

An Improved Adaptive Spiral Dynamic Algorithm for Global Optimization

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ABSTRACT

This paper proposes a new strategy to enhance the performance and accuracy of the Spiral dynamic algorithm (SDA) for use in solving real-world problems by hybridizing the SDA with the Bacterial Foraging optimization algorithm (BFA). The dynamic step size of SDA makes it a useful exploitation approach. However, it has limited exploration throughout the diversification phase, which results in getting trapped at local optima. The optimal initialization position for the SDA algorithm has been determined with the help of the chemotactic strategy of the BFA optimization algorithm, which has been utilized to improve the exploration approach of the SDA. The proposed Hybrid Adaptive Spiral Dynamic Bacterial Foraging (HASDBF) algorithm is designed so that the chemotaxis phase of bacteria represents the exploration part of the search operation. In contrast, the SDA represents the exploitation part.

Additionally, to improve search operation efficiency, the spiral model's radius and angular displacement are adaptively set according to a linear correlation concerning the fitness value. An additional phase, the elimination and dispersal phase, is obtained from BFA and added to the end of the SDA. This phase aims to improve the algorithm's final solution's accuracy by enhancing the algorithm's search strategy and performance. Simulation tests are run on unimodal and multimodal standard benchmark functions to verify the proposed algorithm. The proposed algorithm significantly outperforms SDA and Adaptive SDA (ASDA) algorithms regarding fitness value and accuracy.

Keywords: Hybrid algorithm, Spiral dynamics, Bacterial foraging, Optimization algorithm.

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خوارزمية ديناميكية لولبية متكيفة مُطورة للتحسين الشامل

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الخلاصة

يقترح هذا البحث استراتيجية فريدة لتحسين أداء ودقة خوارزمية الديناميكا الحلزونية (SDA) للاستخدام في حل المشكلات العملية الحقيقية من خلال دمج خوارزمية SDA مع خوارزمية التغذية الراجعة البكتيرية (BFA). يعتبر حجم الخطوة الديناميكي لخوارزمية SDA منهج استثمار مفيد. ومع ذلك، فإنه يحد من التنوع في البحث خلال طور التنوع للخوارزمية، مما يؤدي إلى الاحتجاز في القيم المثلى المحلية. وللمحد من ذلك، فقد تم تحديد الموضع الأمثل لبدء خوارزمية SDA بمساعدة استراتيجية الكيموتاكتيك لخوارزمية BFA التي تم استخدامها لتحسين القدرة التقييمية لخوارزمية SDA. وقد تم بناء خوارزمية الديناميكا الحلزونية والتغذية الجرثومية الهجينة التكيفية (HASDBF) بحيث تمثل مرحلة التغذية الكيموتاكتيكية للجراثيم الجزء التقييمي من عملية البحث، بينما يتم تمثيل جزء الاستثمار بواسطة SDA. بالإضافة إلى ذلك، لتحسين كفاءة عملية البحث، تم تعيين نموذج اللولب الديناميكي وزاوية الانحراف بشكل تكيفي وفقاً للترابط الخطي المتعلق بقيمة اللياقة. بالإضافة إلى ذلك، تم الحصول على مرحلة إضافية تسمى مرحلة الإزالة والتشتت، من BFA وإضافتها إلى نهاية SDA. والهدف من هذه المرحلة هو تحسين دقة الحل النهائي للخوارزمية من خلال تحسين استراتيجية البحث وأدائها. تم اختبار الخوارزمية الجديدة من خلال اختبارات المحاكاة على مجموعة متنوعة من المعادلات القياسية المعيارية الاحادية والمتعددة للتحقق من أداء الخوارزمية المقترحة. وقد أظهرت النتائج تفوق الخوارزمية المقترحة بشكل كبير على خوارزميات SDA و SDA التكيفية (ASDA) فيما يتعلق بقيمة اللياقة والدقة.

الكلمات الرئيسية: خوارزمية هجينة، ديناميكية اللولب الحلزوني، التغذية الجرثومية، خوارزمية التحسين.

1. INTRODUCTION

An optimization problem's optimal solution can be achieved by using a metaheuristic, an iterative process of a variety of subordinate heuristics free of gradients that combine a simple local search approach with an advanced search method (Micev et al., 2021). Researchers all over the world focus on how metaheuristic algorithms can be used to solve problems in the real world. These algorithms draw their inspiration from biological or natural phenomena. Spiral dynamic algorithm (SDA), Bacterial foraging algorithm (BFA), Biogeography-based optimization (BBO), Cuckoo search optimization (CSO), and Galaxy-based search algorithm (GSO) are some examples of the recently introduced algorithms (Passino, 2002; Simon, 2008; Yang and Deb, 2009; Hosseini, 2011; Tamura and Yasuda, 2011a; Sharma et al., 2019; Jawad and Hadi, 2019). These algorithms are becoming increasingly popular because of their efficiency and effectiveness in dealing with practical problems.

As a metaheuristic algorithm, the SDA is motivated by spiral patterns in nature (Tamura and Yasuda, 2011a). A variety of real-world problems have been addressed through the application of SDA. Since its structure is simple, it can be computed quickly. Using four kinds



of benchmark functions with varied spiral angles, **(Tamura and Yasuda, 2011b)** compared SDA's performance to that of Differential Evolution (DE) **(Kasaiezadeh et al., 2014)** and Particle Swarm Optimization (PSO) methods **(Abbas and Abdulsahab, 2016)**. After 100 experiments with various dimensions, they found that the SDA performed better than the PSO and DE at the spiral angle of $\pi/2$.

