



Fletcher–Reeves based Particle Swarm Optimization for prediction of molecular structure



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ABSTRACT

The determination of the most stable conformers of a molecule can be formulated as a global optimization problem. Knowing the stable conformers of a molecule is important because it allows us to understand its properties and behavior based on its structure. The most stable conformation is that involving the global minimum of potential energy. The problem of finding this global minimum is highly complex, and is computationally difficult because of the number of local minima, which grows exponentially with molecular size. In this paper, we propose a hybrid approach combining Particle Swarm Optimization (PSO) and the Fletcher–Reeves algorithm to minimize the potential energy function. The proposed hybrid algorithm is applied to a simplified molecular potential energy function in problems with up to 100 degrees of freedom and also to a realistic potential energy function modeling a pseudoethane molecule. The computational results for both the cases show that the proposed method performs significantly better than the other algorithms.

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1. Introduction

The advent of high speed computers, availability of sophisticated algorithms, and state-of-the-art computer graphics have made it possible to use computationally intensive methods, such as quantum mechanics, molecular mechanics, and molecular dynamics simulations, to determine the physical and chemical properties of a molecule. The problem of determining the most stable conformation of a molecule can be formulated as a global optimization, and belongs to a class of NP problems. This is because molecular conformation identification is based solely on the energy of the interactions between the atoms composing the molecule. Among the many different possible conformations, the most stable is that with the minimum potential energy, as derived by a mathematical function. This energy function is a nonconvex expression involving many local minima, even for small molecules. The number of local minima increases exponentially with the size of the molecule. The various optimization methods applied to this problem include the random method [7,12,14,15], branch and bound method [11], simulated annealing [16], genetic algorithm [3,8,10], and variable neighborhood search [4]. A stochastic swarm intelligence algorithm, known as Particle Swarm Optimization (PSO) [2], has also

been applied to solve the energy minimization problem. PSO is simple, easy to implement, and requires only a small number of user-defined parameters, but it also suffers from premature convergence.

In this paper, we present a hybrid optimization technique that synergistically couples the conjugate gradient-based Fletcher–Reeves method with PSO. The proposed algorithm performs a local search using the Fletcher–Reeves method, whereas the global search is accomplished by a PSO operator. In this way, we manage to balance exploration and exploitation. The aim of the present paper is to investigate the effect of newly developed Fletcher–Reeves-based Particle Swarm Optimization (FRPSO) on the highly complex molecular potential energy function and to check the efficiency of the proposed algorithm to find the global minimum of the function under consideration. The proposed algorithm FRPSO, is therefore applied in two cases: (1) for the minimization of a potential energy problem with up to 100 degrees of freedom, and the results are extensively compared with those from a genetic algorithm (GA), regular PSO, Fitness Distance Ratio (FDR) PSO and Steepest Descent and (2) for the finding the global minimum energy conformation of pseudoethane molecule based on a potential function.

This paper is organized as follows: a mathematical description of the both the problems is given in Section 2, and the proposed FRPSO is described in Section 3. Computational results are presented in Section 4, and we give our conclusions in Section 5.

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2. Problem description

2.1. Simplified molecular potential energy function

The simplified molecular model used herein has been described by various researchers [2–4,8,10]. This three-dimensional molecular model contains a linear chain of N beads, centered at x_i, \dots, x_N . Let $r_{i,i+1}$ represent the bond length, or Euclidean distance, between every pair of consecutive beads x_i and x_{i+1} . $\theta_{i,i+2}$ is the bond angle corresponding to the relative position of x_{i+2} with respect to the line joining x_i and x_{i+1} . Similarly, for every $x_i, x_{i+1}, x_{i+2}, x_{i+3}$, $\omega_{i,i+3}$ represents the torsion angle between the normal through the planes formed by the atoms x_i, x_{i+1}, x_{i+2} and $x_{i+1}, x_{i+2}, x_{i+3}$.

In molecular mechanics, the interaction between molecules is derived by calculating the set of potential energy contributions of a system of atoms. The set of potential energy contributions is termed the force field. This force field is explained through a mathematical function containing adjustable parameters that are tuned to provide the best possible agreement with experimental data. The force field potentials corresponding to bond lengths, bond angles, and torsion angles are as follows:

$$E_1 = \sum_{(i,j) \in M_1} c_{ij}^1 (r_{ij} - r_{ij}^0)^2 \quad (1)$$

$$E_2 = \sum_{(i,j) \in M_2} c_{ij}^2 (\theta_{ij} - \theta_{ij}^0)^2 \quad (2)$$

$$E_3 = \sum_{(i,j) \in M_3} c_{ij}^3 (1 + \cos(3\omega_{ij} - \omega_{ij}^0)) \quad (3)$$

where c_{ij}^1 – bond stretching force constant, c_{ij}^2 – angle bending force constant, c_{ij}^3 – torsion force constant, r_{ij}^0 – preferred bond length, θ_{ij}^0 – bond angle, ω_{ij}^0 – phase angles (position of the minima), and M_k – $k = 1, 2, 3$ represents the set of pairs of atoms separated by covalent bonds.

