Modeling Coevolutionary Genetic Algorithms on Two-Bit Landscapes: Random Partnering

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Abstract. A model of coevolutioinary genetic algorithms (COGA) consisting of two populations coevolving on two-bit landscapes is investigated in terms of the effects of random partnering strategy, different population updating schemes, and changes in mutation rate and evolution rate. The analytical and numerical approaches showed that even in such a simple model, the dynamics can change dramatically with different evolutionary scenarios in such an extent that deserves our attention from the point of view of algorithm design.

1 Introduction

The theory of natural selection is the only acceptable explanation for the origin and maintenance of adaptation among organisms. The Darwin's and Wallace's original idea about organic evolution has gone beyond biology as far as epistemology, psychology and economics *etc.* In computer science, the term evolutionary computation (EC) stands for a family of algorithms based on the belief that modeling the process of natural selection could help us to solve difficult real-world problems. While a mathematical theory of EC is indispensable by all means to constructing effective and efficient evolutionary algorithms (EAs), such a general and coherent theory is still far beyond our grasp.

To develop a mathematical theory of coevolutionary EAs (COEAs) maybe even more difficult. Different from standard EAs, where individuals are evaluated separately from each other according to predefined objective function(s), one main characteristic of COEAs is that the evaluation procedure involves more than one individuals, and the fitness of an individual is depending on its interaction with its partners. It is intuitively comprehensible that the implemented partner selection strategies can have significant influences on the algorithm's dynamics and optimization performance. In this paper, the effects of random partnering strategy, population updating scheme, mutation rate and evolution rate are investigated through a model of coevolutionary genetic algorithms (COGA) that consists of two populations coevolving on two-bit landscapes.

There have been a lot of applications of modeling coevolutionary process to problem-solving [6,10], as well as analytic and empirical results about the dynamics of coevolutionary algorithms [2,3,9]. Our purpose is to give a relatively extensive investigation about the dynamics of COGA. This paper is organized as follows. After a brief review of the Schema Theorem, the basic model is introduced. Section 4 shows analytic and computer simulation results of different coevolutionary scenarios and Section 5 examines the model from an evolutionary game-theoretical point of view. Finally, Section 6 concludes with a brief of our findings and a few remarks about future work.

2   The Schema Theorem

GAs can be described using the well-known Schema Theorem [8]:

$$m(H, t+1) \geq m(H,t)\frac{f(H)}{\bar{f}}\left[1 - p_c\frac{\delta(H)}{l-1} - o(H)p_m\right] \tag{1}$$

where $m(H,t)$ is the number of instances of schema H at time t, $f(H)$ is the average fitness of individuals in the population representing H at time t, $\bar{f}$ is the average fitness of individuals in the population, $\delta(H)$ is the defining length of H, $o(H)$ is the order of H, strings are of length l, p_c is the probability of crossover, and p_m the probability of mutation. The Schema Theorem shows that short, low-order, and highly fit schemata (referred to as building blocks) are given exponentially increasing numbers of instances. The building block hypothesis assumes that instead of building high-performance strings by trying every conceivable combination, GAs work with building blocks and construct better and better strings from the best partial solutions of past samplings [5, p.41]. But, as pointed out by Goldberg, due to the coding and the objective function itself, building blocks sometimes may be misleading, and make it difficult if not impossible to find the optimal solutions. The simplest case is a two-bit problem, which known as minimal deceptive problem (MDP) [5].

Grefenstette [4] however, showed that *deception* is neither necessary nor sufficient for problems to be GA-hard. The reason, he pointed out, lies in the fact that while the notion of deception [5] is defined in terms of the *static* average fitness of hyperplanes, what really important to GAs' ability of finding better solutions is their dynamic behaviour as described by the Schema Theorem. For example, consider the fitness landscape shown in Fig. 1, which can be considered both a two-bit landscape and a landscape of order-two schemata. The fitnesses are given as $f(01) = 1.0$, $f(11) = 0.0$, $f(00) = 0.0$ and $f(10) = 2.0$, 10 is the maximum. The static building block hypothesis assumes no deception existing here since $f(1*) = \frac{f(10)+f(11)}{2} = 1.0 > f(0*) = \frac{f(00)+f(01)}{2} = 0.5$ and $f(*0) = \frac{f(00)+f(10)}{2} = 1.0 > f(*1) = \frac{f(01)+f(11)}{2} = 0.5$. However, consider a GA population consisting of individuals as $p(00) = 16\%$, $p(01) = 64\%$, $p(10) = 4\%$ and $p(11) = 16\%$, respectively. Then the *observed* fitness [4] of the schema $1*$ is $f(1*) = \frac{p(10)f(10)+p(11)f(11)}{p(10)+p(11)} = 0.4$, and in the same sense

$f(0*) = 0.8$, $f(*0) = 0.4$, $f(*1) = 0.8$. Since $f(0*) > f(1*)$ and $f(*1) > f(*0)$, according to the Schema Theorem, the population might also converge to 01, the local optimum, if $p_c = 1.0$ and $p_m = 0.0$. This indicates that whether a problem is GA-hard is searcher-depended, and the characterization of GA-hard problems "must take into account the basic features of the GA, especially its dynamic, biased sampling strategy" [4].

