A Novel Hybrid Spiral Dynamics Bacterial Chemotaxis Algorithm for Global Optimization with Application to Controller Design

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Abstract—This paper presents a hybrid optimization algorithm, referred to as hybrid spiral dynamics bacterial chemotaxis (HSDBC) algorithm. HSDBC synergizes bacterial foraging algorithm (BFA) chemotaxis strategy and spiral dynamics algorithm (SDA). The original BFA has higher convergence speed while SDA has better accuracy and stable convergence when approaching the optimal value. This hybrid approach preserves the strengths of BFA and SDA and thus has the capability of producing better results. Moreover, it has simple structure, hence reduced computational cost. Several unimodal and multimodal benchmark functions are employed to test the algorithm in finding the global optimum point. Furthermore, the proposed algorithm is tested in the design of PD controller for a flexible manipulator system. The results show that the HSDBC outperforms SDA and BFA in all test functions and successfully optimizes the PD controller.

Keywords—Spiral dynamics; bacterial chemotaxis; optimization algorithm; PD control; flexible manipulator.

I. INTRODUCTION

Metaheuristic optimization algorithms have gained a lot of interest by many researchers worldwide. These algorithms are inspired by biological phenomena or natural phenomena. Some of the newly introduced algorithms include biogeography-based optimization (BBO) [1], firefly optimization algorithm [2], cuckoo search optimization [3], galaxy-based search algorithm [4], and spiral dynamics inspired optimization (SDA) [5]. All these algorithms have gained attention due to their simplicity to program, fast computing time, easy to implement, and possibility to apply to various applications. Each of these algorithms has its own unique features, advantages and also disadvantages. Therefore, there are a lot of possibilities to improve the algorithms from various aspects. Many attempts have been made to improve performances of the algorithms such as developing adaptive approaches or incorporating powerful mathematical functions into the algorithms and mostly hybridizing two or more algorithms.

Hybridisation is a common approach used in metaheuristic to enhance capability of optimization algorithms. It may reduce computational cost by making a simple and better structure to lead to higher performance. Moreover, with the rapidly emerging computing tools and efficiency in current technology, hybrid approaches have become increasingly popular to explore. Various combinations of optimization algorithms have been considered by researchers with the aim to increase system performance. [6] developed a hybrid optimization algorithm combining bacterial foraging optimisation algorithm (BFA) with BBO, and referred to it as intelligent biogeography-based optimization. In the algorithm, chemotaxis behaviour of bacteria is adopted into BBO migration process to determine a valid emigration of an individual from one place to another. This ensures the island that receives the emigrated solution preserves its fitness level by only accepting individuals that contribute to a better fitness value. [7] introduced hybrid version of BFA with differential evolution (DE) algorithm called chemotaxis differential evolution. In the algorithm, chemotaxis strategy of bacteria is combined with the mutation process in DE. [8], [9] and [10] introduced hybrid GA-BF algorithm employing modified mutation and crossover operation in GA while applying variation bacterial chemotaxis step size in BFA. [11] developed cooperative (BF-TS) by combining adaptive bacterial foraging optimization algorithm (ABFA) and adaptive tabu search (ATS). With limited exploration capability of ATS in the search space and complexity of ABFA, the chemotaxis strategy of ABFA is incorporated into ATS to provide suitable exploration at the early stage. On the other hand, [12] used hybrid ABFA and ATS called BTSO, to analyze Lyapunov’s stability of linear and nonlinear systems. [13] introduced a hybrid algorithm namely BPSO-DE synergizing BFA, particle swarm optimization (PSO), and DE to solve dynamic economic dispatch problem with valve-points effect. Bacterial chemotaxis strategy with adaptive step-size in BFA is used to perform local search to enhance exploitation while PSO-DE features containing evolutionary operators and velocity update equation are used to perform exploration search over the entire search space. Hybrid BFA and PSO on the other hand, has received the most attention. [14], [15], [16], [17] and [18] employed velocity and position update equation in PSO to act as global search method while utilizing chemotaxis strategy in BFA to serve as local search method. [19] introduced simplified version of BFA employing bacterial chemotaxis strategy and PSO velocity update equation to solve parameter identification problem of heavy oil thermal cracking model. Reproduction and elimination stages were omitted to reduce computational time.