Another force field that measures the two-body interactions between consecutive beads separated by more than two covalent bonds is given by:

$$E_4 = \sum_{(i,j) \in M_3} \left(\frac{(-1)^i}{r_{ij}} \right) \quad (4)$$

where r_{ij} is the Euclidean distance between beads x_i and x_j . The problem is then to minimize the total molecular potential energy function $E = E_1 + E_2 + E_3 + E_4$ so as to determine a stable conformer or the optimal spatial position of the atoms.

The above equation is simplified using the parameters defined by Lavor and Maculan [11], and the resultant expression for potential energy as a function of the torsion angles is as follows:

$$E = \sum_i (1 + \cos(3\omega_{i,j+3})) + \sum_i \left(\frac{(-1)^i}{\sqrt{10.60099896 - 4.141720682 \cos(3\omega_{i,j+3})}} \right) \quad (5)$$

where $i = 1, 2, 3, \dots, n-3$ and n is the number of beads in the given system.

The problem is now to find $\omega_{i,j+3}, i = 1, 2, \dots, n-3$, corresponding to the global minimum of the function E . It was shown by Lavor and Maculan [11] that the number of local minima of the function in Eq. (5) is 2^n , where $n = N-3$ is the total number of beads in a molecule. The global minimum of E is the alternating sequence of

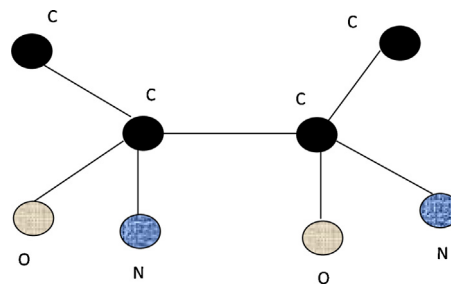


Fig. 1. Pseudoethane.

torsion angles $(a, b, a, b, a, b, a, b, \dots)$, independent of the number of variables, where $a = 1.039195303$ and $b = 3.141592654$. It can also be shown [11] that, for all values of n , the difference between the global minimum value E^* and the second-best local minimum, i.e., E_2 , always satisfies the following relation:

$$|E^* - E_2| = .0816608225 \quad (6)$$

Although the energy function E is simplified, the problem remains very difficult because of the combinatorial explosion caused by the exponential growth in the number of local minima with the size of the molecule. Thus, finding the global minimum for chains of even moderate length is intractable by exhaustive methods.

To find the global minimum of the molecular potential energy function E , we develop a PSO-based method:

$$\text{global}_{x \in X} \min f(x),$$

in the hyper-rectangle

$$X = \{(x_1, x_2, \dots, x_n) : a_i \leq x_i \leq b_i\}$$

for the function $f(x)$ defined by:

$$f(x) = \sum_i (1 + \cos(3x_i)) + \sum_i \left(\frac{(-1)^i}{\sqrt{10.60099896 - 4.141720682 \cos(x_i)}} \right) \quad (7)$$

where

$$0 \leq x_i \leq 5, \quad i = 1, 2, \dots, n.$$

2.2. Potential energy function of a pseudoethane molecule

In order to illustrate the efficiency of the proposed FRPSO algorithm a pseudoethane molecule involving a realistic energy function is considered. A pseudoethane molecule is a fully substituted ethane molecule where all three hydrogen atoms of both carbon atoms are replaced with one Carbon (C), one Oxygen (O) and one Nitrogen (N) atom as shown in Fig. 1.

This one dimensional conformational problem is taken from Adjiman and Floudas [1], where the global potential energy conformation of small molecules is studied. The potential energy of the molecule is expressed by the Lennard–Jones potential. The potential energy of the molecule in terms of single dihedral angle is given by:

