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Biomimicry of Symbiotic Multi-Species Coevolution for Global Optimization

Na Lin

Beijing Shenzhou Aerospace Software Technology Co. Ltd., Beijing 110000, China

Shikai Jing

School of Mechanical Engineering, Beijing Institute of Technology, Beijing 110081, China

Xiaodan Liang, Weitao Yuan, Hanning Chen

School of Computer Science and Software, Tianjin Polytechnic University, 300387, Tianjin, China

Abstract

In recent years, symbiosis as a rich source of potential engineering applications and computational model has attracted more and more attentions in the adaptive complex systems and evolution computing domains. Inspired by different symbiotic coevolution forms in nature, this paper proposed a series of multi-swarm particle swarm optimizers called PS^2Os, which extend the single population particle swarm optimization (PSO) [1] algorithm to interacting multi-swarms model by constructing hierarchical interaction topologies and enhanced dynamical update equations. According to different symbiotic interrelationships, four versions of PS^2O are initiated to mimic mutualism, commensalism, predation, and competition mechanism, respectively. In the experiments, with five benchmark problems, the proposed algorithms are proved to have considerable potential for solving complex optimization problems. The coevolutionary dynamics of symbiotic species in each PS^2O vesion are also studied respectively to demonstrate the heterogeneity of different symbiotic interrelationships that effect on the algorithm's performance.

Key Words: SYMBIOSIS, PARTICLE SWARM OPTIMIZATION, MULTI-SWARM COEVOLUTION, GLOBAL OPTIMIZATION.

1. Introduction

Natural selection tends to enable living organisms to adapt to their environments by the processes of interaction [2]. As in nature, individuals interact constantly. Within a species or a population, Individuals can gain useful information to improve their adaptation by interacting with other member of the same species or population (e.g., individual species member use information of other members to find more food more quickly and allocate more time to feed but less to look for predators than individuals do). Two or more individuals from different species or populations can also interact with each anther to gain food, protection from enemies, a nesting site, or a combination of benefits (e.g., in Africa a species of bird known as honeyguide lead human to bee hives, then human break into these hives to collect honey, and the honeyguide later exploit the damage that human did to the hives to gain access to food) [3]. In biology, such intraspecific interaction (heterogeneous coevolution) and interspecific interaction (homogeneous coevolution) in an ongoing cycle of adaptation are called symbiotic coevolution [4].

In this paper, we implement an entire symbiotic system which consists of both heterogeneous and homogeneous coevolution aspects in formulating our symbiotic simulation models [5]. We introduced several symbiotic species each possesses a number of individuals into this coevolution model to represents the "biological community". The coevolution process in our model is hierarchical and contains three levels (i.e. individual level, species level and community level). Each individual of the biological community evolve base on the knowledge integration of itself (individual-level evolution, associate with individual's own cognition), its species members (species-level coevolution, associate cooperative interaction within species) and its symbiotic partners from other species (community-level coevolution, associate heterogeneous coevolution between individual from different species). Clearly we model more details of the social behaviors in nature ecosystems and tie this model closer to natural evolution. Since the community is made up of a swarm of agents who are species while each species is made up of a swarm of species member (individual), our swarms-within-swarms model is instantiated as a symbiotic coevolutionary optimization algorithm, namely particle swarms swarm optimizer (PS^{2}O).

Inspired by different symbiotic coevolution forms in nature, this work proposed four versions of PS^{2}O to mimic mutualism, commensalism, parasitism, and competition mechanism, respectively. In order to evaluate the performance of the PS2O algorithms, extensive studies based on five widely used benchmark functions have been carried out. The simulation results are encouraging: all the PS^{2}O algorithms have markedly superior search performance in terms of accuracy, robustness and convergence speed on all benchmark functions. We also simulated the coevolution process of a number of distinct species in our biological community model, and the simulation result is consistent with the natural phenomenon (i.e., the biological diversity is sustained after many coevolutionary generations, and the adaptive abilities of the interacting individuals / species are greatly increased).