This paper presents hybrid version of bacterial foraging algorithm (BFA) chemotaxis strategy and spiral dynamics
algorithm (SDA). The rest of the paper is organized as follows. Section II provides a brief literature review of the original BFA and spiral dynamics inspired optimization. The proposed HSDBC is described in section III. Validation of the proposed HSDBC in comparison to SDA and BFA with uni-modal and multi-modal test functions as well as application of the algorithm in optimizing a PD controller is presented in section IV. Section V presents concluding remarks.

II. BFA AND SDA

The original versions of BFA and SDA are briefly described in this section.

A. Bacterial foraging optimization algorithm

The BFA is a biologically inspired algorithm introduced in [20]. It is based on adaptation technique of Escherichia Coli (E. Coli) bacteria to find nutrient or food source during their lifetime or alternatively the technique might be called bacterial foraging strategy. Furthermore, E. Coli bacteria use saltatory search technique, which is the combination of cruise and ambush movement. One of the exceptional features of E. Coli is that it has very high growth rate, which is normally exponential. This extraordinary capability of E. Coli has motivated researchers to adopt the strategy as optimization technique. Bacterial foraging strategy consists of three basic cycles namely chemotaxis, reproduction and elimination & dispersal. These cycles are continuing processes and very effective for optimization purposes [21]. Moreover, it offers flexibility for researchers to manipulate the strategy according to a specific application area. When searching for food or nutrient, tumbling and swimming will take place. Tumbling is similar to cruise and it happens when the E. Coli navigates in the search area and once the food source is found, it swims like ambushing a target area with great speed, up to 20µm/s or faster in a rich nutrient medium. This unique movement is called chemotaxis. Reproduction, elimination and dispersal events then happen to bacteria with high fitness or healthier that has capability to reach food source accurately and quickly. The strength of BFA lies in its spiral dynamics model. An n-dimensional spiral mathematical model that is derived using composition of rotational matrix based on combination of all 2 axes is given as:

\[ x(k+1) = S_n(r, \theta)x(k) - (S_n(r, \theta) - I_n)x^* \]  

where \[ S_n(r, \theta)x(k) = rR^n(\theta_{i,n}, \theta_{j,n}, \ldots, \theta_{n-2,n})x(k) \]  

or \[ S_n(r, \theta)x(k) = \prod_{i=1}^{n-1} \prod_{j=1}^{n-1} (R_{i,j,\text{amb}}(\theta_{i,n,\text{amb}}, \theta_{j,n,\text{amb}})) \]

and \[ R^n_{i,j}(\theta_{i,j}) = \begin{pmatrix} 1 & 1 & \cdots & 1 \\ \cos \theta_{i,j} & 1 & \cdots & -\sin \theta_{i,j} \\ \vdots & \vdots & \ddots & \vdots \\ \sin \theta_{i,j} & \cdots & \cos \theta_{i,j} & 1 \\ 1 & \cdots & \cdots & 1 \end{pmatrix} \]

Parameters and descriptions used in equation (1) are similar to those used in HSDBC optimization algorithm, which are shown in Table 1. Since SDA is relatively new, not much work in the literature involving the algorithm has been reported. The details of the original SDA algorithm for 2-dimension and n-dimension can be found in [5]. The hybrid approach of this algorithm and its details are provided in the next section.

B. Spiral dynamics inspired optimization algorithm

The SDA is another metaheuristic algorithm adopted from spiral phenomena in nature [5]. 2-dimensional and N-dimensional [5] logarithmic spiral discrete models have been tested on several benchmark functions. Moreover, comparisons with other optimization algorithms such as PSO and DE have shown that SDA performance is either better or the same as those [5]. This simple and effective strategy retains the diversification and intensification at the early phase and later phase of the trajectory as diversification and intensification are important features of the optimization algorithm. At the early stage, the spiral trajectory explores a wider search space and it continuously converges with a smaller radius providing dynamics step size when approaching the final point, which is the best solution, located at the centre. The distance between a point in a path trajectory and the centre point is varied constantly if the radius of the trajectory is changing at constant rate thus making the radius an important converging parameter for the algorithm. The strength of SDA lies in its spiral dynamics model. An n-dimensional spiral mathematical model that is derived using composition of rotational matrix based on combination of all 2 axes is given as:

\[ x(k+1) = S_n(r, \theta)x(k) - (S_n(r, \theta) - I_n)x^* \]  

