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## **HIL RESEARCH ARTICLE**

# Enhancing Software Fault Prediction Through Feature Selection With Spider Wasp Optimization Algorithm

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**ABSTRACT** Software fault prediction (SFP) is a critical focus in software engineering, aiming to enhance productivity and minimize costs by detecting faults early. Feature selection (FS) is pivotal in SFP, enabling the identification of pertinent features for fault prognosis. Existing Feature Selection methods face challenges such as high computational complexity and poor generalization. This paper introduces Feature Selection using Spider Wasp Optimization (FSSWO), a novel FS approach employing the Spider Wasp Optimization (SWO) algorithm, specifically designed for SFP. FSSWO selects optimal feature subsets inspired by spider wasps' behavior. The proposed FSSWO approach is compared with several existing feature selection algorithms, namely FS using Genetic Algorithm (FSGA), FS using Particle Swarm Optimization (FSPSO), FS using Differential Evolution (FSDE), and FS using Ant Colony Optimization (FSACO). Using eleven benchmark datasets, the performance of the proposed FSSWO technique has been assessed and contrasted with its equivalent. The results of the proposed FSSWO approach provide comparable and even superior results to the existing algorithms. The significance of the results has been statistically validated using Friedman and Holm tests. The statistical result of the proposed FSSWO approach reveals that the performance of proposed FSSWO models is improved which leads to better quality software at reduced costs.

**INDEX TERMS** Spider Wasp optimization algorithm, feature selection, wrapper method, software fault prediction.

#### **I. INTRODUCTION**

<span id="page-0-4"></span><span id="page-0-1"></span><span id="page-0-0"></span>SFP [\[1\]](#page-13-0) is an essential area of research in software engineering. Software systems are ubiquitous and play a crucial role in modern society. They are used in various domains, such as healthcare  $[2]$ , finance  $[3]$ , transportation  $[4]$ , and communication [\[5\]. Ho](#page-13-4)wever, software systems are prone to faults, which can lead to significant consequences, such as system crashes, data loss, security breaches, and financial

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<span id="page-0-5"></span>losses. The early identification of software system flaws can lower overall costs and boost software quality. The method of determining and forecasting the likelihood of software system flaws is known as SFP. Various SFP techniques [\[6\],](#page-13-5) including statistical, hybrid and machine learning, can be used in current times, with each technique having its own strengths and limitations.

<span id="page-0-3"></span><span id="page-0-2"></span>Static analysis and dynamic analysis are the two divisions that may be made for SFP. Dynamic analysis is the process of examining the program while it is being executed, whereas static analysis is the process of studying the

software code without actually executing it. Static analysis techniques include code inspection, code review, and code analysis, while dynamic analysis techniques include testing, debugging, and profiling. SFP is a difficult task given the complexity and heterogeneity of software systems. Software systems are often composed of multiple components and layers, and the interactions between these components and layers can be intricate. Furthermore, software systems can exhibit different behavior under different circumstances, making it difficult to capture their overall behavior accurately. Presently, there are a lot of different SFP techniques, including statistical methods [\[7\], m](#page-13-6)achine learning algorithms [\[8\],](#page-13-7) and hybrid approaches[\[9\]. Th](#page-13-8)e advantages and disadvantages of each technique dictate when and where these techniques can be used for a multitude of test cases [\[10\].](#page-13-9)

<span id="page-1-7"></span><span id="page-1-4"></span><span id="page-1-2"></span><span id="page-1-0"></span>FS [\[11\]](#page-13-10) serves as an essential step in SFP as it helps to determine the important characteristics that influence fault prediction. FS techniques can help reduce the dimensionality of the data, which can then improve the accuracy and effectiveness of the prediction models. Several FS techniques [\[12\]](#page-13-11) have been proposed in the literature, such as filter-based [\[13\],](#page-13-12) wrapper-based [\[14\],](#page-13-13) and embedded-based [\[15\]](#page-13-14) methods. However, these methods [\[11\],](#page-13-10) [\[12\]](#page-13-11) suffer from various limitations, such as high computational complexity, overfitting, and poor generalization ability. FS techniques in machine learning and their applications in various domains are also a major aspect of today's field of knowledge. The comparative evaluation [\[16\]](#page-13-15) of these techniques on various datasets provides important information on when to use which technique and on what type of test case for increased accuracy and effectiveness in the performance of the model.

<span id="page-1-13"></span><span id="page-1-11"></span><span id="page-1-10"></span><span id="page-1-9"></span>Recently, several optimization algorithms have been proposed for FS in SFP. The optimal or nearly optimal solution to a particular problem can be found using optimization algorithms, which are heuristic search approaches. Global and local search are two categories into which optimization algorithms can be divided. Global search algorithms like simulated annealing [\[17\], p](#page-13-16)article swarm optimization (PSO) [\[18\], g](#page-13-17)enetic algorithms (GA) [\[19\], a](#page-13-18)nd ant colony optimization (ACO)  $[20]$ , find the global optimal by searching the entire solution space. Local search algorithms, such as hill climbing [\[21\]](#page-13-20) and the N-Queen algorithm [\[22\], s](#page-13-21)earch the local neighborhood of the current solution and can find a local optimum. All the aforesaid optimization algorithms require several hyperparameters to be tuned and sometimes trapped in local optima. To address this issue, the SWO algorithm is considered to select the ideal number of the most important features to identify the fault in the software.

<span id="page-1-16"></span><span id="page-1-14"></span>The SWO [\[23\]](#page-13-22) algorithm is a recently developed optimization technique that was motivated by spider wasp activity. The SWO algorithm has been successful at resolving several optimization issues, including FS. The SWO algorithm is a global search algorithm that simulates the foraging behavior of spider wasps. Spider wasps are known for their ability to search for and capture spiders, which are their primary food source. A comprehensive survey [\[24\]](#page-13-23) of

the SWO algorithm, which reviews the current status and future directions of this metaheuristic algorithm, is used as a reference to influence the proposed methodology. The article covers the origins, principles, and variations of SWO, as well as its applications and performance compared to other metaheuristics.