$$f(t) = \frac{58860}{(3r_0^2 - 4\cos\theta r_0^2 - 2(\sin^2\theta \cos(t - (2\pi/3))\cos\theta^2)r_0^2)^6} - \frac{1079.1}{(3r_0^2 - 4\cos\theta r_0^2 - 2(\sin^2\theta \cos(t - (2\pi/3)) - \cos\theta^2)r_0^2)^3} + \frac{600800}{(3r_0^2 - 4\cos\theta r_0^2 - 2(\sin^2\theta \cos(t) - \cos\theta^2)r_0^2)^6} - \frac{1071.5}{(3r_0^2 - 4\cos\theta r_0^2 - 2(\sin^2\theta \cos(t) - \cos\theta^2)r_0^2)^3} + \frac{481300}{(3r_0^2 - 4\cos\theta r_0^2 - 2(\sin^2\theta \cos(t + (2\pi/3)) - \cos\theta^2)r_0^2)^6} - \frac{1064.6}{(3r_0^2 - 4\cos\theta r_0^2 - 2(\sin^2\theta \cos(t + (2\pi/3)) - \cos\theta^2)r_0^2)^3}$$

where r_0 - covalent bond length (1.54 Å), θ - covalent bond angle (109.5°), t - dihedral angle ($0 \leq t \leq 2\pi$).

In the above formulation contribution from 1–2 to 3–4 atom interactions are not considered because they are constant. This potential energy function is a highly nonlinear function having three minima in the range $[0, 2\pi]$. The two local minima occur at: $t = 61.42^\circ$ and corresponding $f(t)_{\min} = -0.7973$ kcal/mol and $t = 296.12^\circ$ and corresponding $f(t)_{\min} = -1.03989$ kcal/mol. The global minimum is observed at $t = 183.45^\circ$ where the potential energy takes the value of -1.0711 kcal/mol. The problem is to find the most stable conformation of this molecule that is to find out the value of t (dihedral angle) that corresponds to the global minimum value of $f(t)$.

The next section describes the proposed methodology for solving this global optimization problem.

3. Fletcher–Reeves-based Particle Swarm Optimization (FRPSO)

The FRPSO technique described in this paper is a hybrid of standard PSO [9] and the gradient-based Fletcher–Reeves method [6]. In FRPSO, the exploitation of the region visited by a particle is done by the Fletcher–Reeves method, and promising results are further explored using standard PSO.

PSO [9] is a swarm intelligence approach inspired by the social behavior of birds flocking and fish schooling. In PSO, a collection of particles moves through the search space towards the optimum solution by updating their position and velocity. Each particle's position represents a possible solution, and the particle's velocity represents the rate of change of the next position with respect to the current position. The position and velocity of a group of particles are initially random. The fitness value of each particle is computed, and if this fitness value is better than the best value obtained thus far, it replaces the best value of the particle. The particle with the best fitness value of all particles is chosen as the global optimum. Finally, each particle's position and velocity is updated according to the global optimum and its own optimum. Owing to this discontinuous behavior, a particle may leave the region in which it arrived only a few moments previously, without staying to exploit the region. As a result, the optimization sometimes misses a better solution, or even converges prematurely [5]. Thus, despite its simplicity, ease of implementation, and good exploration capability, standard PSO lacks sufficient exploitation capability. To address this problem, and further enhance the performance, we introduce a Fletcher–Reeves local search method to PSO.

The Fletcher–Reeves [6] method is a variant of the conjugate gradient method that uses the first-order derivative of the objective

function. Instead of looking for the direction in which the objective function decreases the most, the Fletcher–Reeves method determines a number of different directions, resulting in the minimum number of line searches in the optimization process. This not only reduces the numerical errors in the optimization process, but also reduces the computation time.

The computational steps of the FRPSO algorithm are as follows:

Algorithm 1: FRPSO.

```

FOR each particle  $i \in S$  DO
  Initialize  $x_i, v_i$ ;
  FOR each particle  $i \in S$  DO
     $P_i \leftarrow x_i$ ;
     $Y_i \leftarrow f(P_i)$ ;
  REPEAT
    FOR each particle  $i \in S$  DO
      Determine  $g_i$  with respect to given topology;
       $V_i \leftarrow wv_i + c1r1(p_i - x_i) + c2r2(g_i - x_i)$ ;
       $x_i \leftarrow x_i + v_i$ ;
      IF  $f(x_i) < f(p_i)$  THEN
         $p_i \leftarrow x_i$ ;
      IF  $f(x_i) < f(g_i)$  THEN
         $g_i \leftarrow x_i$ ;
      End IF
    End IF
     $x'_i \leftarrow \text{Fletcher-Reeves}(x_i)$ ;
    IF  $f(x'_i) < y_i$  THEN
       $P_i \leftarrow x'_i$ ;
       $Y_i \leftarrow f(x'_i)$ ;
  UNTIL stopping condition is true;

```

where

- v_i represents the rate of position change (velocity) of the i th particle,
- x_i represents the position of the i th particle in the d th dimension,
- P_i represents the historically best position of the i th particle (or the position giving the best fitness value attained by x_i),
- g_i represents the position of the swarm's global best particle (x_g) (or the position giving the global best fitness value attained by any particle in the entire swarm),
- $r1$ and $r2$ are two n -dimensional vectors of random numbers uniformly selected in the range $[0.0, 1.0]$, which introduce useful randomness to the search strategy,
- $c1$ and $c2$ are positive constant weighting parameters, also called the cognitive and social parameters, respectively,
- w represents the inertia weight,
- Y_i represents the position vector of the i th particle,
- x'_i represents the new position of the i th particle found by the Fletcher–Reeves method, $f(x'_i)$ represents the fitness value of the particle position found by the Fletcher–Reeves method.