III. HYBRID SPIRAL DYNAMICS BACTERIAL CHEMOTAXIS ALGORITHM

The HSDBC is a combination of bacterial chemotaxis strategy used in BFA and SDA. BFA has faster convergence speed due to the chemotaxis approach but suffers from oscillation problem towards the end of its search process. On the other hand, SDA provides better stability when approaching optimum point due to dynamic spiral step in its trajectory motion but has slower convergence speed. HSDBC algorithm preserves the strengths possessed by BFA and SDA. Moreover, by incorporating only chemotaxis part
of BFA simple structure of SDA can be retained, thus reducing computational time and enhancing performance of the algorithm. The parameters and description used in n-dimensional HSDBC optimization algorithm are presented in Table 1 and the algorithm is shown in Fig. 1.

TABLE I. PARAMETERS FOR HSDBC OPTIMIZATION ALGORITHM

<table>
<thead>
<tr>
<th>Symbols</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\theta_{i,j}$</td>
<td>Bacteria angular displacement on $x_i - x_j$ plane around the origin</td>
</tr>
<tr>
<td>$r$</td>
<td>Spiral radius</td>
</tr>
<tr>
<td>$m$</td>
<td>Number of search points</td>
</tr>
<tr>
<td>$k_{\text{max}}$</td>
<td>Maximum iteration number</td>
</tr>
<tr>
<td>$N_s$</td>
<td>Maximum number of swim</td>
</tr>
<tr>
<td>$x_i(k)$</td>
<td>Bacteria position</td>
</tr>
<tr>
<td>$R^n$</td>
<td>$n \times n$ matrix</td>
</tr>
</tbody>
</table>

An n-dimensional hybrid spiral dynamics bacteria chemotaxis optimization algorithm.

**Step 0: Preparation**
Select the number of search points (bacteria) $m \equiv 2$, parameters $0 \leq \theta < 2\pi$, $0 < r < 1$ of $S_n(r, \theta)$, maximum iteration number, $k_{\text{max}}$ and maximum number of swim, $N_s$ for bacteria chemotaxis. Set $k = 0$, $s = 0$.

**Step 1: Initialization**
Set initial points $x_i(0) \in R^n$, $i = 1, 2, ..., m$ in the feasible region at random and center $x^*$ as $x^* = x_i(0)$, $i_1 = \arg \min_i f(x_i(0))$, $i = 1, 2, ..., m$.

**Step 2: Applying bacteria chemotaxis**
(i) Update $x_i$
$$x_i(k+1) = S_n(r, \theta)x_i(k) - (S_n(r, \theta) - I_n)x^*$$

(ii) Bacteria swim
(a) Check number swim for bacteria $i$.
   
   If $s < N_s$, then check fitness,
   Otherwise set $i = i + 1$, and return to step (i).
(b) Check fitness
   
   If $f(x_i(k+1)) < f(x_i(k))$, then update $x_i$,
   Otherwise set $s = N_s$, and return to step (i).
(c) Update $x_i$
$$x_i(k+1) = S_n(r, \theta)x_i(k) - (S_n(r, \theta) - I_n)x^*$$

**Step 3: Updating $x^*$
$$x^* = x_i(k+1),$$

$$i_1 = \arg \min_i f(x_i(k+1)), i = 1, 2, ..., m.$$ **Step 4: Checking termination criterion**
If $k = k_{\text{max}}$ then terminate. Otherwise set $k = k + 1$, and return to step 2.

In the proposed hybrid approach, bacterial chemotaxis strategy is employed in step 2 to balance and enhance exploration and exploitation of the search space. The bacteria move from low nutrient location towards higher nutrient location, placed at the centre of a spiral. The most important factor of HSDBC algorithm is the respective diversification and intensification at the early phase and later phase of the spiral motion. In the diversification phase, bacteria are located at low nutrient location and move with larger step size thus producing faster convergence. On the other hand, in the intensification phase, bacteria are approaching rich nutrient location and move with smaller step size hence avoiding oscillation around the optimum point. Another factor contributing to better performance of the algorithm is the swimming action in bacterial chemotaxis. Bacteria continuously swim towards optimum point if the next location has higher nutrient value compared to previous location until the maximum number of swim is reached.