3 A Model of Coevolutionary GA

Bull [3] extended the Schema Theorem to coevolutionary systems. In a $(1 + S)$-population model with random partnering and asynchronous reproduction, suppose scheme $H = \{H_k, H_{c_1}, H_{c_2}, \ldots, H_{c_S}\}$, where H_k is sub-schema in current population and H_{c_i} sub-schema in the other S populations, the Schema Theorem reads

$$m(H, t + 1) \geq m(H_k, t)\frac{f(H_k)}{\bar{f}} \cdot \left[1 - p_c\frac{\delta(H_k)}{l_k - 1} - o(H_k)p_m\right] \cdot \prod_{i=1}^{S} \frac{m(H_{c_i}, t)}{P_{op}} \quad (2)$$

where P_{op} stands for population size and

$$m(H_{c_i}, t) \geq m(H_{c_i}, t - 1)\frac{f(H_{c_i})}{\bar{f}} \cdot \left[1 - p_c\frac{\delta(H_{c_i})}{l_{c_i} - 1} - o(H_{c_i})p_m\right]. \quad (3)$$

As shown in Eqn. (2), the basic idea of COGA is "divide-and-conquer", namely divide the problem at hand into a number of subproblems and challenge each of them separately, then construct the complete solutions from the subproblems' solutions. This kind of COGA has been named as cooperative coevolutionary GA [10]. To our purpose of investigating coevolutionary behaviour of GA, a model that consists of two populations coevolving on two-bit landscapes is constructed, where finding the maximum is divided into two subproblems, and each is challenged by a Simple GA (SGA). Individuals in the two population A and B represent the first and second bit respectively, and to evaluate individuals in A, individuals from B are required and *vice versa*. Unless otherwise stated, of the two-bit strings used in this paper, the first bit corresponds to individuals of A, the second to that of B.

4 Random Partnering Strategy

Let P_a (P_b) be the proportion of "0" individuals of A (B), f_a^0 (f_a^1) the fitness of "0" ("1") individuals of A, f_b^0 (f_b^1) that of B, respectively. By using random partnering strategy, an individual's partners are picked up from the other population at random, and the expectation of the individual's fitness reads

$$\begin{cases} E(f_a^0) = P_b \cdot f(00) + (1 - P_b) \cdot f(01) = 1 - P_b \\ E(f_a^1) = P_b \cdot f(10) + (1 - P_b) \cdot f(11) = 2P_b \\ E(f_b^0) = P_a \cdot f(00) + (1 - P_a) \cdot f(10) = 2 - 2P_a \\ E(f_b^1) = P_a \cdot f(01) + (1 - P_a) \cdot f(11) = P_a. \end{cases} \quad (4)$$

Those values can also be considered the fitness obtained when using *complete mixing strategy*, in which an individual interacts in a pairwise way with all individuals in the other population. Because complete mixing strategy is computational expensive, it is seldom used in COGA but is popular in literature of evolutionary game theory. By setting $E(f_a^0) = f_a^0$, $E(f_a^1) = f_a^1$, $E(f_b^0) = f_b^0$ and $E(f_b^0) = f_b^0$, the resulting behaviour of COGA with complete mixing strategy can also be interpreted as the "expected" behaviour of COGA with random partnering strategy. Let F_a (F_b) be the average fitness of individuals in A (B), it holds

$$\begin{cases} F_a = P_a \cdot f_a^0 + (1 - P_a) \cdot f_a^1 = P_a + 2P_b - 3P_aP_b \\ F_b = P_b \cdot f_b^0 + (1 - P_b) \cdot f_b^1 = P_a + 2P_b - 3P_aP_b. \end{cases} \quad (5)$$