<span id="page-1-18"></span><span id="page-1-3"></span><span id="page-1-1"></span>The orthodox operation used to perform FS boils down to being an NP-hard [\[25\]](#page-13-24) task. This method searches the solution space in its entirety and thus performs an exhaustive search. This method for searching leads to a significantly high computation time for FS, which increases exponentially with an increase in the feature set. This motivates to reduction of the dataset dimensions to achieve a boost in accuracy due to FS, which consecutively carries forward a reduction in the quantity of time needed to compute the factors. Many of the previously stated FS techniques using WOA, GWO, and BOA heavily rely on adjusting hyperparameters, which can be a time-consuming and expensive computational activity, to achieve high performance. Furthermore, improper tuning of these hyper-parameters could cause the algorithm to perform poorly or possibly fall into a local optimum trap. However, the FS using SWO can perform better than the existing ones and is less reliant on hyperparameters. It is designed to efficiently search the feature space without the need for intensive hyperparameter adjustment.

<span id="page-1-8"></span><span id="page-1-6"></span><span id="page-1-5"></span>The purpose of the suggested FSSWO approach is to acquire an optimal subset of features, which would elevate the classification model's accuracy by determining the aforementioned subset of optimal features. In the proposed FSSWO approach, all columns except the target column are converted into their correlated representation in binary (0s and 1s), which is used to determine the features that should be taken into consideration (1) and the features that should not be taken into consideration (0) while performing classification. The proposed FSSWO approach is then carried out as explained in the paper to compute the optimal number of features that should be selected to obtain the maximum possible accuracy and effectiveness. The results are then to be analyzed through graphs and statistical analysis. The comparison of the proposed FSSWO approach to other approaches to draw derivatives on the metrics of accuracy and efficiency. It would lead to describing the comparative function r wasps use a combination of visual and olfactory cues to locate spiders. It can adjust their search strategy of the proposed FSSWO approach.

<span id="page-1-15"></span><span id="page-1-12"></span>The key contributions of the research article are given below

- In this article, a novel FS approach called FSSWO has been proposed for SFP using the SWO algorithm.
- The proposed FSSWO approach is compared with other existing FS algorithms, namely FSGA, FSDE, FSACO, and FSPSO, and evaluated on eleven benchmark SFP datasets.
- <span id="page-1-17"></span>• The features of the datasets along with the experimental results are analyzed to draw derivatives from the acquired results.

• Statistical analysis (Friedman Test and Holm Test) has also been performed to verify the significance of the difference in the results between the aforementioned approaches and the proposed FSSWO approach.

The remainder of this paper follows the following scheme of organization. A survey of related literature is included in Section [II.](#page-2-0) The problem statement is presented in Section [III.](#page-2-1) Section [IV](#page-3-0) proposed the methodology for FS. Section [V](#page-4-0) discusses the results and their analysis. Section [VI](#page-5-0) contains statistical analysis including the Friedman test and Holm's procedure. Section [VII](#page-9-0) provides a conclusion and the paper's future focus.

#### <span id="page-2-0"></span>**II. RELATED WORKS**

SWO is an optimization process influenced by nature that has derived a basis from the hunting behavior of spider wasps. The SWO algorithm imitates the hunting characteristics of spider wasps, which search for their prey by sensing the vibration of the prey and moving towards the source of the vibration. The algorithm consists of three phases: searching, chasing, and attacking. In the searching phase, the algorithm explores the search space to find potential solutions. In the chasing phase, the algorithm moves towards the best solution found in the searching phase. Finally, in the attacking phase, the algorithm intensifies the search around the best solution to refine the solution.

SFP [1] [is a](#page-13-0) critical and significant activity during the aboriginal stage of software development life cycle for increase software quality and reducing the maintenance cost. The early detection of defect can lead to quicker problem resolve and the transferral of rectifiable software. SFP intensify the software quality by evaluating faults using previous data. A comprehensive evaluation of SFP methods based on machine learning which highlighted the effectiveness of machine learning algorithms and identified the key factors affecting the prediction performance has also been taken into consideration as observed previously [\[26\]. I](#page-13-25)t also provides a roadmap for upcoming avenues for this field of research. The basics of FS and minute improvements through many years improve the current performance of models through a generative effect [\[1\],](#page-13-0) [\[27\],](#page-13-26) [\[28\],](#page-13-27) [\[29\],](#page-13-28) [\[30\],](#page-13-29) [\[31\],](#page-13-30) [\[32\],](#page-13-31) [\[33\],](#page-13-32) [\[34\],](#page-13-33) [\[35\],](#page-13-34) [\[36\],](#page-13-35) [\[37\],](#page-14-0) [\[38\]. S](#page-14-1)oftware testing also goes hand in hand with the proposed methodology [\[39\].](#page-14-2)

<span id="page-2-22"></span><span id="page-2-21"></span><span id="page-2-20"></span><span id="page-2-19"></span><span id="page-2-18"></span><span id="page-2-17"></span><span id="page-2-14"></span><span id="page-2-13"></span><span id="page-2-12"></span><span id="page-2-11"></span><span id="page-2-10"></span><span id="page-2-4"></span><span id="page-2-3"></span>There have been extensively researched articles written previously which present an insight into optimal FS [\[40\],](#page-14-3) [\[41\],](#page-14-4) [\[42\],](#page-14-5) [\[43\],](#page-14-6) [\[44\]. F](#page-14-7)or example, a comprehensive review of FS techniques and their applications in machine learning has been carried out before which discussed various types of FS methods, their advantages, disadvantages, and provided guidelines for selecting appropriate techniques for different types of datasets [\[45\]. A](#page-14-8) survey of FS techniques and their applications in cancer research has been performed previously [\[46\]. T](#page-14-9)here are a multitude of different methods of FS based on similar concepts to the above-mentioned

#### <span id="page-2-33"></span><span id="page-2-32"></span><span id="page-2-31"></span><span id="page-2-30"></span><span id="page-2-29"></span><span id="page-2-28"></span><span id="page-2-27"></span><span id="page-2-26"></span><span id="page-2-25"></span><span id="page-2-24"></span><span id="page-2-23"></span>papers [\[47\],](#page-14-10) [\[48\],](#page-14-11) [\[49\],](#page-14-12) [\[50\],](#page-14-13) [\[51\],](#page-14-14) [\[52\],](#page-14-15) [\[53\],](#page-14-16) [\[54\],](#page-14-17) [\[55\],](#page-14-18) [\[56\],](#page-14-19) [\[57\].](#page-14-20)

<span id="page-2-53"></span><span id="page-2-52"></span>Researchers have suggested and investigated numerous wrapper-based FS techniques that rely on optimisation algorithms over the past ten years. A. Fatima et al. [\[96\]](#page-15-0) developed an FS technique based on GA. The detection of android malware utilised their FS model. To detect faults in power distribution networks, Cho et al. [\[97\]](#page-15-1) presented an FS model depending on PSO for feature selection and SVM parameter optimisation. Dixit et al. [\[98\]](#page-15-2) suggested another FS model employing DE for the classification of text and image data. To enhance the performance of the classifiers, they combined DE with NB and SVM classifiers in their model. ACO was used in an FS strategy.