Simple and effective tactics, like those used in the SDA, ensure that the algorithm's diversification and intensification components remain in the early and late stages of the trajectory, respectively. The search area is wider early in the spiral trajectory and narrows toward the end, where the optimal solution is situated in the center; the radius decreases gradually to give dynamic step size. Given that the distance from any given point on a path trajectory to the path's center constantly changes as its radius changes, making the radius a crucial convergence parameter for the method. The SDA algorithm excels due to the spiral dynamics model it employs. The original SDA's rotating angle and radius remained constant throughout the search. Therefore, when confronted with high-dimensional problems, The algorithm converges to and stays in local optima **(Nasir et al., 2013a; Nasir et al., 2014; Nasir et al., 2015a)**. Several attempts made by researchers to improve the algorithm's performance yielded different versions of the algorithm that involved either modifying the technique of searching or using a hybrid algorithm. To prevent trapping in the local optima, an adaptive formulation for varying the spiral model's radius and displacement is introduced **(Nasir et al., 2012a; Nasir et al., 2013b)**. They proposed that the radius and rotational angle continuously vary using exponential, quadratic, and linear functions. Fuzzy logic and a non-mathematical method were utilized to associate fitness values with the spiral's radius and arrive at a suitable place inside the searching area. Dimensionally distinct unimodal and multimodal reference functions were used to evaluate the algorithm's performance.

In **(Nasir et al., 2016)**, an enhanced version of the spiral dynamics algorithm called the linear adaptive spiral dynamics algorithm (LASDA) is suggested. In LASDA, a new mathematical equation is used to modify the angular displacement and spiral radius according to a linear function that shows a connection between the angular displacement, the fitness value, and the spiral radius. The results of LASDA are demonstrated regarding fitness accuracy and convergence speed to the optimal point and compared to those of SDA, BFA, and IBFA. It was found that the proposed method was more effective at finding the optimal solution.

Many studies have used hybridization, where one algorithm is combined with another, to improve the algorithm's performance. For example, the research of **(Nasir et al., 2012b)** has created a combination of SDA and BFA in which the algorithm permits the bacterium swimming and tumbling in a spiral shape during the search. Because of this, the algorithm's capability for exploration was increased. On the other hand, the adaptive approaches described by **(Nasir et al., 2012a; Nasir et al., 2013b)** improved the performance by changing the radius and the rotation angle with each iteration. Also, based on step size variation, **(Nasir et al., 2015b)** presented a hybrid technique by merging the SDA algorithm with the BFA. In light of the bacterial swimming mechanism, they offered two different approaches. The first involves the bacteria swimming in a spiral to find the optimal value, while the second involves a random process. With a random strategy, the bacteria can swim freely about their current location, increasing their probability of discovering the best possible value. In spiral swimming, however, the spiral itself determines the search direction. According to the supplied data, the spiral swimming strategy is superior to the random swimming method.



To enhance the SDA's exploration capabilities, **(Nasir et al., 2015a)** adopted a BFA elimination dispersal approach. The issue of settling on local optima can be reduced by expanding the capacity of the search space to discover more suitable solutions. The strategy was evaluated using a variety of benchmark function tests and analyses. Furthermore, by instructing the bacteria to swim spirally, the authors have created a hybrid technique combining SDA and BFA **(Nasir et al., 2013a)**. Two distinct hybrid methods were developed by sequentially combining SDA and BFA. The SDA or BFA is carried out initially, and the other is carried out. According to **(Nasir et al., 2012b)**, this method can solve the algorithm's high-dimensionality problem. The first hybrid approach that has been presented can provide a higher level of fitness accuracy, but it suffers from a significant computational time disadvantage as it takes longer to complete the SDA and BFA stages than the original SDA. The method was created by incorporating spiral search patterns into the exploration and chemotaxis phases. The bacteria are progressively led in a spiralling pattern toward the optimal solution at each round of the search process. The proposed method is a development of the first hybrid technique presented by **(Nasir et al., 2013a)**. In the first phase, bacteria utilize chemotaxis for exploration, whereas in the second phase, they employ spiral movement for exploitation. The hybrid spiral-dynamic bacteria-chemotaxis (HSDBC) combines the spiral-dynamic algorithm (SDA) with the bacterial chemotaxis utilized in the bacterial foraging algorithm (BFA) **(Goher et al., 2017)**. To solve the limitations found when using the SDA or BFA methods separately, HSDBC took advantage of the convergence speed and fitness accuracy of SDA and the chemotactic approach of BFA. Results comparing the proposed approach to the original BFA and SDA algorithms showed its ability to improve the outcomes for highly nonlinear systems.

Further, a new hybrid approach that combines SDA and BFA is introduced by **(Kasruddin et al., 2022)**. By adding a spiral model to the chemotaxis of the BFA algorithm, the exploration and exploitation capabilities of both algorithms are improved, resulting in greater fitness accuracy for the SDA and quicker convergence time for the BFA, in addition to greater fitness accuracy. The suggested method has been shown to have superior results compared to competing algorithms in benchmark function tests. Furthermore, the work of **(Matajira et al., 2018)** presented a performance analysis of the Stochastic Spiral Optimization (SSO) method and an objective comparison of five population-based optimization techniques. Performance tests showed that the stochastic spiral dynamic enhances the algorithm's exploration and exploitation characteristics, resulting in fewer errors in a number of benchmark functions.