Denote the changes of P_a and P_b due to selection by ΔP_a and ΔP_b, then the proportion of "0" in A and B after selection will be

$$\begin{cases} P_a' = P_a + \Delta P_a \\ P_b' = P_b + \Delta P_b \end{cases} \quad (6)$$

and the implemented roulette-wheel selection scheme in SGA leads

$$\begin{cases} \Delta P_a = K_a P_a \left(f_a^0/F_a - 1 \right) \\ \Delta P_b = K_b P_b \left(f_b^0/F_b - 1 \right) \end{cases} \quad (7)$$

where K_a and K_b are coefficients that scale the rate of evolutionary change [1]. Let M_a and M_b be mutation rate of A and B, then the proportion of "0" in the next generation can be expressed as

$$\begin{cases} P_a'' = P_a'(1 - M_a) + (1 - P_a')M_a \\ P_b'' = P_b'(1 - M_b) + (1 - P_b')M_b. \end{cases} \quad (8)$$

4.1   Without Mutation

The behaviour of the above model can be characterized by its fixed points and their stability properties. At the beginning, suppose $M_a = M_b = 0$, then the fixed points of Eqn. (8) must satisfy $\Delta P_a = \Delta P_b = 0$ and this leads

$$\begin{cases} P_a(1 - P_a)(1 - 3P_b) = 0 \\ P_b(1 - P_b)(2 - 3P_a) = 0. \end{cases} \quad (9)$$

In consequence, there are 5 fixed points: (0,0), (1,0), (0,1), (1,1) and $(\frac{2}{3}, \frac{1}{3})$. Since the sign of ΔP_a and ΔP_b in Eqn. (7) depends on f_a^0, F_a, f_b^0 and F_b, by comparing f_a^0 and f_a^1, f_b^0 and f_b^1 in Eqn. (4), we obtain

$$\begin{cases} f_a^0 > f_a^1 \text{ if } 0 < P_b < \frac{1}{3} \\ f_a^0 < f_a^1 \text{ if } \frac{1}{3} < P_b < 1 \end{cases} \quad \text{and} \quad \begin{cases} f_b^0 > f_b^1 \text{ if } 0 < P_a < \frac{2}{3} \\ f_b^0 < f_b^1 \text{ if } \frac{2}{3} < P_a < 1. \end{cases}$$

As a result, the phase space is divided into four regions I, II, III and IV (Fig. 2), all orbits in region II converge to (0,1) and all orbits in region IV to (1,0).

Since any perturbations that made the system apart from (1,0) and (0,1) but still remain in region II and IV respectively will not change the system's ultimately ending up to them, those two fixed points are stable. By contrast, any perturbation that causes the system to apart from (0,0) and (1,1) will make the system ultimately converge to (1,0) and (1,0) respectively. So, (0,0) and (1,1) are unstable fixed point. For $(\frac{2}{3}, \frac{1}{3})$, the Jacobian of Eqn. (6) at this point is

$$A = \begin{bmatrix} \frac{\partial P'_a}{\partial P_a} & \frac{\partial P'_a}{\partial P_b} \\ \frac{\partial P'_b}{\partial P_a} & \frac{\partial P'_b}{\partial P_b} \end{bmatrix} = \begin{bmatrix} 1 & -K_a \\ -K_b & 1 \end{bmatrix} \tag{10}$$

where the two eigenvalues are $1 \pm \sqrt{K_a K_b}$. As $0 < (1 - \sqrt{K_a K_b}) < 1 < (1 + \sqrt{K_a K_b})$, $(\frac{2}{3}, \frac{1}{3})$ is a saddle, and there are two orbits converging to it, one of them in region I and the other in region III. Those two orbits consist the separatrix that divides the phase space into two basins of attraction, all orbits above the separatrix converge to (0,1), and all orbits below it converge to (1,0).

Fig. 3 shows a set of evolutionary trajectories where A and B evolving at the same rate $K_a = K_b = 0.1$. It can be seen that almost all trajectories end at one of the two stable fixed points, (1,0) and (0,1), which correspond to the global and local maximum respectively. The eventual end-point is completely determined by the initial starting positions, all orbits beginning at points on the same side of the separatrix lead to the same fixed point.

A point is called a *sink* (*source*), if very orbit converges to it when time runs toward $t \to +\infty$ ($t \to -\infty$). In the model, by setting $t \to -\infty$, the original problem can be converted to a problem of searching the minimum on the landscape, where the two minima have the same value 0.0. The time-reversed evolution processes can be realized by rewriting Eqn. (7) as

$$\begin{cases} \Delta P_a = -K_a P_a (f_a^0 / F_a - 1) \\ \Delta P_b = -K_b P_b (f_b^0 / F_b - 1) \end{cases} \tag{11}$$

Fig. 4 shows a set of evolutionary trajectories of this case. All trajectories start from the points satisfying $P_a + P_b = 1$ will end up to the saddle point $(\frac{2}{3}, \frac{1}{3})$, and the seperatrix $P_a + P_b = 1$ divides the phase space into two basins of attraction of the same size since the two minima have the same fitness value. All orbits above the separatrix converge to (1,1), all orbits below it converge to (0,0).