2. Symbiotic Coevolution

Symbiosis, initially defined by Anton de Bary in 1879, is simply the living together of organisms from different species [6]. Here, we denote symbiosis as relationships that are constant and intimate between dissimilar species. Symbiosis is almost ubiquitous in nature. There are practically no plants or animals free of symbionts (organisms in symbiotic relationship) living on or in them. Research shows different types of symbiotic interactions. Some involve internal interactions, like bacteria in human intestines. Some of these interactions have seemed to lead to the evolution of organisms (e.g., the eukaryote cells, form which all plants and animals are descended have symbiotic origin). Others appear to be purely behavioural, as in a human-honeyguide mutualism that discussed above. Currently, enlightened evolutionary theory recognizes symbiosis as an integral process, and a fundamental source of innovation in evolution [7].

It is impossible to describe a set classifications for all types of symbiotic coevolution. Since an arbitrary number of individuals can be involved it would be ludicrous to try. However, the typical approach is to look at how pairs of individuals can form symbiotic relationships. It is possible to describe the various forms of symbiosis that exist in nature in the following listing.

Commensalism: commensalism occurs between two individuals *Host* and *Commensal* if and only if *Host* protagonizes *Commensal* and *Commensal* does not affect the fitness of *Host* (i.e., *Commensal* benefits from *Host* and *Host* is unaffected).

Competition: competition occurs between two individuals *Competitor* A and B if and only if both *Competitors* antagonize each other (i.e., both *Competitors* suffer because of each other).

Mutualism: mutualism occurs between two *Symbiont A* and *B* if and only if *Symbiont A* protagonizes *Symbiont B* and *Symbiont B* protagonizes *Symbiont A* (i.e., both *Symbionts* benefit from and/or need each other).

Predation: predation occurs between two individuals *Predator* and *Prey* if and only if *Predator* antagonizes *Prey* and *Prey* protagonizes *Predator* (i.e., *Predator* benefits from *Prey* while *Prey* suffers due to Predator).

3. Model

In this paper, we mimic four types of symbiotic coevolution, namely mutualism, commensalism, predation, and competition, to design our multi-swarm algorithms.

3.1 Canonical PSO (PSO)

The canonical PSO is a population-based technique, similar in some aspects to evolutionary algorithms [8], except that potential solutions (particles) move, rather than evolve, through the search space. The rules of particle dynamics that govern this movement are inspired by models of swarming and flocking. In PSO population, each particle has a position and a velocity, and experiences linear spring-like attractions towards two attractors:

i. Its previous best position.

ii. Best position of its neighbors.

In mathematical terms, the *i*th particle is represented as $x_i = (x_{i1}, x_{i2}, ... x_{iD})$ in the D-dimensional space, where $x_{id} \in [l_d, \ u_d], d \in [1, \ D]$, l_d, u_d are the lower and upper bounds for the *d*th dimension, respectively. The rate of velocity for particle i is represented as $v_i = (v_{i1}, v_{i2}, ..., v_{iD})$ is clamped to a maximum velocity V_{max} which is specified by the user. In each time step *t*, the particles are manipulated according to the following equations:

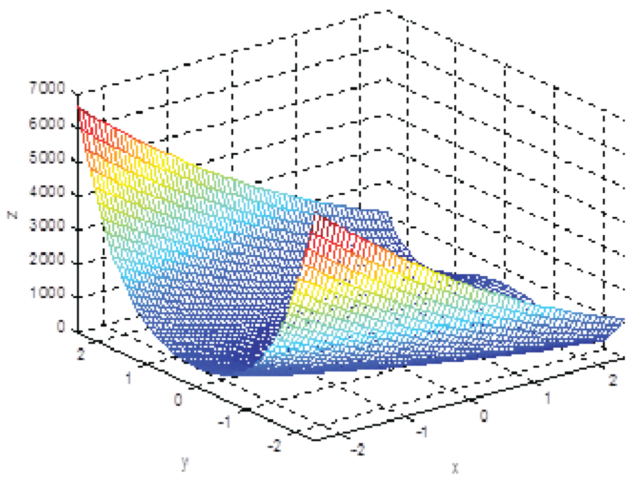


Figure 1. Rosenbrock function.