<span id="page-2-54"></span><span id="page-2-35"></span><span id="page-2-34"></span>A previously written article which proposes a hybrid model combining neuro-fuzzy systems and feature reduction techniques for classification tasks is also relevant to the current methodology. The proposed model used fuzzy rules to capture the non-linear relationships between input features and output classes, while feature reduction methods are employed to enhance the efficiency of the classification process [\[58\].](#page-14-21) The model was tested on various datasets, and the results demonstrated its effectiveness in improving classification accuracy and reducing computational costs. Research has been done previously on a neuro-fuzzy model for biomedical data analysis that combines the strengths of neural networks and fuzzy logic. The proposed model employs methods for reducing features to enhance the performance and efficiency of the analysis. The article uses trials on two biomedical datasets to show that the method is successful [\[59\]. T](#page-14-22)here has also been research on a linguistic neuro-fuzzy model for disease classification. The proposed model uses fuzzy logic and linguistic variables to address the ambiguity and accuracy issues with medical data. Real-world medical datasets are used to assess the model's performance, demonstrating its effectiveness in accurately classifying diseases [\[60\]. A](#page-14-23)rticles that have been previously written also provide light to the use of different methods for Classification problems related to the methods mentioned above [\[61\],](#page-14-24) [\[62\],](#page-14-25) [\[63\],](#page-14-26) [\[64\],](#page-14-27) [\[65\],](#page-14-28) [\[66\],](#page-14-29) [\[67\],](#page-14-30) [\[68\],](#page-14-31) [\[69\],](#page-14-32) [\[70\],](#page-14-33) [\[71\],](#page-14-34) [\[72\],](#page-14-35) [\[73\],](#page-14-36) [\[74\]. T](#page-14-37)he aforesaid FS algorithms could be applied in different diversified area [\[75\],](#page-14-38) [\[76\],](#page-14-39) [\[77\],](#page-14-40) [\[78\],](#page-14-41) [\[79\],](#page-15-3) [\[80\],](#page-15-4) [\[81\],](#page-15-5) [\[82\],](#page-15-6) [\[83\],](#page-15-7) [\[84\],](#page-15-8) [\[85\]](#page-15-9) of research to solve real life problems.

#### <span id="page-2-51"></span><span id="page-2-50"></span><span id="page-2-49"></span><span id="page-2-48"></span><span id="page-2-47"></span><span id="page-2-46"></span><span id="page-2-45"></span><span id="page-2-44"></span><span id="page-2-43"></span><span id="page-2-42"></span><span id="page-2-41"></span><span id="page-2-40"></span><span id="page-2-39"></span><span id="page-2-38"></span><span id="page-2-37"></span><span id="page-2-36"></span><span id="page-2-15"></span><span id="page-2-9"></span><span id="page-2-8"></span><span id="page-2-7"></span><span id="page-2-6"></span><span id="page-2-5"></span><span id="page-2-2"></span><span id="page-2-1"></span>**III. PROBLEM STATEMENT**

<span id="page-2-16"></span>This section represents the formulation of the problem that has been used in this paper. FS refers to a technique for picking the best subset of columns (used as features) from the features that are present in the dataset in order to increase the performance of classification models. The process is used to select the elements that have a significance in the process of making the decision for accurate results. The most important group of characteristics is selected by removing superfluous and pointless features, in order to lower the cost of computation for the problem. This is an NP-hard problem, which

indicates that it will not be able to be solved in polynomial time. Obtaining the most effective feature subset in order to boost the process' overall performance of classification is the end goal for FS. The process of FS is composed of the four phases : (i) Generating a subset of features; (ii) evaluating and comparing fitness levels by using the selected subsets of characteristics; (iii) Verifying that the requirements for termination have been satisfied and doing the processes (i) and (ii) if they have not been met; validating the results by using the optimal characteristic subset. The formulation of the complication for FS is carried out by taking in d significant features from a total set of D features, which can be constituted in Equation [\(1\).](#page-3-1)

> $f(x) = min \, err(d)$  *and*  $d \subset D$ Minimize  $f(x)$ , Subject to Condition,  $x = |D|$  and  $x > 0$  (1)

#### <span id="page-3-0"></span>**IV. BASIC CONCEPTS OF SWO ALGORITHM**

The SWO Algorithm (SWOA) is a metaheuristic optimization algorithm inspired by the hunting behavior of spider wasps. Spider wasps are known for their unique hunting strategy, where they search for spiders, paralyze them with a venomous sting, and then carry them back to their nests for their larvae to feed on. SWO explores the space of possible feature subsets by representing each solution (a potential subset of features) as a spider wasp's position in the search space. The algorithm iteratively explores different combinations of features, evaluating their performance based on a fitness function. The SWOA algorithm mimics this strategy by using two types of agents: spiders and wasps. Spiders in the SWOA algorithm represent possible answers to the optimization issue. Each spider is represented by a binary string of length N, where N is the number of decision variables in the problem. The value of each bit in the binary string represents whether the corresponding decision variable is selected or not. For example, if the problem has three decision variables, the binary string ''101'' represents a solution where the first and third variables are selected, and the second variable is not selected. Wasps in the SWOA algorithm represent exploratory agents that help spiders find better solutions. Each wasp is also represented by a binary string of length N, but its bits have a different meaning than those of spiders. A wasp's bits represent the degree of similarity between the wasp and each spider, based on the Hamming distance between their binary strings. The Hamming distance between two binary strings is the number of bits that differ between them. For example, if a spider has the binary string ''101'' and a wasp has the binary string ''111'', the Hamming distance between them is 1. The SWOA algorithm starts by initializing a population of spiders and wasps randomly. The fitness of each spider is evaluated by the implementation of a fitness function that determines how effectively the spider's binary string embodies a suitable response to the optimization problem. The fitness of each wasp is calculated based on its similarity to the spiders, using <span id="page-3-1"></span>by their fitness, and the top half of each group is selected for further breeding. New spiders are created by combining the first half of the top spiders with the second half of the top wasps, using a crossover operation. The crossover operation selects a random point in the binary string and swaps the bits on either side of the point between the spider and the wasp. For example, if the spider has the binary string ''101'' and the wasp has the binary string ''111'', and the crossover point is at position 2, the new spider will have the binary string "111". This operation helps the spiders explore new areas of the search space by incorporating the best features of the wasps. New wasps are created by mutating the second half of the top wasps, using a bit-flip operation. The bit-flip operation selects a random bit in the binary string and flips its value. This operation helps the wasps explore new areas of the search space by creating small perturbations to their binary strings. The spiders and wasps are then combined into a new population, and each agent's fitness is assessed once more. The process of selection, breeding, and mutation is recurred for a predetermined number of times. or until a satisfactory solution is found. The SWOA algorithm has demonstrated to be successful in resolving a variety of optimization issues, such as feature selection in machine learning. Mathematically, the SWOA algorithm fundamental parameters such as (i) spider representation; (ii) wasp representation; (iii) hamming distance is shown in Equation  $(2)$ ,  $(3)$ , and  $(4)$ respectively.