To show how changing of the evolution rate K_a and K_b affects dynamics, Fig. 5 gives trajectories where B evolves 5 times faster than A. It can be seen that although the number and positions of the fixed points do not change, the shape of the separatrix is bent. As shown in Fig. 2, since orbits that beginning in region II and region IV end up to (0,1) and (1,0) respectively, the ultimate end-up point of orbits that beginning in region I and III depends on which region, namely II or IV, is reached first. If it is region II reached first, the orbits will end up to (1,0), otherwise end up to (0,1). The evolution rate K_a and K_b in this sense, represent velocity of the orbits moving along x axis and y axis. B evolving 5 times faster than A means that the velocity along y axis is 5 times faster than
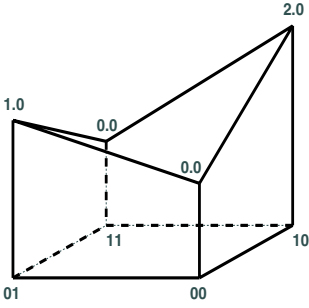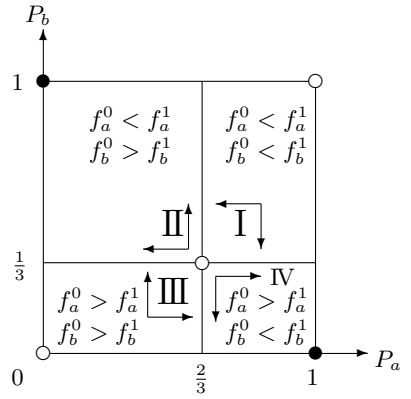
Fig. 1. A two-bit deceptive fitness landscape.

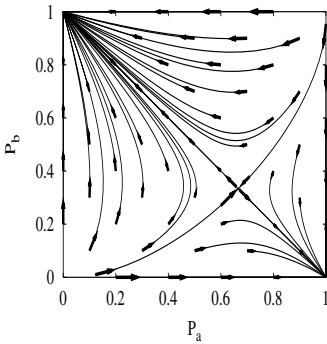**Fig. 2.** Phase portrait of the model with random partnering strategy.
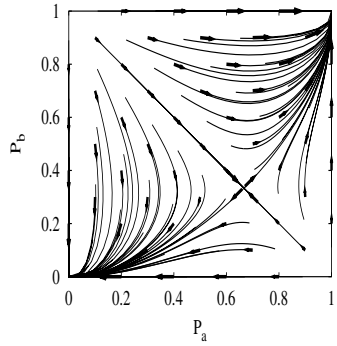

Fig. 3. $K_a = K_b = 0.1$, $M_a = M_b = 0$.

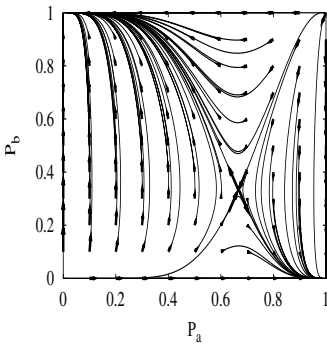**Fig. 4.** $t \to -\infty$, $K_a = K_b = 0.1$, $M_a = M_b = 0$.

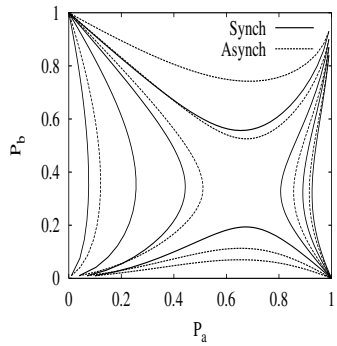**Fig. 5.** B evolves fast than A. $K_a = 0.02, K_b = 0.1$, $M_a = M_b = 0$.

Fig. 6. Updating A first then B. $K_a = K_b = 0.1$, $M_a = M_b = 0$.

that along x axis. In region III, since $f_b^0 > f_b^1$, increasing K_b will increase the velocity translating positively along y axis, and make more orbits beginning in region III reach region II first and end up to (1,0). On the other hand, In region I, since $f_b^0 < f_b^1$, increasing K_b will increase the velocity translating negatively along y axis, and make more orbits beginning in region I reach region IV first and end up to (1,0).