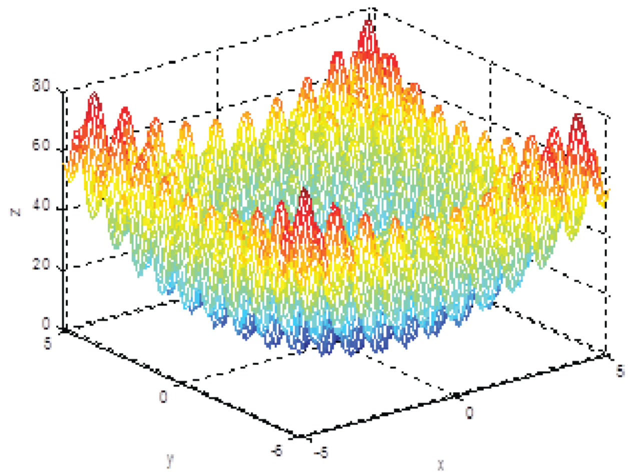


Figure 2. Rastrigrin function.

$$v_{id}(t+1) = \chi(v_{id}(t) + R_1 c_1 (p_{id} - x_{id}(t)) + R_2 c_2 (p_{gd} - x_{id}(t))) \quad (1)$$

$$x_{id}(t+1) = x_{id}(t) + v_{id}(t+1) \quad (2)$$

where R_1 and R_2 are random values between 0 and 1, c_1 and c_2 are learning rates, which control how far a particle will move in a single iteration, p_{id} is the best position found so far of the i^{th} particle, p_{gd} is the best position of any particles in its neighborhood, and χ is called constriction factor [9], give by:

$$\chi = \frac{2}{\left| 2 - \varphi - \sqrt{\varphi^2 - 4\varphi} \right|} \quad (3)$$

Where $\varphi = c_1 + c_2, \varphi > 4$.

Kennedy and Eberhart proposed a binary PSO [10] in which a particle moves in a state space restricted to zero and one on each dimension, in terms of the changes in probabilities that a bit will be in one state or the other. The velocity formula (1) remains unchanged except that x_{id}, p_{id}, and p_{gd} are integers in {0, 1} and v_{id} must be constrained to the interval [0.0, 1.0]. This can be accomplished by introducing a sigmoid function $S(v)$, and the new particle position is calculated using the following rule:

$$\text{if } rand < S(v_{id}), \text{ then } x_{id} = 1; \text{ else } x_{id} = 0; \quad (4)$$

where *rand* is a random number selected from a uniform distribution in [0.0, 1.0] and the function $S(v)$ is a sigmoid limiting transformation as follows:

$$S(v) = \frac{1}{1 + e^{-v}} \quad (5)$$

3.2 Predation PS^{2}O (PS^{2}O-P)

Inspired by predation phenomenon, in our PS^{2}O-P algorithm, a population consists of one predator swarm (symbiont S_1) and one prey swarm (symbiont S_2).

In the commensal swarm, each particle adjusts its trajectory according to its own experience, the experience of its swarm members, and the experience of its symbiotic partners in the prey swarm. Hence, the evolution equation of the predation swarm is the same as the commensal swarm in PS^2O-C agorithm (equation (6) and (7)). While in the prey swarm, the prey particles move away from those positions that are found by predator swarm and explore new sections of the search space. Then at each generation *t*, the prey swarm escapes from the predation swarm's global best position and evolves according to the following equations:

$$v_i^{S_2}(t+1)=\chi(v_i^{S_2}(t)+R_1c_1(p_i^{S_2}-x_i^{S_2}(t)) + R_2c_2(p_g^{S_2}-x_i^{S_2}(t))-R_3c_3(p_g^{S_1}-x_i^{S_2}(t))) \quad (6)$$