Algorithm 2.

```

Fletcher-Reeves algorithm
Require  $x^0$  = starting point
REPEAT
  Compute  $\nabla f(x^0)$  and  $h^0 = \nabla f(x^0)$ 
  FOR  $i = 1, \dots, n-1$  DO
    Replace  $x^i = x^{i-1} + \lambda^{i-1} h^{i-1}$ 
    where  $\lambda^{i-1}$  minimizes  $f(x^{i-1} + \lambda^{i-1} h^{i-1})$ 
    Compute  $\nabla f(x^i)$ 
    IF  $i < n$  THEN  $h^i = -\nabla f(x^i) + \frac{\nabla f(x^i)^2}{\nabla f(x^{i-1})^2} h^{i-1}$ 
  END IF
   $x^0 = x^n$ 
END FOR
UNTIL halting criterion;

```

where, $\nabla f(x^i)$ - gradient of function, λ^{i-1} - step length, h^i - search direction, $(\nabla f(x^i)^2 / \nabla f(x^{i-1})^2)$ - method parameter, i - iteration counter.

Table 1
Parameter settings of the GA.

Cross over probability (P_c)	Mutation probability (P_m)	Tournament size	Population size
0.7	0.08	2	$5n$

Table 2
Parameter settings of PSO, FDR PSO, and FRPSO.

C1	C2	C3 (FDR PSO)	Population size
1.495	1.495	1.495	30

4. Results

Experiments were performed on Windows XP with a 2 GHz processor and 512 MB of RAM. The proposed algorithm was tested against a GA, PSO, and FDR PSO [13]. Table 1 presents the parameter settings for the GA, and Table 2 gives the parameter settings for PSO, FDR PSO, and FRPSO. The inertia weight w was initially set to 0.9, and then linearly decreased to 0.4 to ensure better convergence. The maximum velocity, V_{\max} , was limited to the upper limit of the dynamic range of the search, i.e., $X_{\max}()$. FRPSO uses a local Fletcher–Reeves search method with 100 iterations and step size $\chi = (\text{upper} - \text{lower}) / \text{number of iterations}$, where upper and lower are the maximum and minimum values of the variable for a given function.

4.1. Minimization of potential energy function E

The potential energy function E was minimized in the specified search space $[0, 5]^n$, where n is the total number of beads in a system, or the number of dimensions. Table 3 lists the global minimum value of E corresponding to different dimensions. For all algorithms, the stopping criterion was set to 1000 iterations or an error limit of 0.0001. To evaluate the performance of each algorithm, the following criteria were considered:

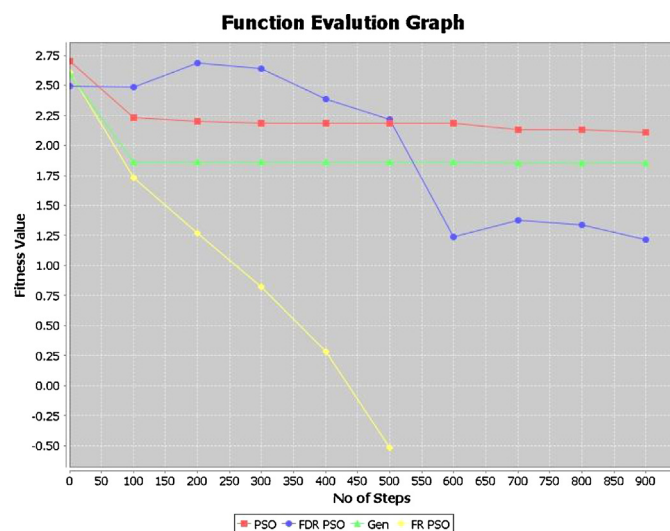
(1) *Quality of the solution*: The mean, standard deviation, standard error mean, and the optimum value of the best solution from 50 independent runs for each of the four algorithms are

Table 4
Computational results for a simplified molecular model of different dimensions using PSO, FDRPSO, GA, and FRPSO.