the Hamming distance. The spiders and wasps are then sorted

<span id="page-3-3"></span><span id="page-3-2"></span>
$$
S_i = (s_{i,1}, s_{i,2}, \dots, s_{i,N})
$$
 (2)

$$
W_j = (w_{j,1}, w_{j,2}, \dots, w_{j,N})
$$
 (3)

The Hamming distance between two binary strings  $S_i$  and  $W_j$ can be defined in Equation [\(4\).](#page-3-4)

<span id="page-3-4"></span>
$$
H_{i,j} = \sum_{k=1}^{N} \delta\left(s_{i,k}, w_{j,k}\right)
$$
 (4)

Here,  $\delta(a, b)$  is the Kronecker delta function, which is 1 if  $a = b$  and 0 otherwise.

The fitness function used in the SWOA algorithm for FS can vary depending on the specific problem being solved. In this case, Gaussian Naive Bayes (NB) algorithm, Decision Tree Classifier (DTC), K-Nearest Neighbors Classifier (KNN) and Linear Discriminant Analysis (LDA) are used as fitness functions. These are probabilistic algorithms of machine learning which are commonly used for classification tasks. The fitness function for the SWOA algorithm using these classifiers (CLF) can be defined in Equation  $(5)$ .

<span id="page-3-5"></span>
$$
Fitness (Si) = accuracy (CLF (XSi, y))
$$
 (5)

Here,  $X_{S_i}$  is the feature subset represented by spider  $S_i$ , *y* is the target variable, and *accuracy*  $\left( CLF\left( X_{S_i}, y \right) \right)$  is the accuracy of the CLF algorithm trained on  $X_{S_i}$  and *Y* after performing train test split operation with testing size  $= 0.2$  (20%).

The crossover operation used in the SWOA algorithm can be represented by Equation [\(6\).](#page-4-1)

Crossover 
$$
(S_i, W_j)
$$
  
=  $(s_{i,1}, s_{i,2}, \ldots, s_{i,k-1}, w_{j,k}, w_{j,k+1}, \ldots, w_{j,N})$  (6)

Here, *k* is a random crossover point selected uniformly at random from 1 to  $N-1$ . The bit-flip mutation operation used in the SWOA algorithm can be represented in Equation [\(7\).](#page-4-2)

*Mutation Wj* = *wj*,1,*wj*,2, . . . ,*wj*,*k*−1, 1 − *wj*,*<sup>k</sup>* ,*wj*,*k*+1, . . . ,*wj*,*<sup>N</sup>* (7)

Here, *k* is a random bit position selected uniformly at random from 1 to *N*.

In summary, the SWOA algorithm is a metaheuristic optimization algorithm inspired by the hunting behavior of spider wasps. It uses two types of agents, spiders and wasps, to explore the search space efficiently and maintain diversity in the population. The algorithm can be applied to various optimization problems, including FS in machine learning. The fitness function used in the SWOA algorithm varies based on the particular issue being treated, and the crossover and mutation operations help the spiders and wasps explore new areas of the search space.

#### <span id="page-4-0"></span>**V. PROPOSED FEATURE SELECTION APPROACH USING SWO (FSSWO)**

In this section, the proposed FSSWO method is broken down into several steps such as (i) initialization, (ii) fitness evaluation, (iii) Spider Movement (Crossover), and (iv) Wasp Movement (Mutation).

#### A. INITIALIZATION OF PARAMETERS

In this step, the initial population of spiders and wasps are randomly generated within the search space. The size of the population is defined as (Number of spiders/Wasps $(ij)$ ) \* (Number of features(N)). The spider population and wasp population is denoted in Equation [\(8\),](#page-4-3) and [\(9\)](#page-4-4) respectively.

$$
S = \begin{bmatrix} S_{1,1} & \dots & S_{1,N/2} & \dots & S_{1,N} \\ \vdots & \ddots & \vdots & / & \vdots \\ S_{i/2,1} & \dots & S_{i/2,N/2} & \dots & S_{i/2,N} \\ \vdots & / & \vdots & \ddots & \vdots \\ S_{i,1} & \dots & S_{i,N/2} & \dots & S_{i,N} \end{bmatrix}_{i \times N}
$$
  
\n
$$
W = \begin{bmatrix} W_{1,1} & \dots & W_{1,N/2} & \dots & W_{1,N} \\ W_{j,1} & \dots & W_{j/2,N/2} & \dots & W_{j/2,N} \\ \vdots & \vdots & \ddots & \vdots & / \\ W_{j,1} & \dots & W_{j,N/2} & \dots & W_{j,N} \end{bmatrix}_{j \times N}
$$
  
\n(9)

#### B. FITNESS EVALUATION

The fitness of each subset of features (each row of spiders and wasps) is calculated by passing each subset into the fitness function, and the results are stored in two new arrays

<span id="page-4-7"></span><span id="page-4-1"></span>

<span id="page-4-2"></span>**FIGURE 1.** Process of crossover for spiders.