Motivated by the simplicity and effectivity of the SDA algorithm and its successes in real-world applications, the main target of this study is to improve the SDA optimization method and test and validate its performance using several benchmark functions. This research introduces a new approach combining the spiral dynamic with the bacteria foraging method. In this proposed algorithm, three techniques have been used:

1. Chemotaxis strategy of bacterial foraging is used to find the optimum initialization point of the dynamic spiral algorithm.
2. To improve the search efficiency, the spiral model's radius and angular displacement are adaptively set according to a linear correlation with regard to the fitness value.
3. An additional phase, called the elimination and dispersal phase, obtained from BFA, is added to the end of SDA.

Tests on different benchmark functions showed that this new proposed method is more effective than the original SDA and adaptive SDA (ASDA) algorithms, as shown in subsequent sections.



2. SPIRAL DYNAMIC ALGORITHM AND BACTERIA FORAGING ALGORITHM

Algorithms for optimization have been used in a wide range of applications (**Madinehi et al., 2011**). This section briefly summarizes the initial versions of the dynamic spiral algorithm (SDA) and the bacterial foraging algorithm (BFA). The SDA is based on natural evolution, whereas the BFA is based on the foraging strategies of E. Coli bacterial cells.

2.1 Spiral Dynamic Algorithm

Motivated by natural spiral patterns such as the form of DNA molecules and hurricanes, tornadoes, and galaxies, (**Tamura and Yasuda, 2011b; Tamura and Yasuda, 2011c**) presented the dynamic spiral algorithm in 2011. The logarithmic spiral method was first applied to problems of two dimensions. SDA is easy to implement due to its simple structure and low computational requirements. Early in the process, when a better solution has yet to be located, diversification is used to execute a wide-ranging examination of the search space. Once the algorithm has finished its initial exploration, it will look for a more probable answer close to the optimal solution. The term "intensification" describes trying to find the best possible solution. When the path of a spiral moves exponentially to its center, this provides a natural model for the diversification and intensification procedures used in SDA (**Tamura and Yasuda, 2011a**). **Fig. 1** illustrates how the logarithmic spiral adapts to exploration and exploitation. It is evident that diversification occurs in the early stages, and the size of the small steps becomes smaller towards the End when intensification takes place. The SDA search starts at the point of initial and moves on to the next point counterclockwise until it reaches the inner layer of the spiral's center. As the search locations get closer to the spiral's center, the step size in this process will gradually decrease. As a result, the SDA can find globally optimal solutions to various uni-modal and multi-modal problems. The SDA converges faster since it always has the highest fitness, leading the spiral search to the best possible solution at each iteration.

A mathematical model of SDA in n-dimension is defined as:

$$x_i(k + 1) = S_n(r, \theta)x_{i(k)} - [S_n(r, \theta) - I_n]x^*, i = 1, 2, \dots, m \quad (1)$$

where θ is the rotational angle, which can range from 0 and 2π , I_n is the identity matrix, x^* is the center of the spiral, k is the number of iterations, r is the spiral radius, which can range from 0 to 1 while multiplying the radius by the composition of a rotational $n \times n$ matrix R^n using the addition of the two axes yields S_n that $S_n(r, \theta) = r R^{(n)}(\theta_{1,2}, \theta_{1,3}, \dots, \theta_{n,n-1})$, where rotation $n \times n$ matrix is $R^{(n)}(\theta_{1,2}, \theta_{1,3}, \dots, \theta_{n,n-1})$. The general mathematical n dimensional spiral model employing $R^{(n)}(\theta_{1,2}, \theta_{1,3}, \dots, \theta_{n,n-1})$ is as follows:

$$R^{(n)}(\theta_{1,2}, \theta_{1,3}, \dots, \theta_{n,n-1}) = \prod_{i=1}^{n-1} \left(\prod_{j=1}^i R_{n-i,n+1-j}^{(n)}(\theta_{n-i,n+1-j}) \right) \quad (2)$$

In general, the performance of SDA is determined by the r and θ parameters. The algorithm may converge towards local optima, and increasing the number of iterations will not be beneficial to find a better solution. In addition, when the size of the spiral model's matrix increases, the computational time required to solve problems of high dimension grows.