$$x_i^{S_2}(t+1)=x_i^{S_2}(t)+v_i^{S_2}(t+1) \quad (7)$$

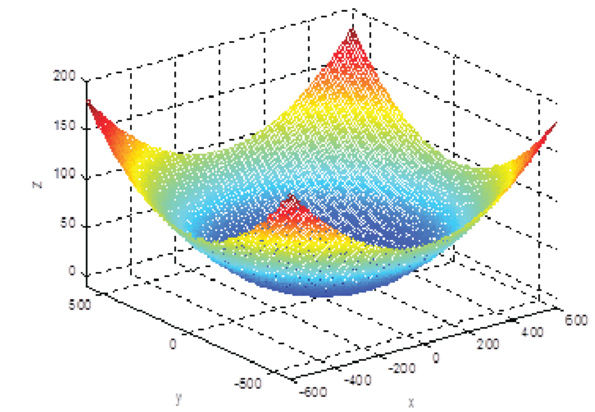


Figure 3. Griewank function.

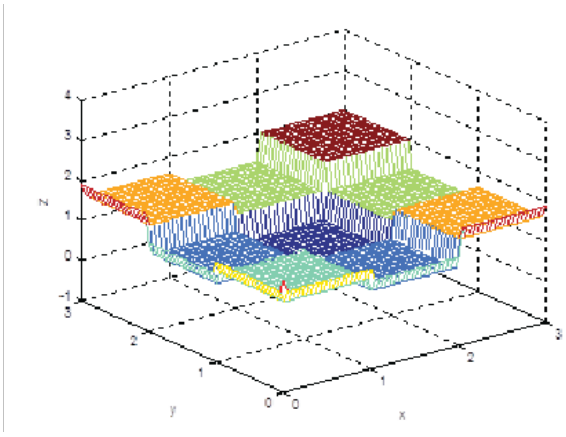


Figure 4. Golderg's order-3 function.

3.3 Mutualism PS^2O (PS^2O-M)

Inspired by mutualism phenomenon, in our PS^2O-M algorithm, a population consists of two cooperative swarms (symbiont S_1 and S_2). In each swarm, each particle adjusts its trajectory according to its own experience, the experience of its swarm members, and the experience of its symbiotic partners in the other swarm. That is, each particle in a swarm pursues the strongest individual in the other swarm. Hence, the evolution equation of both cooperative swarms are the same as the commensal swarm in PS^2O-C agorithm or predator swarm in PS^2O-P (equation (6) and (7)).

3.4 Competition PS^2O (PS^2O-T)

Inspired by competive phenomenon, in our PS^2O-T algorithm, a population consists of two competitive swarms (symbiont S_1 and S_2). In each swarm, each particle adjusts its trajectory according to its own experience, the experience of its swarm members, and the experience of its symbiotic partners in the other swarm. Hoever, contrary to mutulism swarms in PS^2O-M algorithm, each particle in one swarm moves away from those positions that are seen as best position found by the other swarm. Hence, the evolution equation of both competitive swarms are the same as the prey swarm in PS^2O-P agorithm (equation (6) and (7)).

We should note that, for solving discrete problems, we still use equation (4) and (5) to discrete the position vectors in PS^2O algorithms.

1. Experiment

From Fig. 3 [27], we can understand the basic behavior characteristics of bee colony foraging behaviors better. Assume that there are two discovered food sources: A and B. At the very beginning, a potential bee forager will start as unemployed bee. That bee will have no knowledge about the food sources around the nest.

