A New Hybrid Firefly Algorithm for Complex and Nonlinear Problem

Afnizanfaizal Abdullah, Safaai Deris, Mohd Saberi Mohamad,
and Siti Zaiton Mohd Hashim

Abstract. Global optimization methods play an important role to solve many real-world problems. However, the implementation of single methods is excessively preventive for high dimensionality and nonlinear problems, especially in term of the accuracy of finding best solutions and convergence speed performance. In recent years, hybrid optimization methods have shown potential achievements to overcome such challenges. In this paper, a new hybrid optimization method called Hybrid Evolutionary Firefly Algorithm (HEFA) is proposed. The method combines the standard Firefly Algorithm (FA) with the evolutionary operations of Differential Evolution (DE) method to improve the searching accuracy and information sharing among the fireflies. The HEFA method is used to estimate the parameters in a complex and nonlinear biological model to address its effectiveness in high dimensional and nonlinear problem. Experimental results showed that the accuracy of finding the best solution and convergence speed performance of the proposed method is significantly better compared to those achieved by the existing methods.

Keywords: Firefly Algorithm, Differential Evolution, hybrid optimization, parameter estimation, biological model.

1 Introduction

Global optimization is an important task in most scientific and engineering problems. These problems include finding the minimal vehicle routing [1-2] and

Afnizanfaizal Abdullah · Safaai Deris · Mohd Saberi Mohamad
Artificial Intelligence and Bioinformatics Group (AIBIG), Faculty of Computer Science and Information Systems, Universiti Teknologi Malaysia, 81310 UTM, Johor, Malaysia

Siti Zaiton Mohd Hashim
Soft Computing Research Group (SCRG), Faculty of Computer Science and Information Systems, Universiti Teknologi Malaysia, 81310 UTM, Johor, Malaysia

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the optimal design in electronic systems [3]. For the past few years, many global optimization methods have been proposed to solve these problems. Most of these methods are metaheuristics methods such as Genetic Algorithm (GA) [4], Particle Swarm Optimization (PSO) [5] and Evolutionary Programming (EP) [6]. These methods have received remarkable attentions as they are known to be derivative free, robust and often involve a small number of parameter tunings. However, applying such single methods is sometimes too restrictive, especially for high dimensional and nonlinear problems [8]. This is because these methods usually require a substantially huge amount of computational times and are frequently trapped in one of the local optima. Recently, different methods have been combined to overcome these disadvantages. The hybrid optimization methods have proved their effectiveness in several high dimensional and nonlinear problems including in bioinformatics [7] and electrical engineering [8].

In this paper, a new hybrid optimization method is introduced. The proposed method, called Hybrid Evolutionary Firefly Algorithm (HEFA), combines the recently introduced Firefly Algorithm (FA) [9] with the evolutionary operations adopted from the Differential Evolution (DE) [10]. In this method, the population is firstly ranked according to the fitness value. Then, the sorted population is divided into two sub-populations. The first sub-population; which contains the solutions with potential fitness values, is subjected to undergo neighborhood-based optimization, whereas the other sub-population is subjected to perform the evolutionary operations. The proposed method is used to estimate parameters in a complex and nonlinear biological model. The experimental results showed that the accuracy and speed performance of the HEFA method had outperformed the other existing methods. This paper is organized as follows: in Section 2, the proposed HEFA method is introduced and the details of the method are presented. In Section 3, the experimental results of evaluating the effectiveness of the proposed method to the parameter estimation of nonlinear biological model are described. Lastly, in Section 4, the conclusion of the contribution and the future works are discussed.

2 Hybrid Evolutionary Firefly Algorithm (HEFA) Method

The proposed HEFA method is basically a combination of the FA [9] and DE [10] methods. In this method, each solution in a population represents a solution which is located randomly within a specified searching space. The ith solution, X_i, is represented as follows:

$$X_{i(t)} = \left\{x_{i1(t)}, x_{i2(t)}, \dots, x_{id(t)}\right\} \tag{1}$$

where x_{ik} is the vector with $k = 1, 2, 3, \dots, d$, and t is the time step. Initially, the fitness value of each solution was evaluated. The solution that produced the best fitness value would be chosen as the current best solution in the population. Then, a sorting operation was performed. In this operation, the newly evaluated solutions were ranked based on the fitness values and divided into two sub-populations.