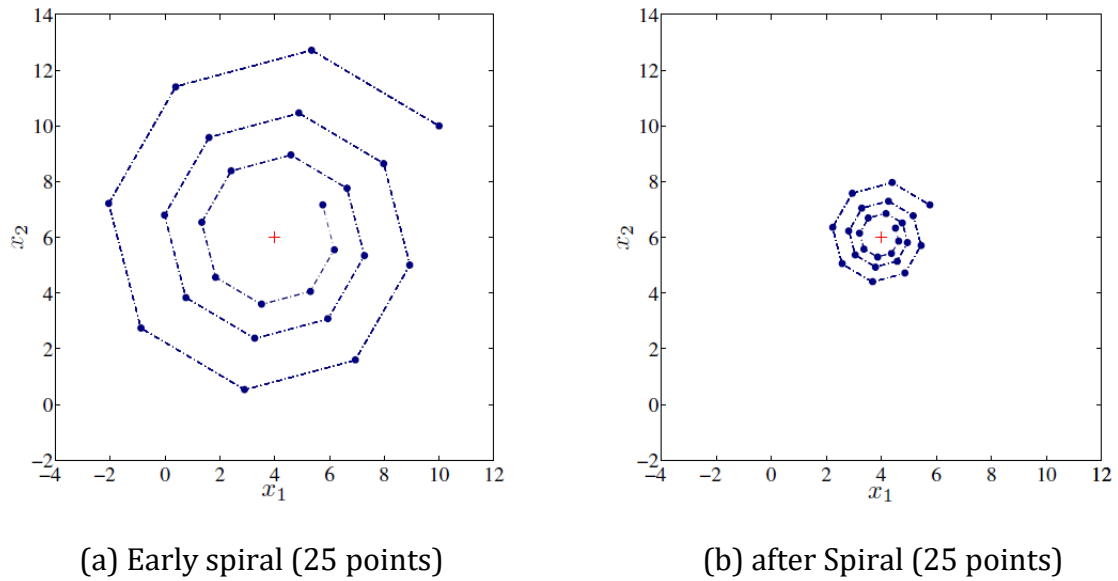


Figure 1. The Spiral Trajectory (Tamura and Yasuda, 2011c)

2.2 Bacterial Foraging Algorithm

A biologically based algorithm known as the BFA was introduced by (Passino, 2002). Escherichia coli (E. Coli) bacteria use an adaptation technique to obtain nutrients or food sources throughout their lifetimes. The method is also referred to as a bacterial foraging strategy.

There are typically three distinct stages of a BFA strategy. The initial and most visible stage of BFA is called chemotaxis, consisting of swimming and tumbling movements. An initial search action known as a "tumble" involves each bacteria taking a random one-step forward from its initial location. $\theta_i(j, k, l)$ where $i, j, k,$ and l represent the i th bacteria, the indexes for chemotactic activity, reproduction, and elimination-dispersal, respectively. The i th bacteria modify their swimming action if the nutrient level at the current position $\theta_i(j+1, k, l)$ is more significant than that at the original location $\theta_i(j, k, l)$. If the i th bacterium's new position $\theta_i(j+1, k, l)$ has a lower nutrient level than its initial position $\theta_i(j, k, l)$, it will tumble again to change the direction of its initial search.

Below is a mathematical expression for the recent position of the i th bacteria following the tumbling movement

$$\theta_i(j + 1, k, l) = \theta_i(j, k, l) + C(i) \phi(j) \tag{3}$$

where $C(i)$ represents the step size of i th bacterium and $\phi(j)$ is a random direction of unit length. A bacterium will swim if the position after the tumble is better than the position before the tumble, and it will take one or more steps parallel to the direction of the tumble. If the bacteria's new position is preferable to its initial one, it will keep going to swim in that direction. The mathematical expression of the i th bacteria's new location after the swim action is represented as:

$$\theta_i(j + 1, k, l) = \theta_i(j + 1, k, l) + C(i) \phi(j) \tag{4}$$



The reproductive phase follows Chemotaxis. Once the maximum chemotactic N_c is reached, the bacteria are divided into two groups, one for weaker bacteria and another for stronger bacteria, based on their fitness. The fitness of a bacterium is based on how close it is to the global optimal position. The healthiest member of the bacterial population is the one with the highest nutritional content. The i th bacteria's health is calculated as follows:

$$J_{health}^i = \sum_{j=1}^{N_c+1} J(i, j, k, l) \quad (5)$$

The i th bacterium is the most robust member of the population by having the lowest cost value. When all the bacteria have been sorted, the first group will contain the healthiest half of the bacteria. The second group of bacteria, as opposed to that, are at a poor fitness level. After that, the bacteria that exhibited the greatest fitness levels are precisely replicated in the first group, so the new bacteria have the same characteristics as their origins. Finally, a method known as "elimination and dispersal" is employed, at which several healthy bacteria that are still present are eliminated.

In contrast, the others are dispersed randomly throughout the search space. This way, the bacteria will have a better chance of being clustered around the most nutrients or the best global solution. The original BFA algorithm and pseudocode are detailed (**Passino, 2002; Das et al., 2009; Abraham et al., 2008**).

3. THE PROPOSED HASDBF ALGORITHM

One alternative approach to enhance algorithm performance is to combine more than two algorithms. This strategy builds a new algorithm by combining the best features of each algorithm. It is expected that a hybrid approach will result in a more accurate algorithm and performs better than the original algorithms in different applications (**Biswas et al., 2007; Nasir et al., 2013a; Nasir et al., 2015b; Nasir et al., 2016; Goher et al., 2017; Jadon et al., 2017; Stretch et al., 2018; Al-Araji and Al-Zangana, 2019; Jawad and Hadi, 2019**). SDA has a quick computation time and speed of convergence, but its accuracy is low. Furthermore, SDA can easily be trapped at a local optimum solution. Whereas BFA has a high accuracy level but is slow in convergence speed and computation time. A new strategy of hybridizing the SDA and BFA algorithms is proposed in this section to enhance the performance and accuracy of SDA and to use the SDA to address actual world issues more effectively. The proposed HASDBF algorithm combines SDA and BFA to create a better balance between the two algorithms' exploration and exploitation phases. This algorithm is constructed so that the chemotaxis phase of bacteria represents the exploration part of the search operation, while the SDA represents the exploitation part. The bacteria chemotactic property has been used to improve the SDA's exploration phase to find the optimal initialization position for the SDA algorithm.

