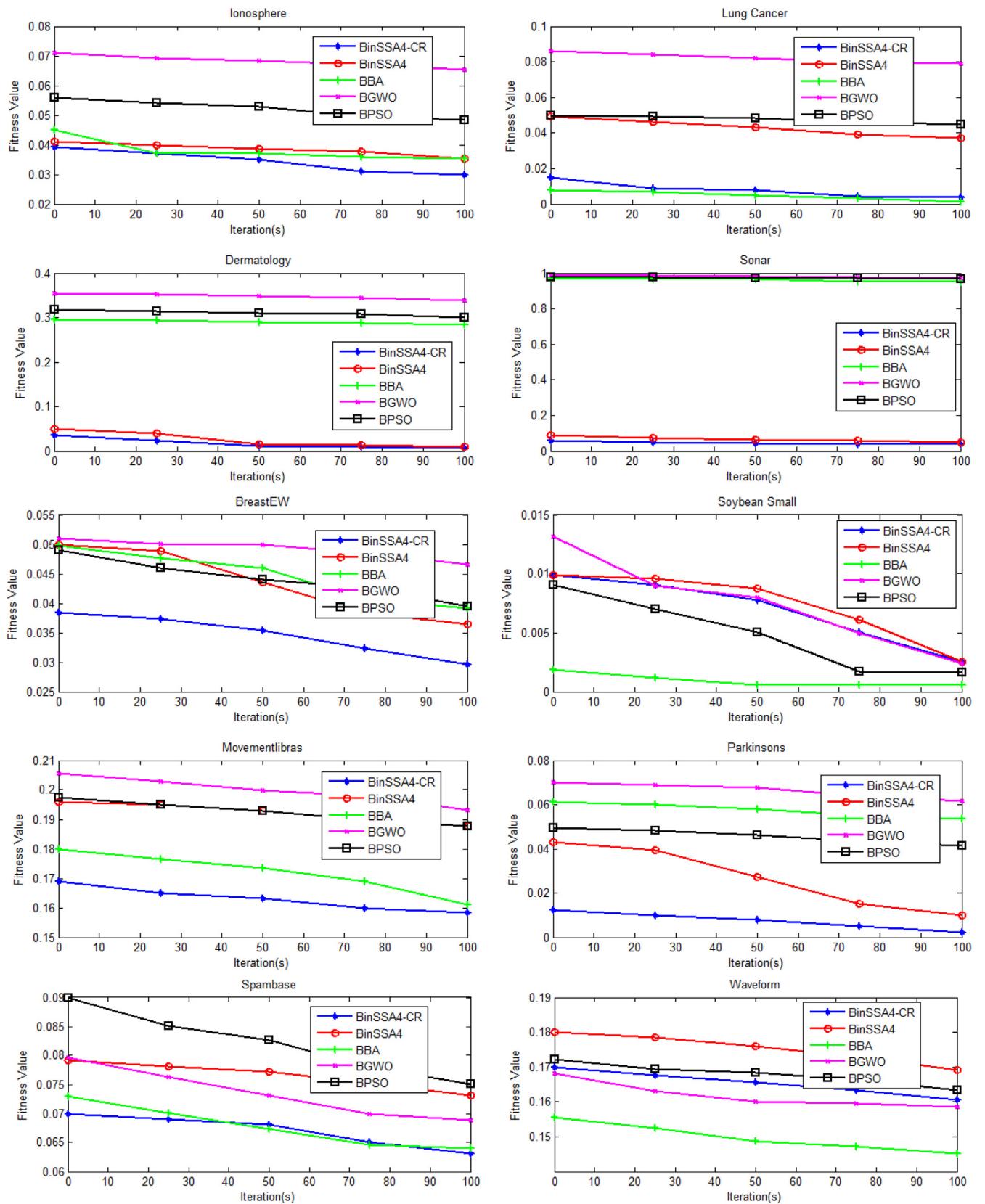
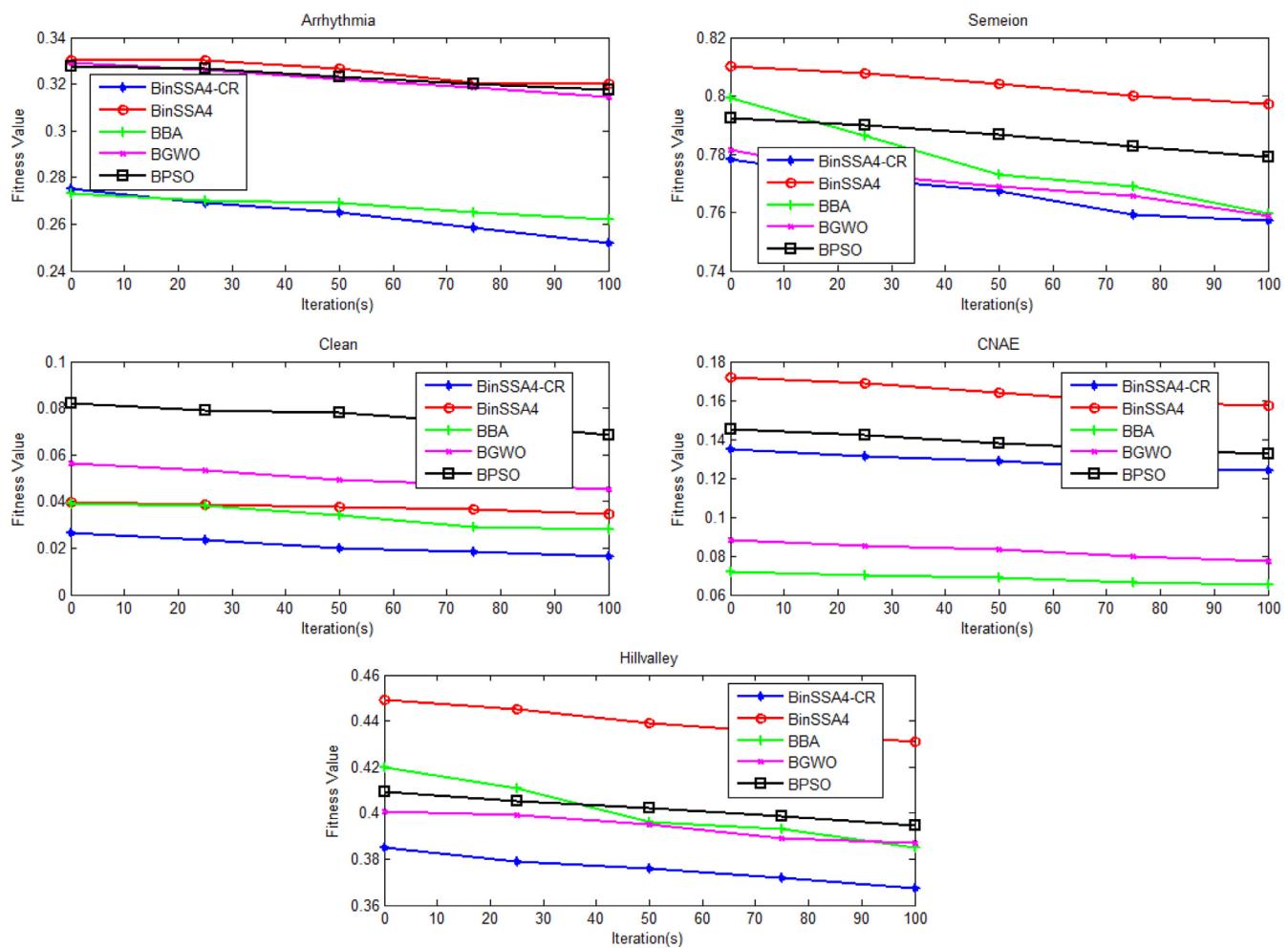