S. No	Dimension	Criterion	PSO	FDR PSO	GA	FR PSO
1	20	Mean	8.119366	2.86039344	4.55176	0.19446631
		Stand. dev.	0.859325	3.766	2.0996	0.3422
		Std. error mean	0.157	0.688	0.383	0.062
		Best	5.647296	−0.41348616	0.90011	−0.41175531
2	40	Mean	21.83672	5.11165677	11.8789	0.02453293
		Stand. dev.	2.8553	6.18961	5.3106	0.23513
		Std. error mean	0.521	1.13008	0.971	0.04293
		Best	8.78631	−0.41406194	4.36526	−0.79192928
3	60	Mean	38.14261	9.36684177	15.2233	1.32941712
		Stand. dev.	1.4817	9.5428	5.6036	0.7531
		Std. error mean	0.271	1.742	1.023	0.137
		Best	32.90896	2.37512642	6.97719	−0.41866821
4	80	Mean	54.95146	5.52360254	21.6016	2.67661501
		Stand. dev.	2.0916	1.73276672	8.3184	1.3131
		Std. error mean	0.382	0.317	1.519	0.24
		Best	49.77881	1.67622757	6.61434	−0.25477077
5	100	Mean	71.643	9.464805929	23.82008	3.514852567
		Stand. dev.	2.4152	1.9934	8.7781	1.731
		Std. error mean	0.441	0.364	1.603	0.316
		Best	63.82602	4.85021429	9.54119	−0.262831769

Table 3
Global minimum value for chains of different sizes (n).

S. No	Dimension (n)	Global optimum
1	20	−0.822366
2	40	−1.644732
3	60	−2.467098
4	80	−3.289464
5	100	−4.11183

**Fig. 2.** Comparative convergence of all algorithms for $n = 20$.

presented in Table 4. The best solution in each case is shown in bold. The numerical results show that the proposed FRPSO performs better than the other three algorithms. To further see the advantages of FRPSO, a t -test was conducted. A comparison of the algorithms by two-tailed t -test with 98 degrees of freedom at a 0.05 level of significance is shown in Table 5, along with the confidence interval (CI), t -value, and two-tailed p -value. From the results of this t -test, we can again conclude that FRPSO has better performance in all instances.

(2) *Speed of convergence*: Figs. 2–6 show the rate of convergence of the four algorithms for different values of n . The convergence

Table 5Results of a *t*-test between all algorithms for the simplified molecular model of different chain lengths.

S. No	Dimension	Algorithms	<i>t</i> -Value	Ci	<i>p</i> -Value	Significance
1	20	PSO-FRPSO	46.9213	7.5828, 8.2672	<.00001	Extremely significant
		FDR PSO-FRPSO	3.8615	1.254, 4.078	0.0006	Significant
		GA-FRPSO	11.2204	3.5648, 5.1512	<.00001	Extremely significant
2	40	PSO-FRPSO	41.6176	20.7422, 22.8818	<.00001	Extremely significant
		FDR PSO-FRPSO	4.4982	2.7741, 7.3999	<.00001	Extremely significant
		GA-FRPSO	12.1955	9.8661, 13.8419	<.00001	Extremely significant
3	60	PSO-FRPSO	121.2982	36.2019, 37.4261	<.00001	Extremely significant
		FDR PSO-FRPSO	4.5992	4.4636, 11.6124	<.00001	Extremely significant
		GA-FRPSO	13.4593	11.7857, 16.0023	<.00001	Extremely significant
4	80	PSO-FRPSO	115.9326	51.3679, 53.1809	<.00001	Extremely significant
		FDR PSO-FRPSO	7.1659	2.0505, 3.6435	<.00001	Extremely significant
		GA-FRPSO	12.3089	15.785, 22.065	<.00001	Extremely significant
5	100	PSO-FRPSO	125.5816	67.0394, 69.2166	<.00001	Extremely significant
		FDR PSO-FRPSO	12.344	4.9845, 6.9155	<.00001	Extremely significant
		GA-FRPSO	12.4304	16.9735, 23.6365	<.00001	Extremely significant