Additionally, to improve the search operation efficiency, the spiral model's angular displacement and radius are adaptively specified in accordance with a linear dependence on the fitness of each bacteria. The fitness accuracy and speed of convergence of an algorithm can be improved by including this strategy in the spiral model. The linearly adoptive relationship is mathematically formulated as follows:



$$r_{la} = \frac{r_l - r_u}{1 + \frac{c_1}{c_2 |f(x_i(k)) - \min J|}} + r_u \tag{6}$$

where r_{la} is the radius of the linear adaptive spiral, linear adaptive angular displacement is θ_{la} , positive constants are c_1 and c_2 , while the absolute value of a point's fitness is $|f(x_i(k))|$, $\min J$ is the best fitness at the current iteration. Within the range $[0,1]$, r_u and r_l specify a spiralling path's largest and smallest radius at a certain point. For the angular displacement that is linearly adaptive θ_{la} , the same formula is used for the linearly adaptive spiral radius r_{la} . In the range $[0,2\pi]$, r_l and r_u can be changed to θ_l and θ_u , respectively.

Table 1. The HASDBF Parameters and Description

Parameter	Description	Parameter	Description
$f(x_i(k))$	Fitness of i th point in k th generation	r	Spiral radius to be replaced by the linear adaptive formulae
s	Number of bacteria	m	Number of search point
C	Bacteria step size	k_{max}	Maximum number of iteration
N_c	Number of chemotaxis	k	Index of number of iterations
N_s	Number of swims	$x_i(k)$	Position of i th point in k th generation
i	Index of the number of search points	I_n	Identity matrix with $n \times n$ dimension
$p_i^n (Best)$	Optimum bacteria location found in the exploration phase	$\theta_{i,j}$	Search point angular displacement on $x_i - x_j$ the plane around the point of origin
x^*	Centre point of a spiral model or global best position	R^n	Composition of rotational $n \times n$ matrix based on a combination of all two axes
n	Number of dimensions	N_{ed}	Elimination and dispersal steps

Elimination and dispersal is an additional phase implemented to enhance the algorithm's search strategy and overall performance, with a special emphasis on the accuracy of the final result. BFA is used to obtain the elimination and dispersal phases. The SDA structure is maintained the same as the original in the HASDBF; nonetheless, the bacteria chemotaxis strategy determines the optimum location for its initialization. In addition, the $((1/5) \times m)$ points with the greatest value of fitness, such as the best value of fitness (x^*), are kept and saved to be used later for elimination and dispersal phase once the maximum number of iterations (k_{max}) have been completed. If the largest amount of elimination and dispersal (N_{ed}) is not achieved, then a total of $(m - ((1/5) \times m))$ new search points are generated at random and redistributed into a viable part of the search area at new places together with the removal of the previous search nodes $(m - ((1/5) \times m))$.

From the previous iteration, Both the fittest search points and the best point (x^*) are retained to direct the remaining points' spiralling motion and to hasten their convergence to an optimal position in this current period, while the entire set of search points is regenerated. Continuous iterations are performed until the largest quantity of cycles of elimination and dispersal (N_{ed}) is achieved.