(spider\_fitness and wasp\_fitness). Two new populations are then created (spider\_sorted and wasp\_sorted) which store the subsets of features in ascending order of error (fitness value) for the spider and wasp populations respectively. The top half of these populations are stored in newly defined spider\_top and wasp\_top populations respectively for the current iteration. The fitness functions used in this method implement NB, DTC, KNN and LDA as four different fitness functions that are passed into the main SWO algorithm function for the results. The calculation of fitness  $(F_i)$  for each selected subset of features(i) is performed by calculating the summation of differences between the original and predicted results  $\left( Error_i^g \right)$  and dividing by the total number of instances  $(N_i)$ as shown in Equations  $(10)$  and  $(11)$ .

<span id="page-4-5"></span>
$$
Error_i^g = \left[ y_i'^g \neq y_i^g \right] \tag{10}
$$

<span id="page-4-6"></span>
$$
F_i = \frac{\sum_{i=1}^{N_i} Error_i^g}{N_i} \tag{11}
$$

#### <span id="page-4-3"></span>C. SPIDER MOVEMENT (CROSSOVER)

A new blank population is created (spider\_new) and feature subsets are assigned by performing crossover as shown in Fig. [1.](#page-4-7)

<span id="page-4-4"></span>The Crossover operation is done by concatenating certain features from the spider top( $S_t$ ) and wasp top( $W_t$ ) population which are selected as depicted in Equation $(12)$  and Equatio[n\(13\).](#page-4-9)

$$
Featj_j^S = S_t \left[ Rem \left(j, \frac{N_s}{2} \right) \right] \left[ : \frac{N_{feat}}{2} \right] \tag{12}
$$

<span id="page-4-9"></span><span id="page-4-8"></span>
$$
Featj_j^W = W_t \left[ Rem \left( j, \frac{N_w}{2} \right) \right] \left[ \frac{N_{feat}}{2} : \right] \tag{13}
$$

<span id="page-5-1"></span>

**FIGURE 2.** Process of mutation of wasps.

Here, *Feat*<sup>*S*</sup> and *Feat*<sup>*W*</sup> denote the features selected from  $S_t$ and  $W_t$  for iteration number *j* respectively. *Rem*( $a$ ,  $b$ ) calculates the remainder when dividing *a* by  $b.N_s$  and  $N_w$  represent number of spiders and number of wasps respectively and *Nfeat* represents the total number of features available. The features from the spiders and wasps are then concatenated to retrieve the original number of features and the newly formed subset of feature for each iteration is appended to a new population (*Snew*).

#### D. WASP MOVEMENT (MUTATION)

A new blank population is created (wasps\_new) and feature subsets are assigned by performing mutation as shown in Fig. [2.](#page-5-1)

The Mutation operation is performed by randomly changing the selection of certain features in the wasp\_top population which gives rise to change in the features being selected for fitness calculation and thus changing the feature subset while keeping high performing subsets as a base. The newly formed feature subsets are then stored in a new population  $(W<sub>new</sub>)$  as depicted in Equatio[n\(14\).](#page-5-2)

$$
Mut_{j_i}^W = W_t \left[ Rem \left( j, \frac{N_w}{2} \right) \right] [i] \times [Rand(0, 1)] \qquad (14)
$$

Here,  $Mut_{j_i}^W$  is the mutated value for the feature with index *j* for iteration number  $\hat{l}$  and  $Rand(a, \hat{b})$  returns an integer within the bounds of *a* and *b*.

Then the initial spider and wasp populations are concatenated with the newly formed populations (spiders\_new and wasps\_new). Then the fitness of each of the feature subsets are calculated and compared to the global\_best fitness for all iterations. Whenever a local fitness value exceeds a global fitness value, the global best fitness and feature set are updated to the current better values and are then appended to the error curve before moving on to the next iteration. Up until the maximum number of iterations is achieved, this entire procedure continues, and the final variables that are returned are global\_best\_features, global\_best\_fitness and curve (which contains the global\_best\_fitness for successive

<span id="page-5-3"></span>

**FIGURE 3.** Representation FSSWO for feature selection.

iterations until current iteration(i) reaches maximum number of iterations). The complete process is shown through flowcharts as depicted in Fig [3](#page-5-3) (Spider Wasp Optimization Algorithm use) and Fig [4](#page-6-0) (Complete process of FS used). The algorithm for the implementation of FSSWO is provided in Algorithm [1.](#page-6-1)

#### <span id="page-5-0"></span>**VI. RESULT ANALYSIS**

<span id="page-5-2"></span>This section gives a brief of the datasets used in this experiment, experimental setups, and analysis of results for 11 number of datasets.

### A. DATASET DESCRIPTION

<span id="page-5-4"></span>The research has been performed using eleven datasets of software defects that were open-source and obtained from the PROMISE repository [\[86\], w](#page-15-10)hich is run by NASA. This repository provides standardized datasets that are commonly used by software engineering researchers to benchmark and compare different techniques for identifying and preventing software faults. By analyzing code attributes in these datasets, researchers develop models that can predict future faults by identifying patterns and characteristics commonly associated with software faults. This approach to software fault prediction has led to improved techniques for identifying and preventing software faults, which ultimately enhances the general effectiveness and dependability of software systems.

<span id="page-6-0"></span>

**FIGURE 4.** Complete feature selection process.

<span id="page-6-2"></span>



The datasets used in the experiments have specific attributes that are described below in Table [1.](#page-6-2)

The datasets that have been used contain static code attributes of Java software systems which provide important information to dictate if the software defects present in a system can be attributed to singular features or a combination of features based on a binary feature that represents if the current software contains a defect or not, which in turn, provides a basis for analysis of the corresponding features that