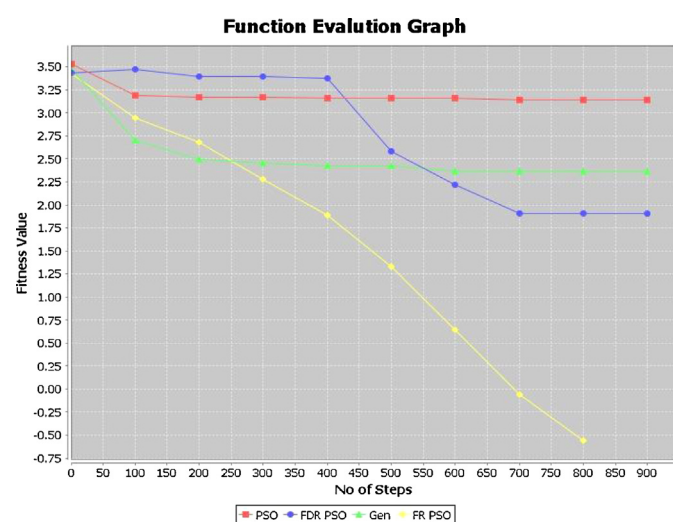
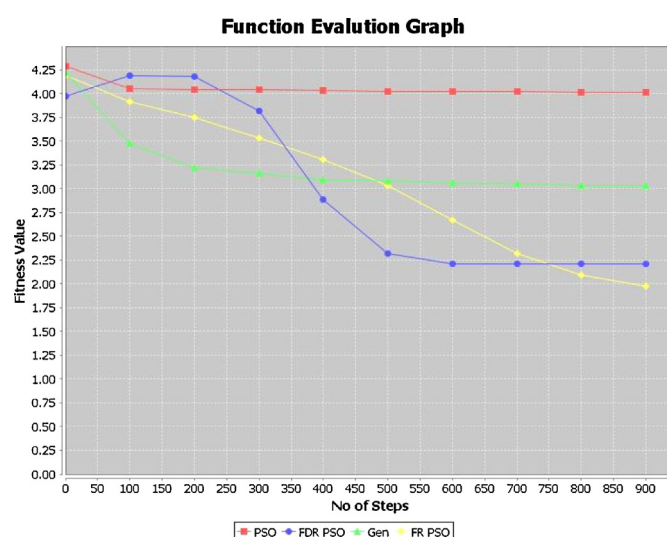
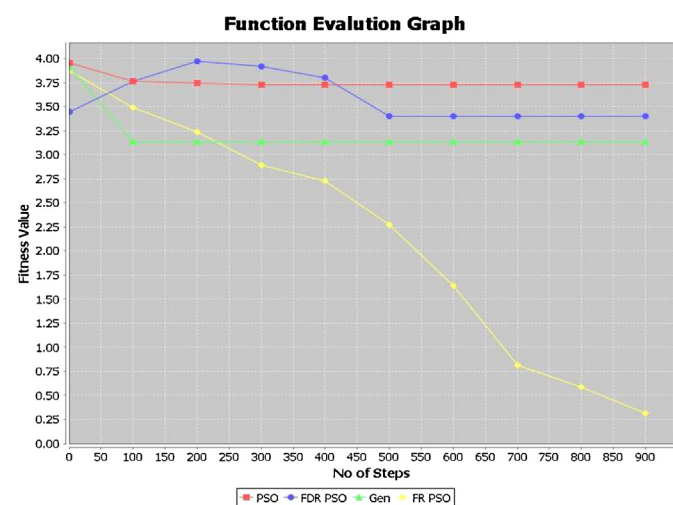
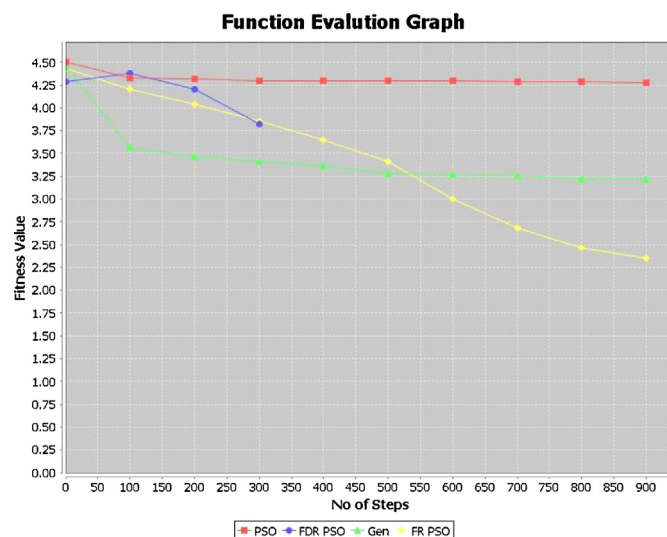
**Fig. 3.** Comparative convergence of all algorithms for $n = 40$.**Fig. 5.** Comparative convergence of all algorithms for $n = 80$.**Fig. 4.** Comparative convergence of all algorithms for $n = 60$.**Fig. 6.** Comparative convergence of all algorithms for $n = 100$.