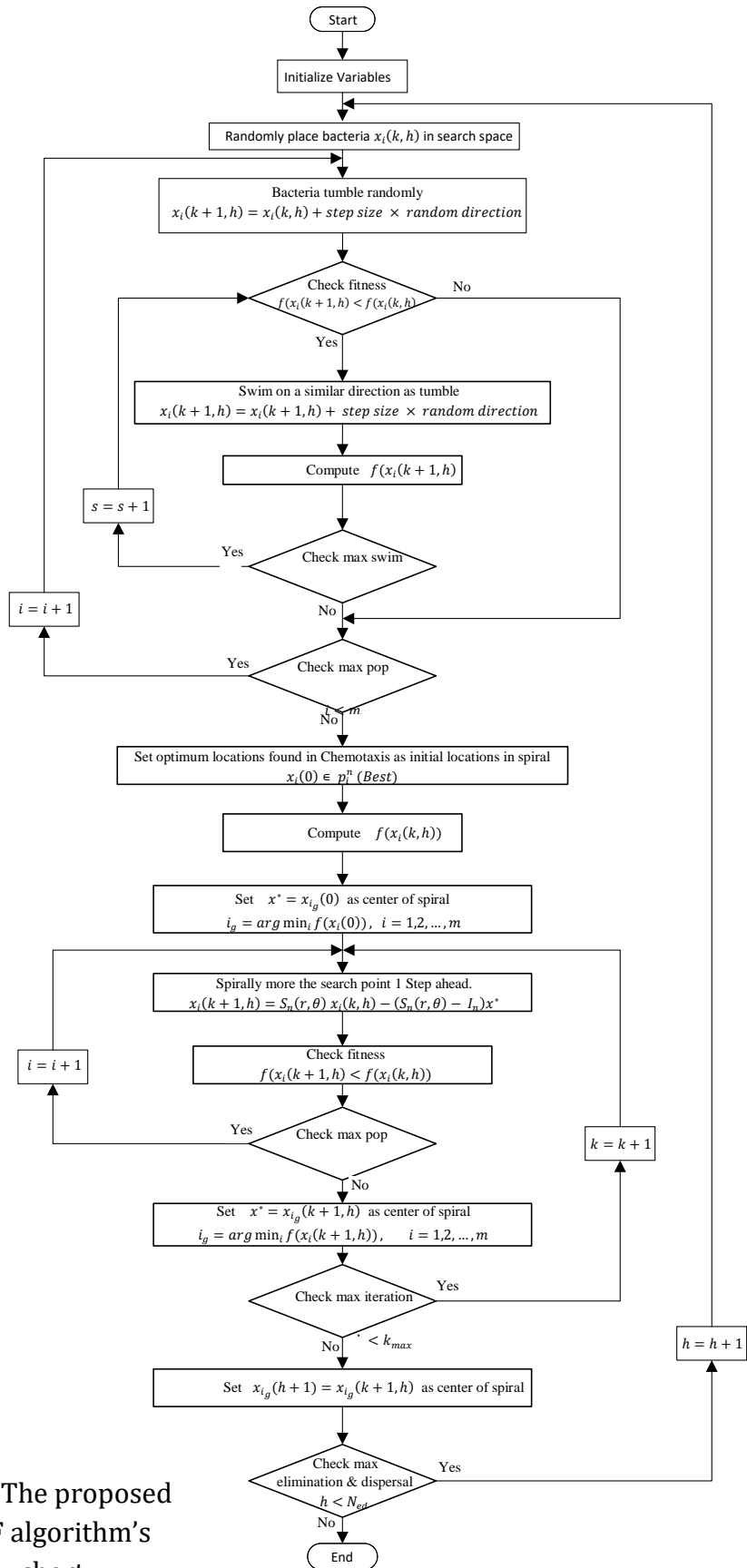


Figure 2. The proposed HASDBF algorithm's flowchart



With this technique, the algorithm can avoid getting stuck on localized optimal solutions and instead achieves the global best solution. Despite adding a new phase to the structure, the parameters of HASDBF are set in the same way as in SDA, making it effortless for the user to select the suitable parameters for achieving the best performance. The HASDBF notations and parameters are listed in **Table 1**, whereas **Fig. 2** shows the algorithm's flowchart.

4. VALIDATION WITH BENCHMARK FUNCTIONS

In this part, the suggested algorithm is verified via simulation tests using five standard benchmark functions, including two benchmarks that are unimodal (Sphere and Rosenbrock) and three benchmarks that are multimodal (Ackley, Rastrigin, and Griewank). The evaluation uses the benchmark functions presented in (**Abdel-Rahman, 2004; Biswas et al., 2007; Dasgupta et al., 2009; Blondin et al., 2018**). $f(x) = 0$ is the optimal fitness value for all benchmark functions. Comparisons among SDA, ASDA, and HASDBF using five benchmark functions are provided to demonstrate the enhanced HASDBF's performance. After exhaustive testing, the optimal parameter values were determined using a trial-and-error approach with various values for the initial parameters across the whole set of benchmark functions. The algorithms were compared fairly by setting the sum of all fitness evaluations to the same value.

The parameters used for SDA are $r = 0.95$, $\theta = 0.785$, and for both SDA and HASDBF algorithms are $m=20$ and $k_m = 50$. The testing requirements for the ASDA radius are $r_l = 0.1$, $r_u = 1$, $c_1 = 1$, and $c_2 = 1$, while for ASDA angle is defined as $\theta_l = 0.1$, $\theta_u = 6.283$, $c_1 = 1$, and $c_2 = 1$, which are the same adaptive values used in HASDBF. The BFA parameters for this function are $s=20$, $N_c = 20$, $C=0.01$, $N_s = 10$, and $N_{ed} = 2$. $n=4$ and variable x_i is in the range $[-10,10]$ for all algorithms.

Table 2. Statistical results obtained by using standard benchmark functions

Function		SDA	ASDA	HASDBF
Ackley	Mean	6.1940	4.9154	1.9456
	SD	1.7888	2.0211	1.3787
Rastrigin	Mean	28.3191	28.1583	16.5829
	SD	13.7267	18.1503	11.6128
Sphere	Mean	11.4310	6.0320	1.2044E-07
	SD	7.5710	7.1676	5.9208E-07
Griewank	Mean	0.1867	0.0558	0.0410
	SD	0.1504	0.0654	0.0449
Rosenbrock	Mean	1577.7127	9314.5572	642.9292
	SD	5576.1038	11582.5266	1011.3268

As shown in **Table 2**, 30 runs of the benchmark functions were simulated and analyzed statistically by recording their mean and standard deviation (SD). The mean and standard deviation demonstrate the average accuracy and consistency of the outcome (**To'aima et al., 2015; George et al., 2018**). If the mean value is smaller, the solution is more accurate and more closely approximates the global optimal solution, while a smaller standard deviation indicates that the generated solutions are more tightly clustered around the mean value and the reverse. In other words, it demonstrates the algorithm's robustness to obtain