Fig. 11. Convergence graphics for BinSSA4-CR, BinSSA4, BBA, BGWO, and BPSO for low-scale datasets.



**Fig. 12.** Convergence graphics for BinSSA4-CR, BinSSA4, BBA, BGWO, and BPSO for middle-scale datasets.



**Fig. 13.** Convergence graphics for BinSSA4-CR, BinSSA4, BBA, BGWO, and BPSO for large-scale datasets.

**Table 28**  
Parameters of BinSSA-CR and comparison algorithms.

Parameters	Values
Population size(n)	10
Maximum iteration	50
Number of runs	20
Problem dimension(N)	Number of features in the dataset
$\rho$	0,9
$\varphi$	0,1
K	5 (K value in K-NN) ( <a href="#">Zawbaa et al., 2015</a> )
k	10 (k value in k-fold)
c1,c2	1,4 (PSO learning factors) ( <a href="#">Hegazy et al., 2018</a> )
$\omega$	0,7 (Inertia factor of PSO) ( <a href="#">Hegazy et al., 2018</a> )
Cross_val	0,9 (GA Crossover Fraction) ( <a href="#">Hegazy et al., 2018</a> )
Mut_val	0,1 (GA Mutation Fraction) ( <a href="#">Hegazy et al., 2018</a> )
Search space	{0, 1}
Paramters for BinSSA and BinSSA-CR	$r_a = 1; p_c = 0,7; p_m = 0,1$ ( <a href="#">Yu &amp; Li, 2015</a> )

that BinSSA-CR provides an advantage thanks to the crossover operator according to comparison algorithms. According to the mean of the fitness values, the second-best comparison algorithm after BinSSA-CR is ALO. ALO shows performance at roughly 10% of benchmark datasets for 2 out of 21 datasets.