The first sub-population contained solutions that produced potential fitness values. The fitness value of each *i*th solution in this sub-population was then compared with its *j*th neighboring solution. If the fitness value of the neighboring solution was better, the distance between every solution would then be calculated using the standard Euclidean distance measure. The distance was used to compute the attractiveness, β:

$$\beta = \beta_0 e^{-\gamma r_{ij}^2} \tag{2}$$

where β_0, γ and , r_{ij} are the predefined attractiveness, light absorption coefficient, and distance between *i*th solution and its *j*th neighboring solution, respectively [9]. Later, this new attractiveness value was used to update the position of the solution, as follows:

$$x_{id} = x_{id} + \beta\left(x_{jd} - x_{id}\right) + \alpha(\delta - \tfrac{1}{2}) \tag{3}$$

where α and δ are uniformly distributed random values between 0 to 1. Thus, the updated attractiveness values assisted the population to move towards the solution that produced the current best fitness value [9, 11].

On the other hand, the second sub-population contained solutions that produced less significant fitness values. The solutions in this population were subjected to undergo the evolutionary operations of DE method. Firstly, the trivial solutions were produced by the mutation operation performed on the original counterparts. The ith trivial solution, V_i, was generated based on the following equation:

$$V_{i(t)} = \left\{v_{i1(t)}, v_{i2(t)}, \dots, v_{id(t)}\right\} \tag{4}$$

$$v_{i(t)} = x_{best(t)} + F \cdot (x_{r1(t)} - x_{r2(t)}) \tag{5}$$

where $x_{best(t)}$ is the vector of current best solution, F is the mutation factor, x_{r1} and x_{r2} are randomly chosen vectors from the neighboring solutions [10]. Next, the offspring solution was produced by the crossover operation that involved the parent and the trivial solution. The vectors of the ith offspring solution, Y_i, were created as follows:

$$Y_{i(t)} = \left\{y_{i1(t)}, y_{i2(t)}, \dots, y_{id(t)}\right\} \tag{6}$$

$$y_{i(t)} = \begin{cases} v_{i(t)} \; if \; R < CR \\ x_{i(t)} \; Otherwise \end{cases} \tag{7}$$

where R is a uniformly distributed random value between 0 to 1 and CR is the predefined crossover constant [10]. As the population of the offspring solution was produced, a selection operation was required to keep the population size constant. The operation was performed as follows:

$$X_{i(t+1)} = \begin{cases} Y_{i(t)} \; if \; f(Y_{i(t)}) \leq \; f(X_{i(t)}) \\ X_{i(t)} \; \; if \; f(Y_{i(t)}) > \; f(X_{i(t)}) \end{cases} \tag{8}$$

This indicates that the original solution would be replaced by the offspring solution if the fitness value of the offspring solution was better than the original solution. Otherwise, the original solution would remain in the population for the next iteration. The whole procedure was repeated until the stopping criterion was met. Figure 1 shows the outline of the proposed HEFA method.

Hybrid Evolutionary Firefly Algorithm (HEFA)

Input: Randomly initialized position of *d* dimension problem: X_i
Output: Position of the approximate global optima: X_G
Begin
  Initialize population; Evaluate fitness value;
  X_G ←Select current best solution;
  For $t \leftarrow 1$ to *max*
    Sort population based on the fitness value;
    $X_{good} \leftarrow first\_half(X)$; $X_{worst} \leftarrow second\_half(X)$;
    For $i \leftarrow 0$ to number of X_{good} solutions
      For $j \leftarrow 0$ to number of X_{good} solutions
        If $(f(X_i) > f(X_j))$ **then**
          Calculate distance and attractiveness;
          Update position;
        End If
      End For
    End For
    For $i \leftarrow 0$ to number of X_{worst} solutions
      Create trivial solution, $V_{i(t)}$;
      Perform crossover, $Y_{i(t)}$;
      Perform selection, $X_{i(t)}$;
    End For
    $X \leftarrow combine(X_{good}, X_{worst})$;
    X_G ←Select current best solution;
    $t \leftarrow t + 1$;
  End For
End Begin