Next, the effects of population updating scheme are investigated. Fig. 6 shows eight pairs orbits of which each pair orbits start from the same position but using synchronous and asynchronous updating strategies, respectively. In asynchronous updating, A is updated first, then B. This fact means that all orbits will move along x axis one-step-ahead than y axis, although the direction can be both positive and negative, depending on the value of f_a^0, f_a^1, f_b^0 and f_b^1. As it is shown in Fig. 2, in region III, since $f_a^0 > f_a^1$, updating A first made orbits beginning in this region move positively along x axis one-step-ahead. In consequence, there are more orbits reach region IV first and end up to (0,1). On the other hand, in region I, because $f_a^0 < f_a^1$, updating A first made orbits beginning in this region move negatively along x axis one-step-ahead, and consequently, there are more orbits reach region II first and end up to (1,0).

4.2   With Mutation

Firstly, consider what happens if there were no selection pressure imposed on both A and B. At the equilibrium, where $P_a'' = P_a' = P_a$ and $P_b'' = P_b' = P_b$, we have

$$\begin{cases} P_a = P_a(1 - M_a) + (1 - P_a)M_a \Rightarrow p_a = 0.5 \\ P_b = P_b(1 - M_b) + (1 - P_b)M_b \Rightarrow P_b = 0.5 \end{cases} \tag{12}$$

This means that when no selection pressure imposed, mutation makes all orbits converge to the single fixed point (0.5,0.5).

Now, let us see what happens when both mutation and selection are assumed in A while only selection in B. In this case, from Eqn. (6)(7)(8), we have

$$\begin{cases} \Delta P_a = M_a(1 - 2P_a) + (1 - 2M_a)K_a P_a(f_a^0/F_a - 1) \\ \Delta P_b = K_b P_b(f_b^0/F_b - 1) \end{cases} \tag{13}$$

and at the equilibrium, where $\Delta P_a = \Delta P_b = 0$, we obtain three fixed points:

$$\begin{cases} p_1 = \left(\frac{M_a(1 - 2K_a) + K_a}{2M_a(1 - K_a) + K_a}, 0 \right) \\ p_2 = \left(\frac{M_a}{2M_a(1 - K_a) + K_a}, 1 \right) \\ p_3 = \left(\frac{2}{3}, \frac{1}{3} - \frac{M_a}{K_a(1 - 2M_a)} \right). \end{cases} \tag{14}$$

It can be seen from Eqn. (14) that by keeping M_a constant, increasing K_a will cause p_1 moving along x axis positively ($+x$ direction) toward (1,0), p_2 along $y = 1$ negatively ($-x$ direction) toward (0,1), p_3 along $x = \frac{2}{3}$ with $+y$ direction toward $(\frac{2}{3}, \frac{1}{3})$. On the other hand, taking M_a as constant, increasing M_a will

cause p_1 and p_2 moving toward $(\frac{1}{2}, 0)$, and $(\frac{1}{2}, 1)$ respectively, and p_3 toward $(\frac{2}{3}, 0)$ or even disappear. The conflicting relation between mutation and selection is definitely expressed by the term $K_a(1 - 2M_a)$. Fig. 7 shows simulation results of this case where the three fixed points are $(\frac{108}{118}, 0), (\frac{10}{118}, 1)$ and $(\frac{2}{3}, \frac{88}{294})$.

At last, consider what happens when both mutation and selection are assumed in A and B. Again, from Eqn. (6)(7)(8), we obtain

$$\begin{cases} \Delta P_a = M_a(1 - 2P_a) + (1 - 2M_a)K_a P_a(f_a^0/F_a - 1) \\ \Delta P_b = M_b(1 - 2P_b) + (1 - 2M_b)K_b P_b(f_b^0/F_b - 1). \end{cases} \tag{15}$$

At the equilibrium, it holds that

$$\begin{cases} M_a(1 - 2P_a) = -(1 - 2M_a)K_a P_a(f_a^0/F_a - 1) \\ M_b(1 - 2P_b) = -(1 - 2M_b)K_b P_b(f_b^0/F_b - 1) \end{cases} \tag{16}$$

and this leads to

$$\frac{M_a(1 - 2M_b)K_b}{M_b(1 - 2M_a)K_a} = \frac{P_a(1 - P_a)(1 - 3P_b)(1 - 2P_b)}{P_b(1 - P_b)(2 - 3P_a)(1 - 2P_a)}. \tag{17}$$