According to the mean of the accuracy of the classification results, BinSSA-CR shows superior performance at roughly 95,24% of benchmark datasets for 20 out of 21 datasets except for N20. The BinSSA-CR technique develops classification rates compared to GWO. A classification rate of BinSSA is roughly 10% and the classification rate of GWO is roughly 5%. Thanks to the crossover operator,

BinSSA-CR has passed BinSSA, GA, PSO, ALO, and GWO. It has developed the ability to search locally and search globally in binary space.

The comprehensive experiments demonstrated the merits of BinSSA-CR for dealing with feature selection problems. The proposed algorithm has shown high performance in low-scaled dimensional datasets like wine as well as large-scale dimensional datasets like CNAE. The main reason for the success of BinSSA is the crossover operator. The crossover operator has significantly changed the position and behavior of the spider. This has enabled the spider positions to be located in different regions and

**Table 29**

According to the mean of fitness values and accuracy values, comparison of BinSSA and BinSSA-CR with comparison algorithms (\*related performance comparisons could not be performed).

ID	Benchmark	BinSSA-CR		BinSSA		GA		PSO		ALO		GWO	
		Fitness	Accuracy	Fitness	Accuracy	Fitness	Accuracy	Fitness	Accuracy	Fitness	Accuracy	Fitness	Accuracy
N1	Wine	<b>00,230</b>	<b>09,806</b>	00,230	09,750	<b>00,230</b>	09,570	00,540	09,230	00,372	09,420	00,430	09,120
N2	Hepatitis	<b>00,905</b>	<b>09,100</b>	01,263	09,000	01,600	08,750	01,500	08,605	01,293	08,825	02,195	08,479
N3	Vehicle	<b>02,091</b>	<b>07,432</b>	02,393	07,201	02,300	07,163	02,100	06,695	03,019	06,814	02,945	06,172
N4	Zoo	<b>00,618</b>	<b>09,800</b>	00,758	09,675	01,160	08,540	02,000	08,240	01,875	08,050	01,027	08,750
N5	Heart	<b>01,210</b>	<b>08,630</b>	01,348	08,521	01,250	08,240	01,850	08,220	02,026	08,020	01,301	08,070
N6	Breast Cancer	<b>00,353</b>	<b>09,688</b>	00,399	09,685	00,380	09,550	00,370	09,510	00,425	09,500	00,415	09,530
N7	Ionosphere	<b>00,554</b>	<b>09,486</b>	01,214	09,100	01,270	08,240	01,760	08,480	01,199	08,430	01,415	08,190
N8	Lung Cancer	<b>00,290</b>	<b>09,750</b>	01,296	09,083	01,500	04,820	01,724	05,627	01,902	05,056	02,844	05,014
N9	Dermatology	<b>00,200</b>	<b>09,932</b>	00,522	09,849	00,900	09,645	00,425	09,071	00,214	09,322	00,226	09,488
N10	Sonar	<b>00,67</b>	<b>09,425</b>	00,669	09,375	01,690	07,170	03,190	07,230	01,769	07,140	02,256	07,140
N11	BreastEW	<b>00,410</b>	<b>09,540</b>	00,512	09,520	00,420	09,350	00,540	09,490	00,564	09,420	00,654	09,490
N12	Soybean Small	00,029	<b>1</b>	00,049	<b>1</b>	00,600	09,438	00,400	08,648	<b>00,019</b>	09,098	02,913	09,205
N13	Movementlibras	<b>01,698</b>	<b>08,250</b>	01,749	08,222	02,960	06,902	03,330	06,466	03,889	06,597	02,784	06,866
N14	Parkinsons	<b>00,070</b>	<b>1</b>	00,293	<b>1</b>	00,840	08,492	00,950	08,653	00,936	08,367	01,242	08,367
N15	Spambase	<b>00,880</b>	<b>09,198</b>	00,943	09,098	02,210	08,229	02,760	08,735	02,904	08,804	02,840	08,839
N16	Waveform	<b>01,910</b>	<b>08,149</b>	02,020	08,008	02,180	07,620	02,400	07,620	02,681	07,690	02,648	07,650
N17	Arrhythmia	02,919	<b>06,844</b>	02,935	06,828	00,600	05,802	00,900	05,707	00,374	05,462	00,363	05,641
N18	Semeion*	<b>07,046</b>	<b>02,100</b>	07,286	02,075	–	–	–	–	–	–	–	–
N19	Clean	00,542	<b>09,237</b>	00,965	09,068	00,640	07,648	00,920	07,784	<b>00,161</b>	08,098	00,184	07,953
N20	CNAE	<b>01,586</b>	08,400	02,069	07,900	02,670	08,246	03,270	08,147	01,662	07,962	02,000	08,407
N21	Hillvalley	02,490	<b>06,708</b>	02,920	06,658	<b>02,450</b>	05,627	02,630	05,507	04,052	05,709	04,088	05,544