Fig. 1 The outline of proposed HEFA method

3 Results

To address its effectiveness, the proposed method was used to estimate the parameters in a complex and nonlinear biological model. A general kinetic model

of the Maillard reaction occurring in heated monosaccharide casein systems [12] was used in this experiment. The model is downloaded from the BioModels repository database [14]. The model observed the dynamic of the metabolites concentrations involved in the systems through different reaction environments. Sugars, including glucose and fructose, were utilized to analyze the effect of the reaction kinetics. The model describes the reactions of the glucose, $\dot{Glu}$, and fructose, $\dot{Fru}$, concentrations as [12]:

$$\dot{Glu} = -k_1(Glu) + k_2(Fru) - k_3(Glu) - k_4(Glu)(Lys) \quad (9)$$

$$\dot{Fru} = k_1(Glu) - k_2(Fru) - k_5(Fru) - k_6(Fru) - k_7(Fru)(Lys) \quad (10)$$

where Glu, Fru, and Lys are the concentrations of glucose, fructose and lysine, respectively. The parameter values are k_1 = 0.01 min^{-1}, k_2 = 0.00509 min^{-1}, k_3= 0.00047 min^{-1}, k_4 = 0.00018 L mmol^{-1} min^{-1}, k_5 = 0.0011 min^{-1}, k_6 = 0.00712 min^{-1} and k_7 = 0.00015 L mmol^{-1} min^{-1} [12]. Figure 2 shows the dynamics of glucose and fructose concentration as depicted in Equation 9 and 10.

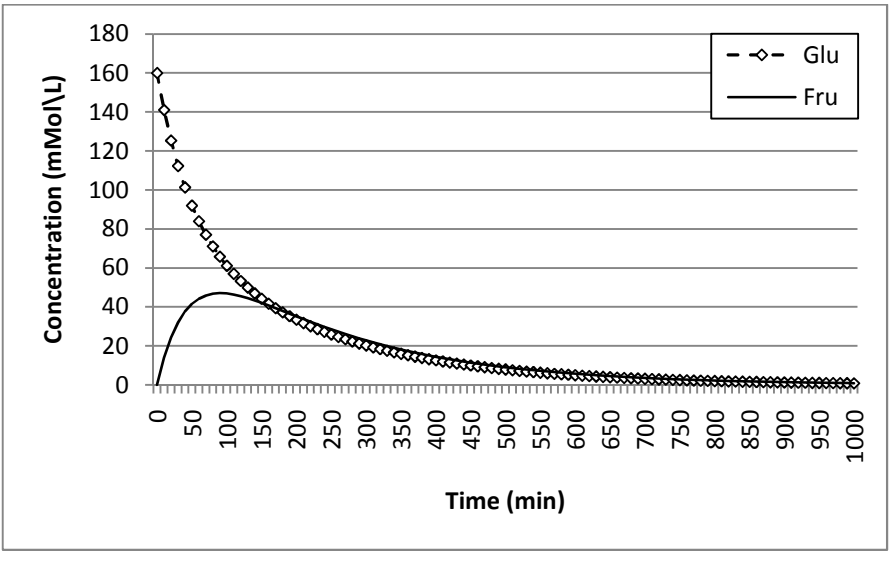

Fig. 2 The dynamics of glucose (Glu) and fructose (Fru) concentration in the system

Parameter estimation was implemented to find the optimal parameter values of the system so that the error difference between the experimental and simulated data would be minimized, as follows:

$$\min f(X_i) = \sum_{n=1}^{N} \sum_{m=1}^{M} (x_{mn}^{exp} - x_{mn}^{model})^2 \quad (11)$$

where N is the number of parameter values, M is the number of observable state variables, x_{mn}^{exp} and x_{mn}^{exp} are the experimental and simulated data points for the mth parameter value in the nth state time, respectively.