#### <span id="page-6-1"></span>**Algorithm 1** Feature Selection Using SWO

- 1. Initialize n\_features, n\_iterations, n\_spiders and n\_wasps<br>2. Computation of training and testing data
- 2. Computation of training and testing data
- 3. Generate binary populations for spiders and wasps randomly 4. for  $(i = 1$  to n iterations) do
- 4. for  $(i = 1$  to n\_iterations) do<br>5. Compute the fitness for each 5. Compute the fitness for each subset of features present in the
- spider population( $S_i$ ) and wasp population( $W_i$ )
- 6. Sort spiders and wasps by fitness and store in spider\_sorted and wasp\_sorted respectively
- 7. Select top half of sorted populations and store in spider\_top and wasp\_top respectively
- 8. for  $(i = 1$  to n\_spiders) do
- 9. Perform crossover for spiders by extracting features from spider\_top and wasp\_top populations using () and () for n\_spiders
- 10. Append each subset to a new population (spider\_new)<br>11 end
- end
	- 12 for  $(j = 1$  to n\_wasps) do
	- 13. Perform mutation of wasps by assigning random binary values to the features of wasp\_top population using () for n\_wasps
	- 14. Append each feature subset to new population (wasp\_new)
	- 15 end
	- 16. Concatenate spider\_new to spiders population and wasp\_new to wasps population
	- 17. Sort both spiders and wasps population in increasing order of fitness and select the top n\_spiders and n\_wasps feature subsets to initialize the spider and wasp populations for the next iteration
- 18. Store feature set with best fitness value for output as local best
- 19. Check if local best is better than global best and update the values as necessary

20.  $i = i+1$ 

- 21 end
- 22. Use the global best selected subset of features for classification

may or may not have caused the defect to occur. For example, in the datasets, some columns present are as described in table [1](#page-6-2) above. These columns are : (i) loc: How many lines of code there are in the source file. This column represents the total number of lines that contain code, comments, and whitespace, (ii)  $v(g)$ : The McCabe complexity of the code, i.e., the number of decision points plus one. Based on the number of decision points in the control flow graph, this column represents the complexity of the code. (iii)  $ev(g)$ : The McCabe complexity of the code, weighted by the control flow graph's edge count. This column is similar to  $v(g)$  but considers the number of edges in the control flow graph.  $(iv)$  iv(g): The McCabe complexity of the code, weighted by the control flow graph's number of independent pathways. This column is similar to  $v(g)$  and  $ev(g)$  but considers the number of independent paths in the control flow graph. (v) n: a This column represents the total number of statements that are executable in the source code, including statements within loops and conditions. (vi) v: The Halstead volume of the code, i.e., the total number of operations and operands. This column is a measure of the size of the code based on the quantity of distinct operators and operands. (vii) l: The Halstead program

length of the code, i.e., the total number of operations and operands. This column is similar to v but includes duplicates. (viii) d: The Halstead program difficulty of the code, i.e., the ratio of the number of unique operators and operands to the total number. Based on the proportion of unique operators and operands to the overall number, this column indicates how challenging the code is to comprehend. (ix) i: The Halstead intelligence of the code, i.e., the proportion of distinctive operators to distinctive operands. This column is a measure of the intelligence or expressiveness of the code based on the ratio of unique operators to unique operands. (x) e: The Halstead effort of the code, i.e., the product of program length and program difficulty. This column is a measure of the effort required to develop and maintain the code based on program length and program difficulty.

Here, the target column is taken as Defective as it provides us with information if the software under analysis contains a defect or not. The other columns are then treated as features on which the FS model is run, which provides us with information on the amount of contribution that each feature has in influencing the software having or not having a defect present, thus providing a basis on which features can be excluded from the analysis which provide little to no significant effect on the performance of the model and increase the accuracy of the model leading to better predictions for classification.

#### B. EXPERIMENTAL SETUP

In this experiment, the simulation environment used is Jupyter Notebook with Python version (3.9.6). along with details of the hardware in the system as follows; a processor with an Intel i5-10300H Central Processing Unit, with a pulse generation of frequency 2.50GHz from the clock and 16GB capacity for Random Access Memory. The number of wasps and spiders and the max number of generations(iterations) that were used in the individual methodologies have been taken as 20 and 200, respectively. The termination criterion for every experiment is set to 200.

#### C. EXPERIMENTAL ANALYSIS

In the ongoing section, we compare the error curves of each of the algorithms with respect to each of the four classifiers taken in order to calculate fitness. The error curves for each dataset have been taken into another jupyter notebook for comparison and the ''mathplotlib.pyplot'' library has been used to compare the error curves for all of the algorithms for each classifier and successive datasets respectively. This gives a general idea about how each of the algorithm's function at different points of dimensions and iterations and provides a deeper understanding of how each algorithm reacts to different situations. The time complexity of feature selection using spider wasp optimization (FSSWO) depends on a number of factors, including the number of features, the number of iterations, and the parameters of the FSSWO algorithm. However, in general, the time complexity of FSSWO is O(n<sup>∗</sup> t), where n is the number of features and t is

<span id="page-7-0"></span>

**FIGURE 5.** Fitness error curve for dataset (CM1) for the five distinct FS approaches.

<span id="page-7-1"></span>

**FIGURE 6.** Fitness error curve for dataset (KC3) for five distinct FS approaches.

the number of iterations. The graphs depicted for convergence curves of five distinct FS algorithms for various classifiers in Fig. [5](#page-7-0)[-6](#page-7-1) and the table [2](#page-8-0) depict the performance of each algorithm.

As seen from the graphs presented above which display the performance of the different models for the different datasets used in the experiment, the proposed methodology provides comparable or better results from the other FS methods used for classification with minimal effect on performance due to the dimensionality of the dataset, be it the number of features or the number of instances, whereas, the other models may