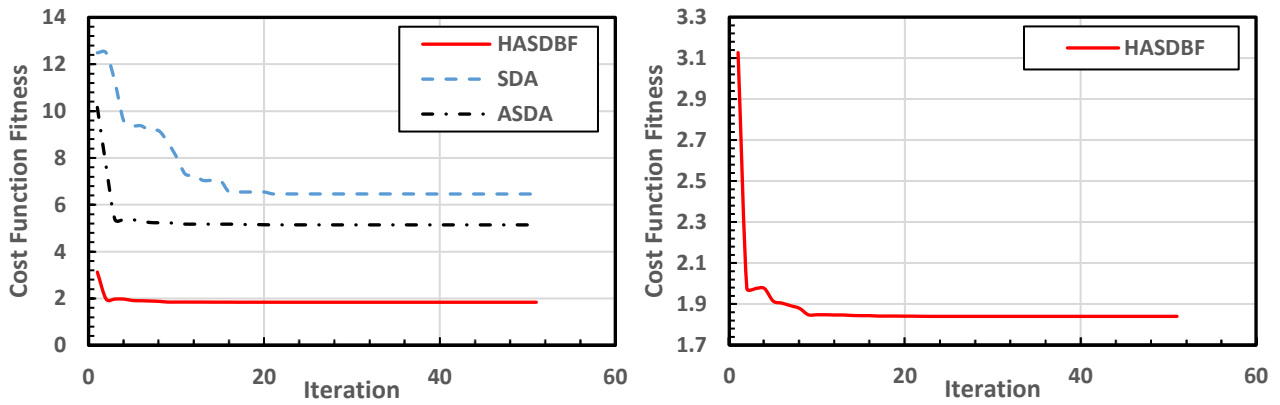


the targeted solution. The statistical performance measures indicate that The HASDBF converged to a near-optimum solution for all benchmark functions.

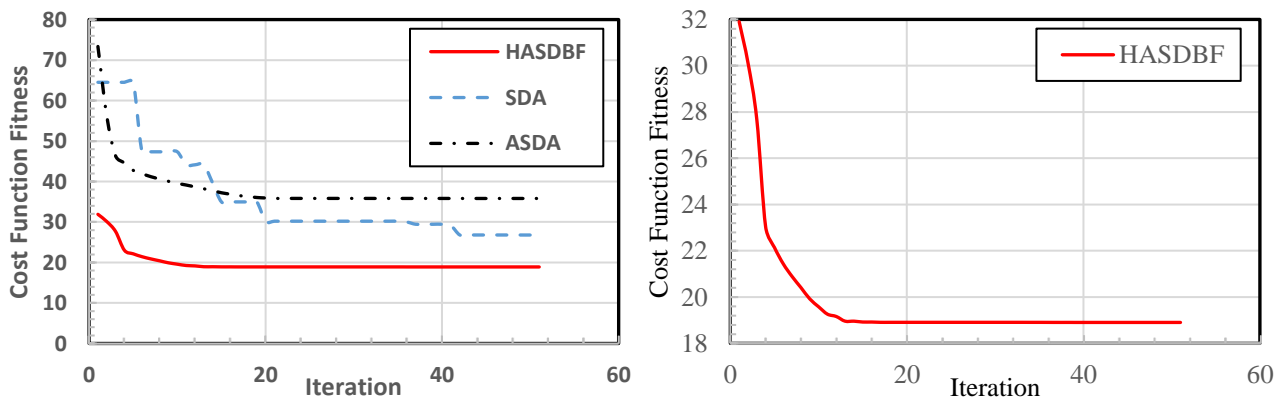
On the other hand, the proposed HASDBF has significantly outperformed SDA and ASDA in terms of accuracy and speed of convergence in all benchmark functions. The proposed algorithm outperforms the SDA for Ackley, Rastrigin, Sphere, Griewank, and Rosenbrock functions by 68.59%, 41.44 %, 99.99%, 78.04%, and 59.25%, respectively. Similarly, the proposed algorithm outperforms the ASDA by 60.42 %, 41.12 %, 99.99%, 26.52%, and 93.10%, respectively.

Fig. 3 shows the convergence graphs for the three methods tested on the benchmark functions. The graphs clearly show that the HSDBF significantly outperformed SDA and ASDA in terms of accuracy and speed of convergence. In contrast to the original SDA and ASDA, the proposed strategy effectively prevented premature SDA convergence and achieved a more optimal solution.

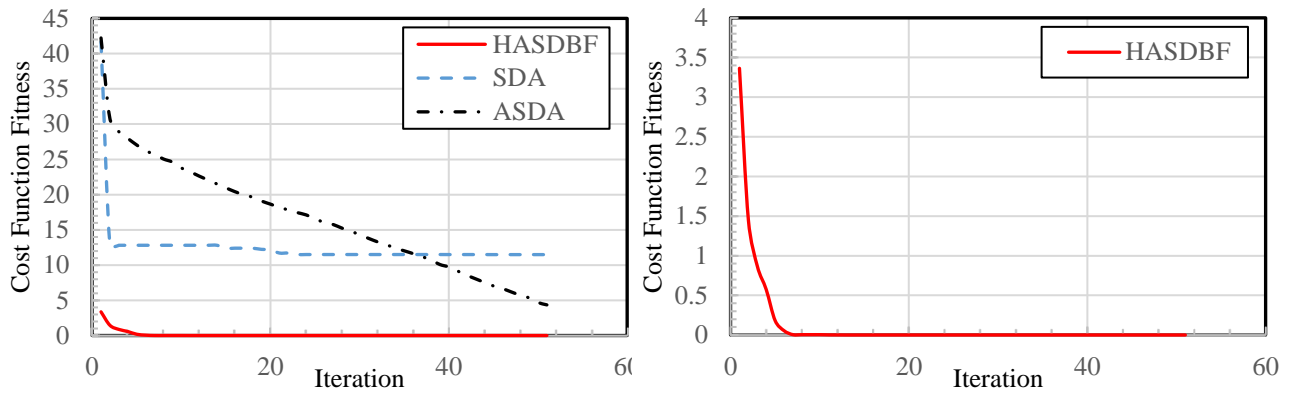
Finally, the statistical and convergence evaluations indicate that the suggested HASDBF algorithm outperformed SDA and ASDA. By combining SDA and BFA, HASDBF can achieve faster convergence to the optimal point than competing methods.