Table 6

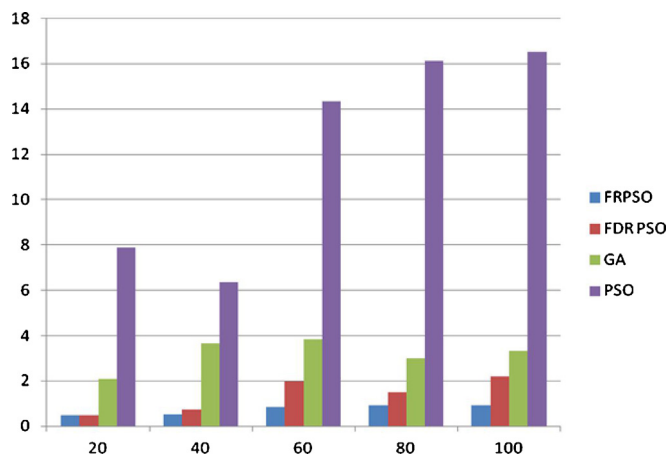
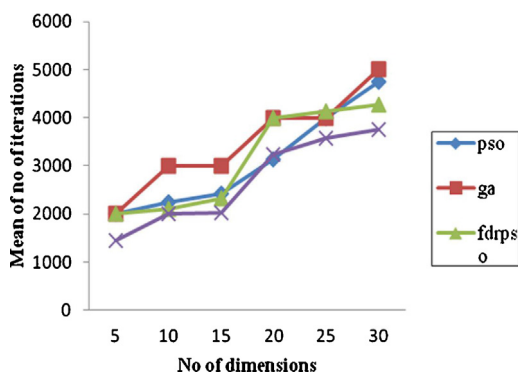
Results of computational time between all algorithms for the simplified molecular model of different chain lengths.

Size (<i>n</i>)	Steepest descent		GA		PSO		FDRPSO		FRPSO	
	No. of steps	CPU time	No. of steps	CPU time	No. of steps	CPU time	No. of steps	CPU time	No. of steps	CPU time
20	512	41	676	28.56	578	24.89	297	22.45	14	21.36
40	965	90.23	897	43.55	763	42.15	357	39.56	176	32.67
60	1000	167.83	989	60.89	920	58.45	578	52.98	234	46.12
80	1000	1189.2	1000	255.93	1000	242.16	638	213.88	397	194.58
100	1000	2856.35	1000	378.65	1000	358.91	1000	312.68	893	286.34

Table 7

Computational results for the pseudoethane molecule.

Algorithm	F_{avg}	F_{min}	F_{max}	F_{sd}	Succ	Time (s)
GA	21,69,771	2,74,424	32,51,614	10,97,602	15	2498
HYB	22,50,405	6,92,753	31,73,252	8,49,153	11	2653
rHYB	20,78,647	7,91,081	32,45,070	10,92,403	7	2855
oHYB	3,94,534	1,57,400	6,71,526	1,09,650	19	1131
PSO	2,84,316	1,49,342	5,81,295	2,03,789	18	1082
FDRPSO	2,58,952	2,54,137	4,37,519	1,25,861	21	1034
FRPSO	21,345	10,641	38,233	8262	29	845

**Fig. 7.** RE of all algorithms with respect to *n*.**Fig. 8.** Scalability of algorithms with respect to *n*.

graphs show that the FRPSO algorithm is able to converge to a more accurate solution in significantly less time than GA, PSO, and FDR PSO.

(3) *Relative error*: The relative error (RE) is defined as follows:

$$RE = \frac{\text{Best optima found} - \text{Global optima value}}{\text{Global optima value}}$$

The REs for all algorithms are compared in Fig. 7. This shows that FRPSO is able to produce more accurate results than GA, PSO, and FDR PSO, even for higher values of *n*.

- (4) *Scalability*: In Fig. 8, we graphically present the scalability of the four algorithms for the energy function *E*. The graph illustrates the change in convergence with the dimensionality of the search space, and shows that the proposed method gives a significant improvement in all cases.
- (5) *Computational time*: Table 6 compares the proposed FRPSO with Steepest Descent, GA, PSO and FDRPSO in terms of number of steps and CPU time (s) taken to reach to the global minimum. It can be clearly seen that FRPSO is able to find the global minimum in less time not only for small dimensions but also for larger dimensions as compared to other four methods.

4.2. Minimizing potential energy function $f(t)$ for pseudoethane

This section presents the numerical results using FRPSO to the energy function $f(t)$ of pseudoethane molecule. 30 independent runs of each algorithm are performed and maximum number of function evaluations are set to 4×10^6 . A run is considered successful if a threshold of 99% of the global minimum function value is reached. All the observations using FRPSO for pseudoethane molecule are recorded in Table 7 along with the earlier published results given in Barbosa et al. [3] and other two algorithms namely PSO and FDRPSO. F_{min} and F_{max} represents the minimum and maximum number of function evaluations needed to achieve the threshold in 30 independent runs while F_{avg} and F_{sd} represents the average and standard deviation considering only successful runs. "Succ" gives the number of successful runs and time is the CPU time (s) to reach 99% of the global minimum of $f(t)$.