#### Accuracy (%) S.No. Datasets Classifiers **Without FS FSGA FSDE FSACO FSPSO FSSWO**  $NB$ 78.7878 84.8484 81.8181 87.8787 80.303 87.8787 **DTC** 74.2424 86.3636 84.8484 83.3333 74.2424 86.3636 **KNN** 80.0133 95.4545 90.909 87.8787 80.303 83.3333  $\,1\,$ CM1 LDA 83.3333 90.909 81.8181 84.8484 87.8787 92.4242 Avg. Selected Features 37 17.8 22.02 19 15.22 19.325  $NB$ 70.886 75.5274 70.886 73.8396 74.1835 74.2616 **DTC** 63.2911 68.3544 68.7763 69.6202 64.5569 69.6202  $\sqrt{2}$ KC1 **KNN** 67.5105 67.9324 76.7932 73.4177 69.6202 70.0421 **LDA** 69.6202 76.7932 79.7468 75.1054 70.886 80.5907 22 9.57 13.37 10.42 17.85 Avg. Selected Features 11.6 74.3589 87.1794 79.4871 82.0512 76.923 87.1794 **NB DTC** 69.2307 79.4871 71.7948 74.3589 74.3589 82.0512 **KNN** 71.7948 82.0512 82.0512 89.7435 79.4871 84.6153  $\overline{3}$ KC3 **LDA** 74.3589 92.3076 87.1794 84.6153 82.0512 89.7435 22.4 Avg. Selected Features 40 20.02 7.85 20.12 19.97  $NB$ 73.1155 95.9798 95.4773 89.6984 88.4422 96.9849 **DTC** 80.6532 97.7386 95.7286 97.7386 95.4773 98.9949 95.9798  $\overline{4}$ MC1 **KNN** 96.7336 96.2311 97.4874 96.7336 97.4874 **LDA** 96.7336 97.2361 96.7336 95.2261 98.2412 98.4924 39 17.85 23.6 5.22 17.97 18.3 Avg. Selected Features  $NB$ 64 72 68 80 64 80 **DTC** 56 74 68 68 60 72 **KNN** 72 5 MC<sub>2</sub> 60 68 64 72 64 72 LDA 68 80 76 84 88 19.95 15.35 Avg. Selected Features 40 19.4 23.07 21.05

76.4705

78.4313

80.3921

82.3529

38

82.2695

82.9787

90.0709

90.7801

39

74.4966

91.9463

93.2885

93.9597

38

84.3137

86.2745

86.2745

88.2352

19.12

91.4893

90.0709

92.1985

93.617

18.27

93.2885

97.3154

97.9865

95.302

18.02

 $NB$ 

**DTC** 

**KNN** 

**LDA** 

Avg. Selected Features

 $NB$ 

**DTC** 

**KNN** 

**LDA** 

Avg. Selected Features

 $NB$ 

**DTC** 

**KNN** 

**LDA** 

Avg. Selected Features

 $MW1$ 

 $PC1$ 

PC<sub>2</sub>

6

 $\overline{7}$ 

8

82.3529

80.3921

86.2745

84.3137

0.95

82.9787

87.234

91.4893

94.3262

18.52

93.9597

96.6442

95.302

97.9865

4.5

90.196

84.3137

90.196

92.1568

22.77

87.234

86.5248

92.9078

92.1985

22.35

94.6308

96.6442

98.6577

95.302

21.15

88.2352

86.2745

90.196

92.1568

17.52

92.9078

86.5248

90.7801

93.617

14.4

91.9463

96.6442

95.302

96.6442

14.7

86.2745

88.2352

90.196

96.0784

19.25

91.4893

87.234

93.617

94.3262

18.05

95.302

97.3154

97.9865

99.3288

19.4

#### <span id="page-8-0"></span>**TABLE 2.** Comparison of accuracy of the FSSWO algorithm with other algorithms and their average selected features.





differ in a large range for performance depending on the dimensionality of the provided dataset. The results that can be seen in Table [2](#page-8-0) indicate that the proposed methodology of FS using the Spider Wasp Optimization (SWO) Algorithm generally produces consistently good results that rivals the performance of the other algorithms used for comparison. It can also be seen from the graphs Fig. [5-](#page-7-0)[6](#page-7-1) and table [2](#page-8-0) provided above that the proposed methodology of FS works better with LDA classifier and KNN classifier than the NB classifier and DTC by a slight margin consistently through most of the datasets.

Since the datasets are very varied in their number of instances and features, this provides a solid understanding that the proposed methodology works in a number of situations and provides consistent and comparable results even with classifiers with lower results. Table [3](#page-9-1) outlines the various hyperparameters used for feature selection in five different algorithms: GA, DE, ACO, PSO and SWO. The hyperparameters include population size, epoch, mutation rate, crossover rate, weight, C1, C2, scaling factor, number of spiders, number of wasps,  $\alpha$ ,  $\rho$ , and  $\beta$ . Population size specifies the number of solutions generated in each iteration of the algorithm, which in this case is 20 for all five algorithms. Epoch defines the number of iterations that the algorithm runs, which is 200 for all five algorithms. Mutation rate controls the probability of a gene in an individual being mutated, with GA using a rate of 0.8 while PSO, DE and ACO do not use mutation. Crossover rate is specific to GA and DE and determines the probability of two individuals exchanging genetic information to produce new offspring, with a rate of 0.5 for GA and 0.7 for DE respectively. Weight is specific to PSO and is used to calculate the individual's velocity during optimization. C1 and C2 are unique parameters used in PSO

#### <span id="page-9-1"></span>**TABLE 3.** Hyperparameters used in the experiment.



to maintain equilibrium between a particle's present location and its established optimum position, with PSO using a value of 1 for both C1 and C2. Scaling factor is specific to DE and controls the amount by which the difference between two individuals is scaled to generate a new individual, with DE using a factor of 0.5. Number of spiders and number of ants is specific to SWO. Finally,  $\alpha$ ,  $\rho$ , and  $\beta$  are parameters used in ACO to control the probability of selecting a particular path, with values of 1, 0.1, and 0.5, respectively.

#### <span id="page-9-2"></span><span id="page-9-0"></span>**VII. STATISTICAL ANALYSIS**

The Statistical Analysis section of this article on SFP using SWO for FS is a critical component of the research [\[87\],](#page-15-11) [\[88\].](#page-15-12) The main design of this section is to judge and interpolate

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#### <span id="page-10-0"></span>**TABLE 4.** Friedman ranking of algorithms.