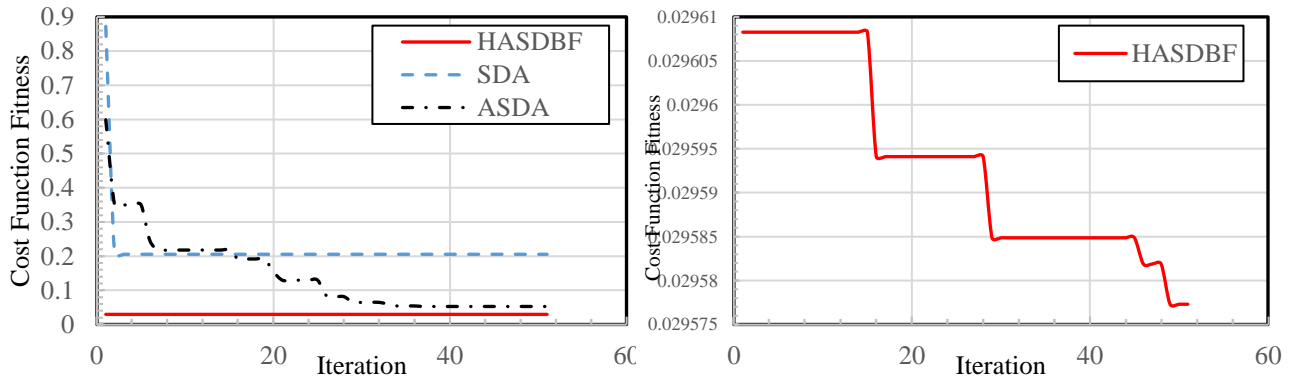
(a) Ackley



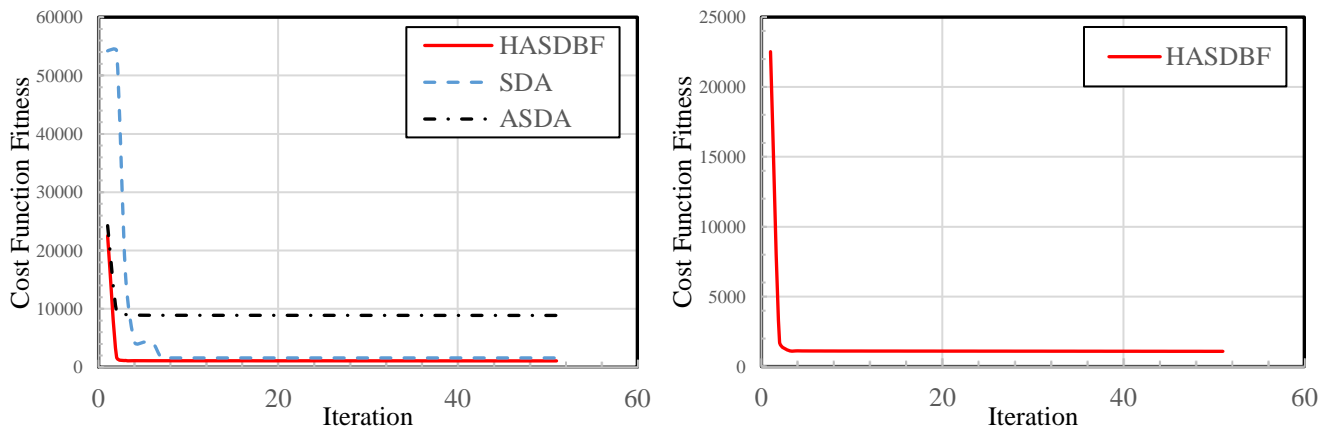
(b) Rastrigin



(c) Sphere



(d) Griewank



(e) Rosenbrock

Figure 3. Convergence plot for benchmark functions.



5. CONCLUSIONS

A new Hybrid adaptive spiral dynamic bacterial foraging algorithm, HASDBF, has been proposed. SDA has adapted the chemotactic technique of bacteria through spiral tumble and swim actions to improve its exploring method. Moreover, a linear function-based adaptation approach that establishes a connection between angular displacement, spiral radius, and fitness function value has been provided to improve search operation efficiency. A new phase has been added at the end of the spiral to prevent early convergence and obtain accelerated convergence. This new phase, the elimination and dispersal phase, was taken from the BFA. By incorporating these three schemes, the SDA successfully avoided trapping in local optima points, resulting in faster convergence. The proposed algorithm, tested on different singular and plural modes common benchmark functions, outperformed the SDA regarding fitness value and exactness. The proposed HASDBF outperformed the SDA for Ackley, Rastrigin, Sphere, Griewank, and Rosenbrock functions by 68.59%, 41.44%, 99.99%, 78.04%, and 59.25%, respectively.

Similarly, the HASDBF algorithm outperforms the ASDA by 60.42%, 41.12%, and 99.99%, respectively, 26.52% and 93.10%. In conclusion, the proposed HASDBF algorithm surpasses SDA and ASDA regarding convergence speed, accuracy, and efficiency. The proposed HASDBF algorithm promotes fast and accurate optimization results if utilized to solve real-world engineering problems.

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