In our experimental studies, a set of 5 benchmark functions was employed to evaluate the PS^2O algorithms in comparison with others. The following benchmark functions can be grouped as continuous unimodal function Rosenbrock (f_1), continuous multimodal functions Rastrigrin (f_2) and Griewank (f_3), and discrete functions Golderg's order-3 (f_4) and Bipolar order-6 (f_5) [11]. The fitness landscapes of these five functions are illustrated in Fig.1 to Fig.5, respectively. The formulas of these functions are presented below:

1. Rosenbrock function

$$f_1(x)=\sum_{i=1}^{n}100\times(x_{i+1}-x_i^2)^2+(1-x_i)^2 \quad (8)$$

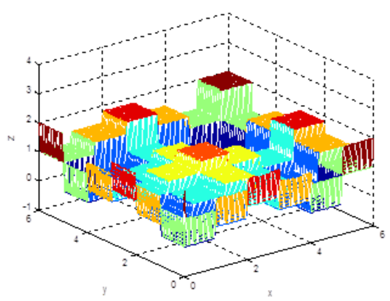
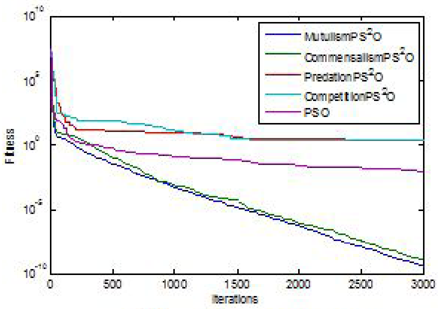
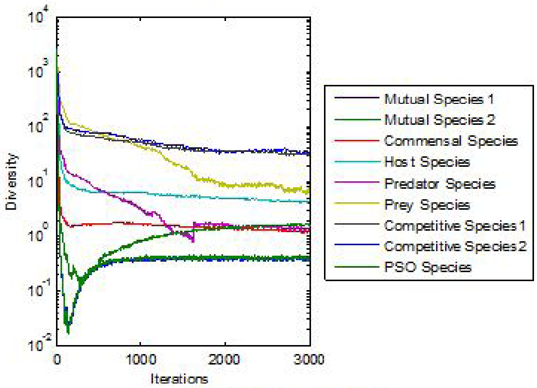


Figure 5. Bipolar order-6 function.

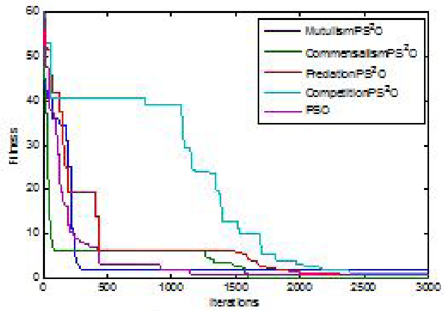


(a) fitness convergence

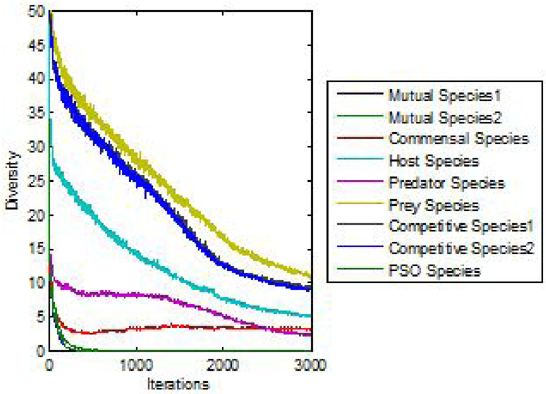


(b) diversity shifting

Figure 6. Simulation result on Rosenbrock.



(a) fitness convergence



(b) diversity shifting

Figure 7. Simulation result on Rastrigrin.