The parameter estimation results of four existing optimization methods, GA, PSO, FA, and EP, were compared with the proposed HEFA. In this comparison, the population size and the number of iterations of all methods were 50 and 1000, respectively. All methods were executed 50 times independently. For the proposed method, the initial attractiveness value, β_0, was set to 0.5 and the light absorption coefficient, γ, value was 0.01 [11]. Furthermore, for GA, EP, and HEFA methods, the mutation factor, *F*, and crossover constant, *CR*, were both set to 0.9 [10]. Table 1 presents the overall performance of these methods. For 50 runs, the average fitness value of the HEFA method was better compared to the other methods. The error percentage of the method for both glucose and fructose concentration are calculated as

$$Error = \sum_{m=1}^{M} \frac{x_m^{exp} - x_m^{model}}{x_m^{exp}} \times 100\% \quad (12)$$

From the table, it shows that the error percentage produced by the HEFA method was substantially small compared to other methods. In term of the computational time, the result showed by GA method was better than the proposed HEFA method. However, the small number of evaluated functions by GA indicated that only a small number of possible solutions were considered through the whole iterations. Thus, even though HEFA method required more computational time, the method tended to evaluate more functions than GA. Figure 3 shows the convergence performance of all tested methods. This proved that the HEFA method managed to escape the local optima more effectively compared to other methods. Overall, the advantages of the HEFA method were majorly due to two main factors. The first factor was the utilization of the solutions that produced least significant fitness values. The results showed that the use of these solutions had increased the exploration capability which allowed the method to escape the local optima effectively. The second factor was the neighborhood information sharing scheme by the evolutionary operations. It had been proven that the used of evolutionary operations could enhance the exploitation of each solution, thus improving the accuracy of finding the optimum solutions.

Table 1 Performance of different methods

	Method				
	GA	PSO	FA	EP	HEFA
Accuracy performance					
Error (Glucose)	1.07%	1.05%	0.42%	1.05%	0.42%
Error (Fructose)	0.28%	0.28%	0.17%	0.28%	0.01%
Average Fitness Value	6.43×10^{-8}	6.38×10^{-8}	9.91×10^{-8}	6.43×10^{-8}	7.79×10^{-18}
Standard Deviation	1.47×10^{-5}	1.47×10^{-5}	2.17×10^{-8}	1.47×10^{-5}	1.66×10^{-25}
Speed performance					
No. of Evaluated Functions	109	25059	29510	25009	35100
Time (second)	0.046	5.413	4.131	5.444	3.521

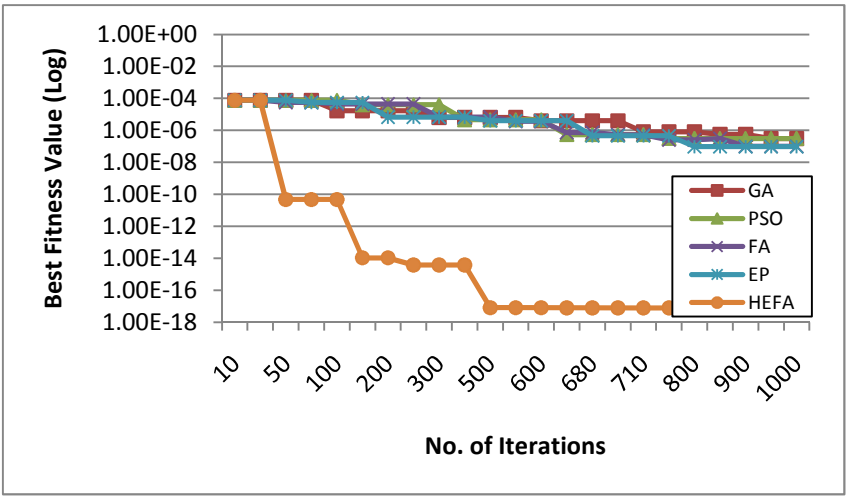

Fig. 3 Convergence behavior of GA, PSO, FA, EP and HEFA methods

4 Conclusion and Future Work

In this paper, the new hybrid optimization called HEFA is introduced. The proposed method combined the FA method with the evolutionary operations adopted from DE. The proposed method is used to estimate the parameters in a biological model. The experimental results showed that the accuracy and speed performance of HEFA had significantly outperformed the results produced by GA, PSO, EP, and the standard FA methods. Moreover, the convergence analysis showed that the proposed method was capable to escape from the local optima more effectively. For the future research, several improvements are suggested to further enhance the performance of the proposed method. Firstly, the adaptive control parameter can be introduced to enhance the function evaluation scheme by the evolutionary operations [13]. This is important to ensure that the speed performance will not be affected by the problem complexity. Secondly, the direction of the fireflies can be added to the method so that the firefly movements can be improved substantially [1]. Lastly, the proposed method should be tested to estimate the parameters in more complex problems such as noise and identifiability.

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