**IV. VALIDATION TEST AND RESULTS**
In this section, the proposed algorithm is validated through simulation tests on two 3-dimensional uni-modal and two 2-dimensional multi-modal benchmark functions. Moreover, the HSDBC algorithm is tested in optimizing PD controller of a flexible manipulator system. Comparison with the original version of SDA and BFA tested on the four benchmark functions is also given to show the improved performance of HSDBC. The parameters used in the simulation are chosen heuristically for all test functions.

**A. Uni-modal sphere function**
The sphere function is defined as:
$$f(x) = \sum_{i=1}^{n} x_i^2$$ (2)
The function has a global minimum at $x_i = [0, 0, 0]$ with fitness $f(x) = 0$. In this simulation, the sphere function is considered to have dimension $n = 3$ and variable $x_i$ is in the range [-5.12, 5.12]. Number of search points, $m = 30$, iteration number, $80$, angular displacement, $\theta = \pi / 4$, and spiral radius, $r = 0.96$ were used for both algorithms. Number of swims with HSDBC was defined as $N_s = 3$, BFA parameters for this function were $S = 30$, $N_c = 30$, $C = 0.01$, $N_s = 4$, $N_{re} = 4$ and $N_{ed} = 2$. The convergence plot for 3 dimensional sphere function thus achieved is shown in Fig 2.

**B. Uni-modal Ackley function**
The Ackley function is mathematically defined as:
$$f(x) = -20 \exp(-0.2 \sqrt{\frac{1}{n} \sum_{i=1}^{n} x_i^2}) - \exp(\frac{1}{n} \sum_{i=1}^{n} \cos(2\pi x_i)) + 20 + e$$ (3)
The function has a global minimum at $x_i = [0, 0, 0]$ with fitness $f(x) = 0$. The Ackley function is considered with dimension $n = 3$ and variable $x_i$ in the range [-32.768, 32.768]. Number of search points, $m = 30$, iteration number
200, angular displacement, $\theta = \pi/4$, and spiral radius, $r = 0.96$ were used in both algorithms. Number of swims for HSDBC with swim radius, $r = 0.6$ was defined as $N_s = 1$. BFA parameters for this function were $S = 20$, $N_c = 20$, $C = 0.02$, $N_s = 4$, $N_{re} = 4$ and $N_{ed} = 2$. The resulting convergence plot for 3-dimension Ackley function is shown in Fig 3.

The function has a global minimum at $x_i = [0, 0]$ with fitness $f(x) = 0$. The Griewank function was considered with dimension $n = 2$ and variable $x_i$ in the range $[-600, 600]$. The number of search points, $m = 50$, iteration number 200, angular displacement, $\theta = \pi/4$, and spiral radius, $r = 0.96$ were used for both algorithms. Number of swims for HSDBC with swim radius, $r = 0.55$ was defined as $N_s = 1$. BFA parameters for Griewank function were $S = 30$, $N_c = 10$, $C = 0.1$, $N_s = 4$, $N_{re} = 4$ and $N_{ed} = 2$. The resulting convergence plot for the 2-dimensional Griewank function is shown in Fig 5.

C. Multi-modal Rastrigin function

The Rastrigin function is defined as:

$$f(x) = \sum_{i=1}^{n} x_i^2 - 10 \cos(2\pi x_i) + 10$$  \hspace{1cm} (4)

The function has a global minimum at $x_i = [0, 0]$ with fitness $f(x) = 0$. The Rastrigin function is considered with dimension $n = 2$ and variable $x_i$ in the range $[-5.12, 5.12]$. The number of search points, $m = 50$, iteration number 120, angular displacement, $\theta = \pi/4$, and spiral radius, $r = 0.96$ were used in both algorithms. Number of swims for HSDBC with swim radius, $r = 0.65$ was defined as $N_s = 2$. BFA parameters for this function were $S = 30$, $N_c = 20$, $C = 0.01$, $N_s = 4$, $N_{re} = 4$ and $N_{ed} = 2$. The resulting convergence plot for the 2-dimensional Rastrigin function is shown in Fig 4.