Assuming $M_a = M_b$ and $K_a = K_b$, Eqn. (17) changes to

$$(P_a + P_a P_b - 2P_b)(1 - P_a - P_b) = 0 \tag{18}$$

and we have

$$P_a + P_a P_b - 2P_b = 0 \tag{19}$$

$$P_a + P_b = 1 \tag{20}$$

Since substitution of Eqn. (19) into Eqn. (16) causes negative M_a, Eqn. (20) must hold. Rewrite Eqn. (16) as

$$M_a = \frac{K_a P_a(f_a^0/F_a - 1)}{2P_a - 1 + 2K_a P_a(f_a^0/F_a - 1)} \tag{21}$$

and substitute Eqn. (20) into it and assume $K_a = K_b = 0.1$, then plot Eqn. (21) in Fig. 11. It can be seen that there is a threshold M_a^*, for $0 < M_a < M_a^*$ three fixed points, $M_a = M_a^*$, two fixed points, $M_a > M_a^*$, a single fixed point exists, respectively. The same can also be done with the evolution rate by rewriting Eqn. (16) as

$$K_a = \frac{M_a(1 - 2P_a)}{P_a(2M_a - 1)(f_a^0/F_a - 1)}. \tag{22}$$

By substituting Eqn. (20) into it and assuming $M_a = M_b = 0.01$, we get Fig. (12), where a threshold K_a^* exists, for $0 < K_a < K_a^*$ a single fixed point, $M_a = M_a^*$, two fixed points, $M_a > M_a^*$, three fixed points exist, respectively. Fig. 8,9,10 show how the number and position of fixed points, in addition with the dynamics behaviours change according to different values of mutation rate and evolution rate.

The population updating strategy is also investigated (data not shown), and the results can be explained from the same way as shown in the case of without mutation.
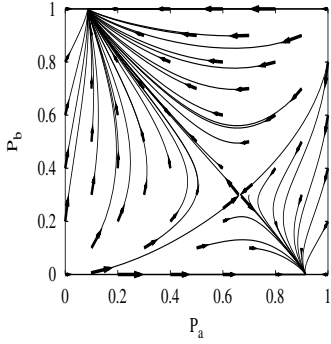
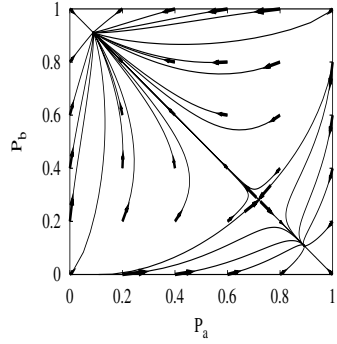**Fig. 7.** Assuming mutation to A only. $K_a = K_b = 0.1$, $M_a = 0.01, M_b = 0$.

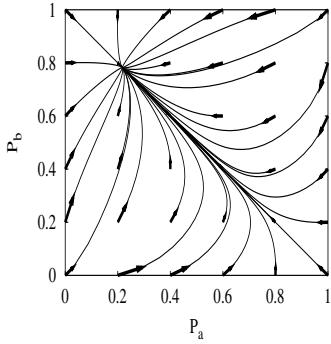**Fig. 8.** $K_a = K_b = 0.1$, $M_a = M_b = 0.01$. Three fixed points.

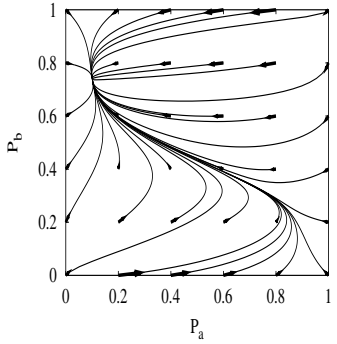**Fig. 9.** $K_a = K_b = 0.1$. $M_a = M_b = 0.03$. One fixed point.

Fig. 10. $K_a = 0.1, K_b = 0.02$, $M_a = M_b = 0.01$. One fixed point.
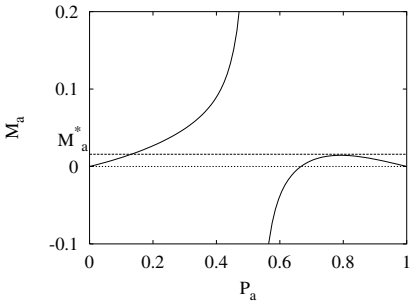

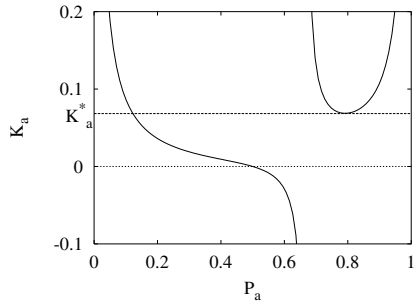**Fig. 11.** $K_a = K_b = 0.1$, $M_a = M_b$.

Fig. 12. $K_a = K_b,$, $M_a = M_b = 0.01$.