2. Rastrigrin's function

$$f_2(x) = \sum_{i=1}^{n}(x_i^2 - 10\cos(2\pi x_i) + 10 \quad (9)$$

3. Griewank function

$$f_3(x) = \frac{1}{4000}\sum_{i=1}^{n} x_i^2 - \prod_{i=1}^{n}\cos(\frac{x_i}{\sqrt{i}}) + 1 \quad (10)$$

4. Golderg's order-3

The fitness f of a bit-string is the sum of the result of separately applying the following function to consecutive groups of three components each:

$$f_4(x) = \begin{cases} 0.9 \ if \ |y| = 0 \\ 0.6 \ if \ |y| = 1 \\ 0.3 \ if \ |y| = 2 \\ 1.0 \ if \ |y| = 3 \end{cases} \quad (11)$$

If the string size (i.e. the dimension of the problem) is D, the maximum value is $D/3$ for the string 111…111. In practice, we will then use as fitness the value $D/3$-f so that the problem is now to find the minimum 0.

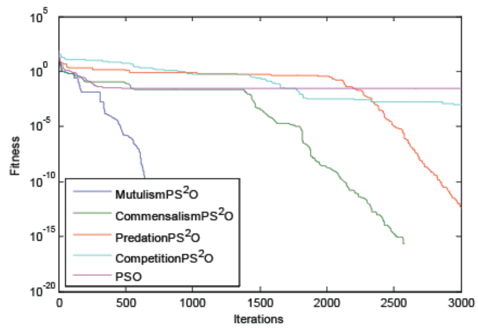
4. Bipolar order-6

The fitness f is the sum of the result of applying the following function to consecutive groups of six components each:

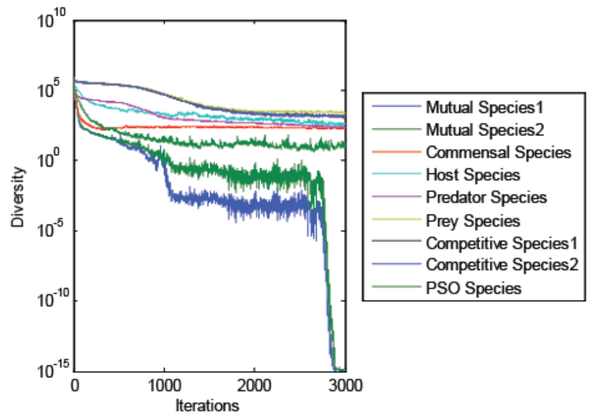
$$f_5(x) = \begin{cases} 1.0 \ if \ |y| = 0 \ or \ 6 \\ 0.0 \ if \ |y| = 1 \ or \ 5 \\ 0.4 \ if \ |y| = 2 \ or \ 4 \\ 0.8 \ if \ |y| = 3 \end{cases} \quad (12)$$

The maximum value is $D/6$. In practice, we will use as fitness the value $D/6$-f so that the problem is now to find the minimum 0.

Experiments were conducted with four variations of PS^{2}O according to the four symbiotic coevolutionary relationships. To evaluate the performance of the proposed PS^{2}O, the canonical PSO was also used for comparisons.

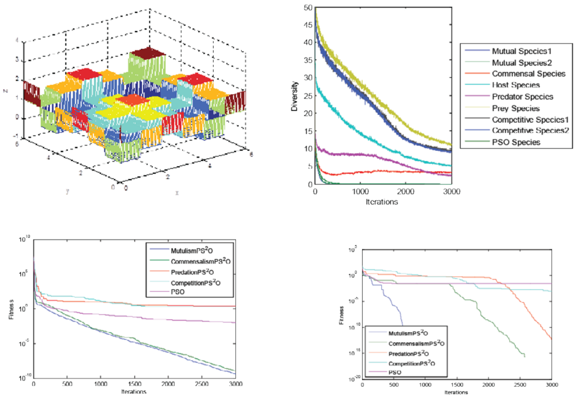


(a) fitness convergence

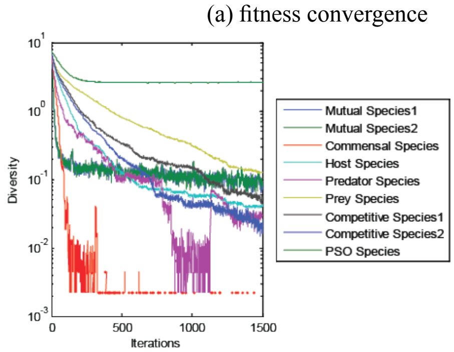


(b) diversity shifting

Figure 8. Simulation result on Griewank.