D. Multi-modal Griewank function

The Griewank function is defined as:

$$f(x) = \frac{1}{4000} \sum_{i=1}^{n} x_i^2 - \prod_{i=1}^{n} \cos \left( \frac{x_i}{\sqrt{i}} \right) + 1$$  \hspace{1cm} (5)

The function can be clearly seen in the plots, in Figures 2-5 that the HSDBC outperformed SDA and BFA in terms of convergence speed and improved accuracy. Numerical results of HSDBC, SDA and BFA performance tests with the benchmark functions are shown in Tables II, III and IV respectively. It is noted that HSDBC has achieved better performance than SDA and BFA with the test functions in terms of convergence speed and accuracy.

<table>
<thead>
<tr>
<th>Cost Function Name</th>
<th>Best fitness</th>
<th>Converge time (iter)</th>
<th>$X_1$</th>
<th>$X_2$</th>
<th>$X_3$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sphere</td>
<td>$6x10^{-7}$</td>
<td>26</td>
<td>$2x10^{-4}$</td>
<td>$6x10^{-7}$</td>
<td>$-7x10^{-4}$</td>
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<tr>
<td>Ackley</td>
<td>$3x10^{-7}$</td>
<td>20</td>
<td>$1x10^{-7}$</td>
<td>$2x10^{-7}$</td>
<td>$-3x10^{-7}$</td>
</tr>
<tr>
<td>Rastrigin</td>
<td>0</td>
<td>15</td>
<td>$-2x10^{-7}$</td>
<td>$4x10^{-10}$</td>
<td>-</td>
</tr>
<tr>
<td>Griewank</td>
<td>$2x10^{-11}$</td>
<td>18</td>
<td>$-3x10^{-10}$</td>
<td>$6x10^{-8}$</td>
<td>-</td>
</tr>
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</table>
TABLE III. SDA PERFORMANCE ON BENCHMARK FUNCTIONS

<table>
<thead>
<tr>
<th>Cost Function Name</th>
<th>Best fitness</th>
<th>Convergence time (iter)</th>
<th>$X_1$</th>
<th>$X_2$</th>
<th>$X_3$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sphere</td>
<td>5x10^{-3}</td>
<td>63</td>
<td>-4x10^{-2}</td>
<td>-5x10^{-2}</td>
<td>-7x10^{-3}</td>
</tr>
<tr>
<td>Ackley</td>
<td>6x10^{-4}</td>
<td>159</td>
<td>9x10^{-4}</td>
<td>2x10^{-3}</td>
<td>2x10^{-3}</td>
</tr>
<tr>
<td>Rastrigin</td>
<td>1x10^{-6}</td>
<td>84</td>
<td>-8x10^{-3}</td>
<td>-2x10^{-3}</td>
<td>-</td>
</tr>
<tr>
<td>Griewank</td>
<td>7x10^{-6}</td>
<td>91</td>
<td>-6x10^{-3}</td>
<td>-1x10^{-2}</td>
<td>-</td>
</tr>
</tbody>
</table>

TABLE IV. BFA PERFORMANCE ON BENCHMARK FUNCTIONS

<table>
<thead>
<tr>
<th>Cost Function Name</th>
<th>Best fitness</th>
<th>Convergence time (iter)</th>
<th>$X_1$</th>
<th>$X_2$</th>
<th>$X_3$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sphere</td>
<td>5x10^{-3}</td>
<td>84</td>
<td>4x10^{-3}</td>
<td>-4x10^{-3}</td>
<td>3x10^{-3}</td>
</tr>
<tr>
<td>Ackley</td>
<td>2x10^{-2}</td>
<td>40</td>
<td>-5x10^{-3}</td>
<td>-9x10^{-3}</td>
<td>-1x10^{-3}</td>
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<tr>
<td>Rastrigin</td>
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<td>85</td>
<td>-8x10^{-4}</td>
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<td>-</td>
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<tr>
<td>Griewank</td>
<td>7x10^{-4}</td>
<td>45</td>
<td>-1x10^{-2}</td>
<td>4x10^{-2}</td>
<td>-</td>
</tr>
</tbody>
</table>

E. Controller design optimization

The HSDBC algorithm is employed here to optimize PD controller of a flexible manipulator system (FMS). Schematic diagram of the flexible manipulator system is shown in Fig. 6. $X_cOY_c$ and $XOY$ represent the stationary and moving coordinate frames respectively. $\tau$ represents the applied torque at the hub. Young modulus, area moment of inertia, mass density per unit volume, cross-sectional area, hub inertia, displacement and hub angle of the manipulator are represented by $E$, $I$, $p$, $A$, $I_h$, $v(x,t)$ and $\theta(t)$ respectively [23].