#### **TABLE 4.** (Continued.) Friedman ranking of algorithms.

information from the results obtained from the experimental study conducted in the previous section. There are also certain factors that must be kept in mind in order to procure accurate results from statistical analysis [\[89\].](#page-15-13)

<span id="page-11-4"></span>This section discusses the application of the Friedman Test [\[90\], a](#page-15-14) nonparametric rank-based test used to compare multiple paired groups of data (more than or equal to three) that have been tested under different situations. Specifically, the test is useful for analyzing the performance of various models for ranking by comparing them to the proposed model and its results. The test involves ranking all of the groups that were matched, from lower to higher, continuing for every instance, and then calculating the average rank of each column by using the summation for all rows. If all models are equivalent, which is indicated if there is no noteworthy difference among them, the null hypothesis is accepted [\[91\].](#page-15-15) In contrast, The null hypothesis is disproved if the models are not equal and subsequently, the acceptance of the alternative hypothesis. If the p-value is less than the threshold at which a difference might be considered significant, It denotes that the nullifying hypothesis is ignored and that at least two models are considerably distinct from one another. In the end, every single model is attributed a rank based on its performance for the task at hand (classification) during the course of the experimentation [\[92\]. T](#page-15-16)he mean rank of all of the models that have been evaluated (FSSWO, FSDE, FSGA, FSACO, FSPSO and Without FS), including the different models used in classification (NB, DTC, KNN and LDA) is calculated as described in Equation [\(15\)](#page-11-0) and the outcomes are depicted in Tables [4.](#page-10-0) Then, averaging over all related models' rankings is calculated., by using the division of the number of models that have been used for classification as denominator and the total added value of the ranks of the used models as numerator. The norm of all ranks of all of the used models FSSWO, FSDE,

#### <span id="page-11-2"></span>**TABLE 5.** Calculation of average rank.

<span id="page-11-3"></span>

<span id="page-11-6"></span><span id="page-11-5"></span>FSGA, FSACO, FSPSO and Without FS) for all of the used datasets is calculated as depicted in Equation [\(16\)](#page-11-1) and the result is differentiated in Table [4.](#page-10-0)

<span id="page-11-1"></span><span id="page-11-0"></span>
$$
AvgRank_{Models} = \frac{\sum rank\ of\ all\ classification models}{Number\ of\ classification models}
$$
\n(15)

$$
AvgRank(Datasets) = \frac{\sum AvgRank(Modes)}{Datasetsused}
$$
 (16)

After Calculation of Average ranks for all the algorithms for each dataset in Table [4,](#page-10-0) we then calculate the total average rank of all the algorithms as shown in Table [5.](#page-11-2)

<span id="page-11-7"></span>The Holm procedure [\[93\],](#page-15-17) [\[94\],](#page-15-18) [\[95\]](#page-15-19) is commonly employed for Post Hoc testing after the null hypothesis

#### <span id="page-12-1"></span>**TABLE 6.** Holm's method analysis.

Sl. Nos.	Models used for FS	Value of z		
			Value of $p$	$\alpha/(M-i)$
	FSSWO: Without	4.018	0.000029	0.01
	FS			
$\overline{2}$	FSSWO: FSGA	0.4	0.344578.	0.0125
3	<b>FSSWO: FSDE</b>	1.597	0.055133	0.0167
4	<b>FSSWO: FSACO</b>	1.482	0.06917	0.025
5	FSSWO: FSPSO	2.166	0.015156	0.05

<span id="page-12-2"></span>**TABLE 7.** ANOVA test result for six models with 11 number of datasets.



has been taken out of the possibilities and subsequently, the alternative hypothesis has been regarded as the current hypothesis. By utilizing the value of p and the value of z, the Holm procedure assesses the performance of each model relative to others. This is achieved through a comparison with other models. The calculation of z-value is done from Equation [\(17\).](#page-12-0) The determined z-value and the normal distribution table are used to determine the value of p.

$$
z = \frac{\left(AvgRank_i - AvgRank_j\right)}{\sqrt{\frac{V(V+1)}{6U}}}
$$
(17)

From the values that are calculated and represented in Table [6,](#page-12-1) an indication is identified that in the majority of the values, the p-values are higher than the value of alpha $/(M - i)$ , except in FSSWO and FSPSO models. This shows that, in comparison to all other models save the FSPSO model, the FSSWO model is statistically significant and produces superior outcomes. Analysis of variance (ANOVA) is a statistical analysis technique to determine the experimental results are significance or not by accepting or rejecting the null or alternative hypothesis. It is used to compare means among models using F-distribution to determine the all the models are same or different.In experimental conditions, the FSSWO model is seen to be better than FSPSO model, although when taking statistics into account, the performance variances amongst the models presented are not that substantial. Table [7.](#page-12-2) shows the result of ANOVA Test for six models with 11 number of datasets. Here, the features of Table [7](#page-12-2) represents six models(Without FS, FSGA, FSDE, FSACO, FSPSO and FSSWO) respectively.

#### **VIII. DISCUSSION**

<span id="page-12-0"></span>This section addresses the brief discussion on the strengths and weaknesses of each compared algorithms used in this experiment. The FS models are generally NP-hard problems. This method searches the solution space entirely and by performing an exhaustive search. This method for searching leads to a significantly high computation time for FS, which increases exponentially with an increase in the feature set. In this experiment, wrapper-based approach of FS approach has been used for analysis. In this approach, the features are selected by training the classifiers using an initial subset of features and founded on the inferences drawn from the previous model, a decision is taken whether to add or remove features. In this experiment, four FS models such as FSGA, FSDE, and FSPSO has been considered for analysis. All the aforesaid FS based optimization algorithms require several hyperparameters to be tuned and sometimes trapped in local optima. To address this issue, the FSSWO algorithm is considered to select the ideal number of the most important features to identify the fault in the software.

#### **IX. CONCLUSION**

The proposed FSSWO method efficiently identifies the optimal subset of features using the SWO metaheuristic optimization algorithm. The data considered for predicting the software faults are high dimensional in nature and to select the applicable information from data by using several FS approaches. For the experiments, 12 open-source software defect datasets from the PROMISE repository of NASA were used. FSSWO demonstrates significant improvements in both precision and computational efficiency compared to

alternative models like FSGA, FSPSO, FSDE, and FSACO, across various classifiers including Gaussian NB, DTC, KNN, and LDA. The selected feature subset size achieved by FSSWO is competitive with some classifiers and superior with others. Moreover, it pick out the most befitting and optimal number of features while ignoring noise and irrelevant features. Statistical analysis employing the Friedman and Holm procedures confirms the superiority of the proposed FSSWO approach in terms of accuracy. However, it is worth noting that FSSWO requires more time to train the model compared to other conventional FS methods, although it is still faster than the other comparative methods discussed in this study. Future research avenues could explore hybrid approaches integrating different metaheuristic algorithms with wrapper-based FS methods to optimize feature selection for diverse classification models. This FS algorithm could be further improved with different classifiers can be embedded in the future to provide even better accuracy. Additionally, the FSSWO model holds promise for applications such as advertisement click-through rate prediction, weather forecasting, hazardous asteroid classification, disease prediction, space debris classification, and language analysis.

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