5   Discussion

Goldberg [5, p.50] has expressed a model of Simple GA (SGA) that consist of only two operators: reproduction and crossover. The COGA model proposed here can also be viewed as a simple GA consisting of three operators, reproduction, mutation and crossover(crossover rate 1.0). That is, the random partnering of two one-bit population has the same effect as a crossover operator to a single two-bit population. Still, from the population genetics viewpoint, the above COGA model can also be interpreted as a model of haploid two-locus two-allele infinite population with random mating and non-overlapping generation.

   In [3], Bull treated situations where two populations are coevolving on their respective fitness landscapes. The model proposed in this paper can be extended to this case by rewriting Eqn. (4) according to the fitness landscapes of each bit. Contrast with Bull, who has started all computer experiments from $P_a = P_b = 0.5$, we gave an relatively overall investigation about different start conditions. For example, Bull showed that on the landscape defined as $f(00) = 0.4$, $f(01) = 0.8$, $f(10) = 1.0$, and $f(11) = 0.1$, starting from $P_a = P_b = 0.5$, both populations will converge at about $P_a = P_b = 0.54$. This can be explained by our model as that in the above landscape, setting $f_a^0 = f_a^1$, $f_b^0 = f_b^1$ in Eqn. (4) [1] causes $P_a = P_b = \frac{7}{13} = 0.538$ at the equilibrium. Furthermore, our simulation results on Bull's landscape (Fig. 13) also show that any start from $P_a = P_b \neq 0$ will end at $P_a = P_b = \frac{7}{13}$, while all the other starting points will end at either $P_a = 1$, $P_b = 0$ or $P_a = 0$, $P_b = 1$ depending on their starting positions.

   In his discussion about fitness level, Bull described a situation where instead of fitness of single bits, only fitness of two-bit strings are available. He referred to this as "global-level fitness", which is exactly what our work concerned in this paper. The experiment as Bull showed, where two populations converged at about $P_a = P_b = 0.62$ can be explained by our model as that since the global-level landscape is defined as $f'(00) = f(00) + f(00) = 0.8$, $f'(01) = f(01) + f(10) = 1.8$, $f'(10) = f(01) + f(10) = 1.8$, and $f'(11) = f(11) + f(11) = 0.2$, setting $f_a^0 = f_a^1$, $f_b^0 = f_b^1$ in Eqn. (4) causes $P_a = P_b = \frac{16}{26} = 0.615$ at the equilibrium. On account of his experiment results, Bull concluded that "using a global fitness has a slight effect on coevoluntary system since each population's landscape is added onto its parters" [3, p.205]. While Bull's comments are true about his landscapes, it is worth pointing out that in general, the effect of global-level fitness on the dynamics of coevolutionary systems depends on the particular landscapes under consideration, *e.g.* if landscapes of the two bits are defined according to the Prisoner's Dilemma, it can be shown that a global fitness approach will induce to a cooperation while a local fitness approach to defection.

   From the viewpoint of Bull's local-level fitness, the landscape shown in Fig. 1 arise a scene where the two bits are facing a asymmetric situations, *e.g.* while a "0" of A partnering with a "1" in B will receive 1.0 as its fitness, a "0" of B partnering with a "1" will receive an increased fitness 2.0. If we think of

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[1] Eqn. (4) should be rewritten as $f_b^0 = f_a^0$ and $f_b^1 = f_a^1$ to treat Bull's local-level fitness assignment. See below.
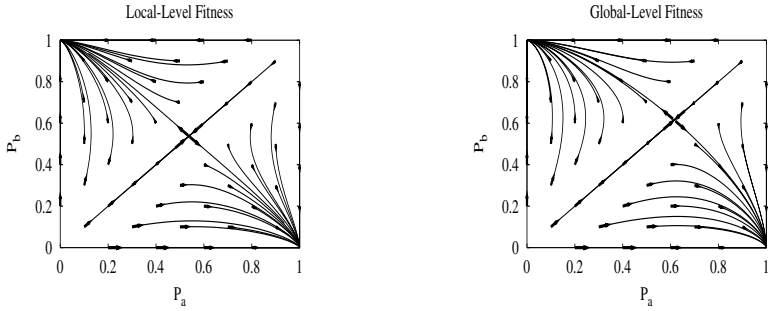
Fig. 13. The COGA model on Bull's landscapes. $M_a = M_b = 0, K_a = K_b = 0.1$.

"0" and "1" as strategies in a game situation instead of values of bits, we can see that this asymmetry has been investigated in evolutionary game theory as asymmetric games. The *battle of sexes* is an example of such game.