![Figure 6. Schematic diagram of flexible manipulator system.](image)

Mathematical model of FMS adopted here is that derived using Lagrange method in [22]. The FMS model has been used by many researchers in testing various types of controller for flexible systems [23], [24]. The dynamic equation of motion of FMS can be represented as:

$$M\ddot{q}(t) + D\dot{q}(t) + Kq(t) = F(t)$$  \hspace{1cm} (6)

where $M$, $D$ and $K$ are mass, damping and stiffness matrices respectively. $F(t)$ and $Q(t)$ are vectors of external forces and modal displacement respectively;

$$F(t) = [\tau \quad 0 \quad 0 \quad \cdots \quad 0]^T$$  \hspace{1cm} (7)

$$Q(t) = [\theta \quad q_1 \quad q_2 \quad \cdots \quad q_n]^T = [\theta \quad q^T]^T$$  \hspace{1cm} (8)

More details of the derivation and parameters of FMS can be found in [22], [23]. A state-space model of FMS is obtained by linearizing (6) and it is used to design PD controller through HSDBC. The control strategy of FMS is adopted from [23] and [24] where PD feedback of collocated sensor signals is employed. A block diagram of the control structure is shown in Fig. 7, where $K_p$, $K_v$ and $A_r$ are the proportional, derivative and motor amplifier gains respectively. The input of the system is reference hub angle, $\theta_l$ and the outputs of the system are hub angle, $\theta$ and hub angle velocity, $\dot{\theta}$. In this simulation, number of search points, $m = 30$, iteration number 100, angular displacement, $\theta = \pi/4$, and spiral radius, $r = 0.96$, and number of swim $N_s = 3$ were used to optimize the PD controller.

![Figure 7. Collocated PD control structure of FMS.](image)

Integral square error (ISE) of hub angle was chosen as cost function for the optimization algorithm. As a means of examining the proposed algorithm, this paper is only dealing with step input tracking capability of FMS. Step input was defined to have final value at 0.8 radians, which is the final location of hub angle. Graphical plot of the hub angle achieved is shown in Fig. 8.

![Figure 8. Hub angle response of FMS.](image)

In this plot, for the purpose of comparison, the hub angle response with PD controller designed using root locus approach from [24] is also shown. Simulation with HSDBC optimization algorithm on the FMS gave $K_p = 72.3459$ and $K_v = 20.6227$ while $K_p = 60$ and $K_v = 19$ using root locus technique [24]. It is clear from Fig. 8, that hub angle response of FMS using HSDBC was better than hub angle response using root locus technique in terms of speed of response. Numerical results of the hub angle response are shown in Table V. It is noted that the HSDBC approach resulted slightly larger overshoot within acceptable range. However, the response rise time with HSDBC was better, which indicates that the algorithm can perform faster with satisfactory response overshoot and no error at steady state.
TABLE V. PERFORMANCE SPECIFICATION OF HUB ANGLE RESPONSE

<table>
<thead>
<tr>
<th>Tuning Method</th>
<th>Performance Specification</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Overshoot, %</td>
</tr>
<tr>
<td>HSDBC</td>
<td>0.84</td>
</tr>
<tr>
<td>Root locus</td>
<td>0.53</td>
</tr>
</tbody>
</table>

V. CONCLUSION

A novel hybrid spiral dynamics bacterial chemotaxis optimization algorithm has been proposed. Validation with uni-modal and multi-modal benchmark functions and comparison with standard SDA and BFA have been carried out. Moreover, the HSDBC has been used in controller design of a flexible manipulator in comparison with root locus design approach. Simulation results have shown that the proposed algorithm outperformed its counterpart in all test functions and it successfully optimized PD controller of flexible manipulator system in terms of convergence speed and accuracy.

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