From Table 7, it is clear that the FRPSO reached the threshold with much less effort, in terms of number of function evaluations as well as time as compared to other six algorithms. Also FRPSO is able to find global minimum 29 times out of 30 runs while other algorithms fail.

5. Conclusion

In this paper, we have proposed the FRPSO, a hybrid of the gradient-based Fletcher–Reeves local search method and a standard PSO. The scheme attempts to make judicious use of the exploration and exploitation abilities of the search space, thus

avoiding false or premature convergence. The proposed FRPSO was successfully applied to solve the molecular potential energy function, whose number of local minima grows exponentially with the problem size. The reported results allow us to conclude that this new variant of PSO outperforms standard PSO, GA, and FDR PSO in a statistically meaningful way. The performance metrics used were the quality of solutions, rate of convergence, relative error, and scalability. FRPSO is also compared with Steepest Descent method in terms of computational time and number of steps to reach the global minimum. Numerical results verify that the proposed FRPSO outperforms the competitors in all cases. Experimental results were also obtained for the realistic molecular potential energy function modeling pseudoethane molecule. It is clearly seen that the FRPSO show a remarkable performance as compared to the other six algorithms. Future work will focus on the application of FRPSO to more realistic complex molecular potential energy functions, and on reducing the number of user-defined parameters.

References

- [1] C.S. Adjiman, C.A. Floudas, Rigorous convex underestimators for general twice-differentiable problems, *Journal of Global Optimization* 9 (1996) 23–40.
- [2] J.C. Bansal, K. Shashi Deep, V.K. Katiyar, Minimization of molecular potential energy function using particle swarm optimization, *International Journal of Applied Mathematics and Mechanics* 6 (9) (2010) 1–9.
- [3] H. Barbosa, C. Lavor, F. Raupp, A GA-simplex hybrid algorithm for global minimization of molecular potential energy functions, *Annals of Operations Research* 138 (1) (2005) 189–202.
- [4] M. Drazic, C. Lavour, N. Maculan, N. Mladenovic, A continuous neighborhood search heuristic for finding the three dimensional structure of a molecule, *European Journal of Operational Research* 185 (3) (2008) 1265–1273.
- [5] R.C. Eberhart, Y. Shi, Comparing inertia weights and constriction factors in particle swarm optimization, *Congress on Evolutionary Computing* 1 (2000) 84–88.
- [6] R. Fletcher, C.M. Reeves, Function minimization by conjugate gradient methods for optimization, *Computer Journal* 7 (2) (1964) 149–154.
- [7] C.A. Floudas, J.L. Klepeis, P.M. Pardalos, Global optimization approaches in protein folding and peptide docking. In *Mathematical Support for Molecular Biology*. DIMACS Series, vol. 47, American Mathematical Society, 1999, pp. 141–171.
- [8] A.R. Hedar, A.F. Ali, T.H.A. Hamid, Genetic algorithm and tabu search based methods for molecular 3D-structure prediction, *Numerical Algebra Control and Optimization* 1 (1) (2011) 191–209.
- [9] J. Kennedy, R. Eberhart, Particle swarm optimization, in: *Proceedings IEEE International Conference Neural Networks*, vol. 4, 1995, pp. 1942–1948.
- [10] K. Shashi Deep, V.K. Katiyar, A.K. Nagar, Minimization of molecular potential energy function using newly developed real coded genetic algorithms, *International Journal of Optimization and Control: Theories & Applications* 2 (1) (2012) 51–58.
- [11] C. Lavor, N. Maculan, A function to test methods applied to global minimization of potential energy of molecules, *Numerical Algorithms* 35 (2–4) (2004) 287–300.
- [12] P.M. Pardalos, D. Shalloway, G.L. Xue, Optimization methods for computing global minima of nonconvex potential energy functions, *Journal of Global Optimization* 4 (2) (1994) 117–133.
- [13] T. Peram, K. Veeramachaneni, C.K. Mohan, Fitness-distance-ratio based particle swarm optimization, in: *Proceeding of IEEE Swarm Intelligence Symposium*, 2003, pp. 174–181.
- [14] J.M. Troyer, F.E. Cohen, Simplified models for understanding and predicting protein structure, *Reviews in Computational Chemistry* (Wiley-VCH) 2 (1991) 57–80.
- [15] D.J. Wales, H.A. Scheraga, Global optimization of clusters, crystals and biomolecules, *Science* 285 (5432) (1999) 1368–1372.
- [16] J. Zhao, H.W. Tang, An improved simulated annealing algorithm and its application, *Journal of Dalian University of Technology* 46 (5) (2006) 775–780.