A sexual population can be considered as a population of males that interacts with a population of females. It is believed that there is a conflict between males and females concerning their respective investment to their offspring. Raising offspring requires a considerable amount of time and energy, and each parent might attempt to reduce its own share at the expense of the other. But the fact that females produce relatively few, larger eggs, whereas males produce many small sperms made males in a better position. This situation can be modeled game-theoretically as that suppose there are two types of male as well as female, and without loss of generality, the payoff matrices for male and female can be wrote as

$$A_m = \begin{bmatrix} 0 & a_{12} \\ a_{21} & 0 \end{bmatrix} \qquad A_f = \begin{bmatrix} 0 & b_{12} \\ b_{21} & 0 \end{bmatrix}. \tag{23}$$

It is shown in [7] that if $a_{12}a_{21} \leq 0$ ($b_{12}b_{21} \leq 0$), one of the two strategies of male (female) dominates the other, and male (female) population remains either constant, or converges monotonically to 0 or 1; when $a_{12}a_{21} > 0$ and $b_{12}b_{21} > 0$, there is a unique rest point

$$F = \left(\frac{b_{12}}{b_{12} + b_{21}}, \frac{a_{12}}{a_{12} + a_{21}} \right) \tag{24}$$

if $a_{12}b_{12} > 0$, F is a saddle, and almost all orbits converge to one or the other of two opposite corners of the phase space, if $a_{12}b_{12} < 0$, then all orbits are periodic orbits surrounding F.

From this game-theoretical point of view, the landscape in Fig. 1 can be rewritten for the first bit and the second bit respectively as

$$A_{1st} = \begin{bmatrix} 0 & 1 \\ 2 & 0 \end{bmatrix} \qquad A_{2nd} = \begin{bmatrix} 0 & 2 \\ 1 & 0 \end{bmatrix}. \tag{25}$$

where the global-level fitness assignment constrains that $a_{12} = b_{21}$ and $a_{21} = b_{12} \leq 0$. In consequence, the sexes battle game where $a_{12}a_{21} \leq 0$ and $b_{12}b_{21} \leq 0$ can be treated by the COGA model by setting $f(00) = 0.0$, $f(01) = -1.0$, $f(10) = 2.0$ and $f(11) = 0.0$, and the resulted landscape will have one global optimum and no local optimum. For the cases where $a_{12}a_{21} > 0$ and $b_{12}b_{21} > 0$ that can be divided into two sub-classes: $a_{12}b_{12} > 0$ and $a_{12}b_{12} < 0$, since the landscape in Fig. 1 satisfies $a_{12}b_{12} = 1 > 0$, all results shown in Section 4 hold in the sexes battle game also. Finally, the sub-class of $a_{12}b_{12} < 0$ can be realized by rewriting P'_a in Eqn.(6) as

$$P'_a = P_a - \Delta P_a \qquad (26)$$

with an interpretation as that while A is searching for the minimum on the landscape, B is for the maximum. This will induce a competitive coevolution between A and B. Generally speaking, competitive coevolution is more difficult to investigate, it often shows more complex behaviour than cooperative coevolution.

6   Conclusion

This paper presented a simple model of coevolutionary genetic algorithms consisting of two populations coevolving on two-bit landscapes. The effects of population updating schemes and changes in mutation rate and evolution rate are investigated in the context of random partnering strategy. The analytic and empirical results show that even in such a simple model produces rich behaviour in different evolutionary scenarios. The model are now being extended to other partnering strategies.

References

1. Cart T. Bergstrom and Michael Lachmann: The red king effect: when the slowest runner wins the coevolutionary race, PNAS 100 (2003) 593-598
2. Bull, L.: Evolutionary Computing in Multi-Agent Environments: Partners. Proc. of ICGA 7 (1997) 370-377
3. Bull, L.: On coevolutionary genetic algorithms, Soft Computing **5** (2001) 201–207
4. Grefenstette, J. J.: Deception considered harmful. Foundations of Genetic Algorithms 2 (1993) 75-91
5. Goldberg D. E.: *Genetic Algorithms in Search, Optimization and Machine Learning*, Addison-Wesley 1989
6. Hillis, W. D.: Coevolving parasites improve simulated evolution as an optimization procedure, Physica D 42 (1991) 228–234.
7. Hofbauer J. and K. Sigmund K.: *Evolutionary Games and Population Dynamics*, Cambridge University Press (1998)
8. Holland J. H.: *Adaptation in Natural and Artificial Systems*, MIT Press 1992
9. Kauffman S. A. and Johnsen S.: Coevolution to the edge of chaos: coupled fitness landscapes, poised states, and coevolutionary avalanches, Artificial Life II (1991) 325-370
10. Potter M. A. and De Jong K. A.: A cooperative coevolutionary approach to function optimization, Proc. of PPSN III (1994) 249-257