increased exploration and exploitation capabilities of the spiders. S-shaped and V-shaped transfer functions can effectively map the continuous values to binary ones. The BinSSA approaches performed well on most of the feature selection problems. The proposed variations of BinSSA and BinSSA-CR have a high potential to provide very superior results.

## 6. Conclusion

Social spider algorithm (SSA) is a heuristic algorithm that is created by imitating spider behaviors in nature. SSA regulates search space of optimization problems as a high dimensional spider web. SSA can be easily adapted to real-world problems and an easy to apply heuristic algorithm. In this paper, the developed binary social spider algorithm both with crossover operator (BinSSA-CR) and without crossover operator (BinSSA) for feature selection problem is proposed. In order to obtain binary search space in BinSSA, eight different transfer functions (S-shaped and V-shaped) are used. According to transfer functions, eight different BinSSA variations (BinSSA1, BinSSA2, BinSSA3, BinSSA4, BinSSA5, BinSSA6, BinSSA7, and BinSSA8) have been developed and eight different BinSSA-CR variations (BinSSA1-CR, BinSSA2-CR, BinSSA3-CR, BinSSA4-CR, BinSSA5-CR, BinSSA6-CR, BinSSA7-CR, and BinSSA8-CR) have been developed. The ability of the balance between exploration and exploitation capabilities of BinSSA has been improved with the crossover operator. The variations of BinSSA and BinSSA-CR are operated in twenty-one different low, middle, and large-scaled benchmark test datasets in order to evaluate their performances. Each benchmark datasets is operated 20 times. Performance of variants of BinSSA and BinSSA-CR is compared in various criteria ((1) the mean and the standard deviation of fitness values, (2) the best and the worst of fitness values, (3) the mean of the accuracy, (4) the mean number of the selected features (5) the mean of CPU time). According to the mean of fitness results, the standard deviation of fitness results, the mean of accuracy values, and the mean number of the selected features, the best variation of BinSSA-CR is determined as BinSSA4-CR. Wilcoxon signed-rank test is applied to BinSSA4-CR and other BinSSA variations.

BPSO, BBA, and BGWO which are well-known heuristics algorithms in the literature are compared with the variations of

BinSSA4 and BinSSA4-CR. In order to the comparison to be fair, all comparison algorithms are run on equal parameters and on equal conditions. The Wilcoxon signed-rank test is applied to BinSSA4-CR variation with Binary Bat Algorithm (BBA), Binary Grey Wolf Optimization (BGWO), and Binary Particle Swarm Optimization (BPSO). According to the mean of fitness values, the mean of standard deviation values, the mean number of the selected feature, and the mean of accuracy, the performance of the BinSSA4-CR is superior. According to the means of fitness values and the means of accuracy results, Genetic Algorithm (GA), Particle Swarm Optimization (PSO), Ant Lion Optimization (ALO), and Grey Wolf Optimization (GWO) which are well-known heuristic algorithms in the literature are compared with BinSSA-CR. According to the results, the variations of BinSSA-CR offers quality solutions for most tests.

In future research, we will design new transfer functions. We will apply some local search algorithms to BinSSA to improve its performance on the high dimensional binary optimization problems.

## Compliance with ethical standards

### Ethical approval

This article does not contain any studies with human participants or animals performed by any of the authors.

### Declaration Of Competing Interest

There is no conflict of interest between the authors to publish this manuscript.

### Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:[10.1016/j.eswa.2020.113185](https://doi.org/10.1016/j.eswa.2020.113185).

### Credit authorship contribution statement

**Emine BAŞ:** Writing - original draft, Writing - review & editing.  
**Erkan ÜLKER:** Writing - original draft, Writing - review & editing.

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