(a) fitness convergence



(b) diversity shifting

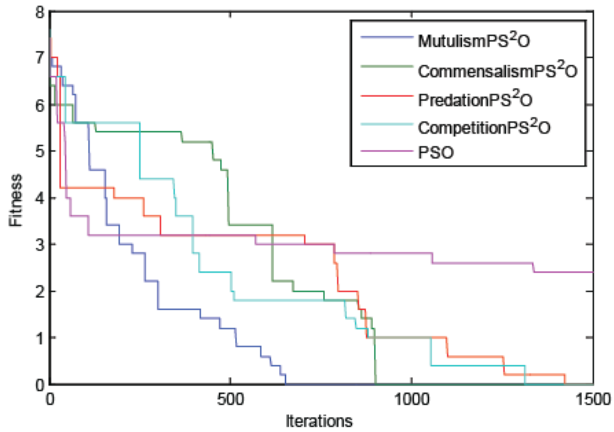
Figure 9. Simulation result on Golderg's order-3.

The population size of all algorithms used in our experiments was set at 60. For canonical PSO, the learning rates c_1 and c_2 were both 2.05 and the constriction factor χ =0.729. For four PS²Os, parameters were set to the values $c_1 = c_2 = c_3$ =1.3667, and χ =0.729. The experiment run 25 times respectively for each algorithm on each benchmark function and max generation is set at 3000.

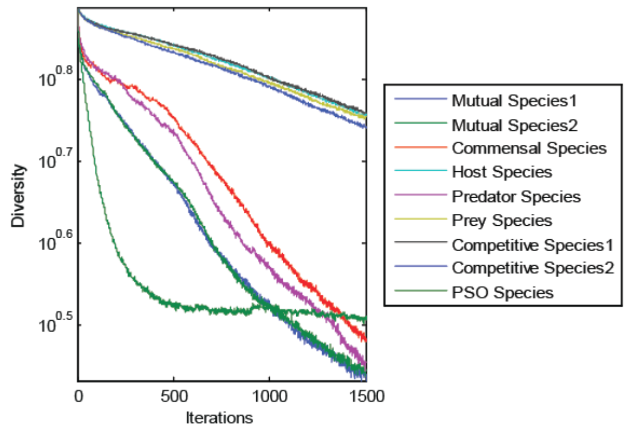
The representative results obtained are presented in Table 1, including the best, worst, mean and standard deviation of the function values found in 25 runs.

Figures 6 through 10 present the evolution process, including the best fitness convergence and the diversity shifting graphs, for all algorithms according to the reported results in Table 1.

From Table 1, we can observe that the four PS²O algorithms obtain an obviously remarkable performance. From the fitness convergence figures, we can see it clearly all PS²O variants converged greatly faster and to significantly better results than the canonical PSO for all unimodal, multimodal, and discrete cases.



(a) fitness convergence



(b) diversity shifting

Figure 10. Simulation result on Bipolar order-6.

From the diversity shifting results, we can observe that all the symbiotic partners do not suffer from premature convergence and are able to reach states of higher fitness with greatly faster rate. Just like in nature, dissimilar species spontaneously establish symbiotic relationships to improve their survivability and adaptability. While the canonical PSO species lost its population diversity quickly and then suffer adaptation stagnation in successive generations. From these simulation results, it maybe concluded that PS²O can accommodate a considerable potential for solving more complex problems.

Table 1. Performance of all algorithms on benchmark fucions $f_1 \sim f_5$.

Func.		PS²O-C	PS²O-P	PS²O-M	PS²O-T	PSO
	Best	1.0803e-009	2.2127	**3.9646e-010**	1.9175	0.0101
	Worst	3.3329	3.2295	**2.9866**	3.0551	4.1661
f_1	Mean	0.3999	0.8763	**0.1793**	0.5315	0.5966
	Std	1.0016	0.9846	**0.1838**	1.3783	1.3883
	Rank	2	5	**1**	3	4
	Best	**0**	0.0428	0.1120	0.5472	0.9950
	Worst	**0**	1.0821	2.9546	2.9281	8.9546
f_2	Mean	**0**	0.9950	1.9899	1.1429	4.3778
	Std	**0**	0.8256	1.2950	1.8891	1.9658
	Rank	**1**	2	4	3	5
	Best	**0**	**0**	**0**	0.0011	0.0295
	Worst	**0**	**0**	**0**	0.1137	0.1697
f_3	Mean	**0**	**0**	**0**	0.0532	0.0773
	Std	**0**	**0**	**0**	0.0273	0.0367
	Rank	**1**	**1**	**1**	4	5
	Best	**0**	**0**	**0**	**0**	2.4000
	Worst	**0**	**0**	**0**	**0**	3.6000
f_4	Mean	**0**	**0**	**0**	**0**	2.1833
	Std	**0**	**0**	**0**	**0**	0.2614
	Rank	**1**	**1**	**1**	**1**	5
	Best	**0**	**0**	**0**	**0**	1.8000
	Worst	**0**	**0**	**0**	**0**	2.8000
f_5	Mean	**0**	**0**	**0**	**0**	3.1800
	Std	**0**	**0**	**0**	**0**	0.3295
	Rank	**1**	**1**	**1**	**1**	5

4. Conclusions

The models of evolution that are being used in evolutionary and swarm intelligence algorithms are becoming increasingly complex. Hence, this work proposed a symbiotic multi-swarm coevolution optimization model named PS²O. The model has been instantiated as four novel multi-species optimizers, which extends the dynamics of the canonical PSO algorithm by adding a significant ingredient that takes into account four different symbiotic coevolution mechanisms respectively.

A set of 5 benchmark functions that including unimodal, multimodal, and discrete cases has been used to test the proposed PS²O algorithms in comparison with the canonical PSO. The simulation results show that, for all benchmark functions, the PS²O variants reach remarkable better fitness values than PSO. We also simulated the coevolution process of symbiotic species' diversity in our model. The results capture some important aspects of the dynamics of biological coevolution that some evolutionary biologists believe takes place in nature.

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Low Frequency Rotating Magnetic Field Generator And Its Application in Blood Pressure Regulation

Yumiao Ren[1, 2]

[1] The Key Laboratory of Biomedical Information Engineering of Ministry of Education, Research Center of Rehabilitation Science and Technology, School of Life Science and Technology, Xi'an Jiaotong University, Xi'an, 710049, shaanxi,China
[2] School of Electronics and Information Engineering, Xi'an Technological University, Xi'an, 710032, shaanxi, China

Jianbao Zhang, Xiaoni Wang, Lin Xie, Binbin Liu

The Key Laboratory of Biomedical Information Engineering of Ministry of Education, Research Center of Rehabilitation Science and Technology, School of Life Science and Technology, Xi'an Jiaotong University, Xi'an, 710049, shaanxi,China

Abstract
On the basis of predecessors' research and the existing theory, for convenient and reliable to study the biological effect of low frequency rotating magnetic field, design a high precision and low frequency rotating magnetic field generator, which could be used to stimulate the small area. Choose stepper motor to drive permanent magnet for produce a rotating magnetic field, which can reduce the magnetic field coverage area and improve the positioning accuracy. Adopt high precision stepper motor controller and step motor to control motor speed for high precise frequency of the rotating magnetic field. Using the motor controller can output three road motor control pulse at the same time, to realize frequency is 1-15 Hz, 0.3-0.4 T surface magnetic field strength and three same characteristics rotating magnetic field. Using light touch switch and LCD display for the frequency, the direction of the spin magnetic control