Evolutionary Games with Randomly Changing Payoff Matrices

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Evolutionary games are used in various fields stretching from economics to biology. In most of these games a constant payoff matrix is assumed, although some works also consider dynamic payoff matrices. In this article we assume a possibility of switching the system between two regimes with different sets of payoff matrices. Potentially such a model can qualitatively describe the development of bacterial or cancer cells with a mutator gene present. A finite population evolutionary game is studied. The model describes the simplest version of annealed disorder in the payoff matrix and is exactly solvable at the large population limit. We analyze the dynamics of the model, and derive the equations for both the maximum and the variance of the distribution using the Hamilton–Jacobi equation formalism.

1. Introduction

Evolutionary game theory[1–3] describes a process of evolution, characterized by population dependent selection (the fitness depends on the structure of population). Today, there is no reasonable alternative within evolutionary theory to this mathematical concept. Evolutionary games are usually described through pair interaction; some fixed strategies and fixed payoff matrices are generally assumed. The latter defines the fitness of a population for a given distribution of population via different strategies. Analytical investigation of games with a finite population has been covered.[4–8]

While most literature focuses on evolutionary games with fixed payoff matrices, there have been several works with stochastic choice of strategies in repeated games,[9] mixed strategies,[10] as well as simple analytical dynamics for payoff matrices,[11] or the evolutionary choice of payoff matrix.[12]

Evolutionary games have already been applied to describe the evolutionary dynamics of cancer cells[13,14] and bacteria,[15,16] the theory of biological polymorphism,[17] and public traffic networks.[18] Understanding the social cooperation of cancer cells and acting against this cooperation[19] is one of the most promising directions in curing cancer. Another forward-looking direction of modern virology and cancer biology is the concept of a mutator gene[20] — a gene whose mutation drastically changes the properties of the whole genome, including the whole fitness landscape change (contrary to a simple epistasis between two genes).[21,22]

As both games and mutator genes are assumed to describe the real evolution of microbes and cancer cells, it is reasonable to consider the evolutionary dynamics of a population with mutator genes, i.e., evolutionary games with a mutator gene. In this article we follow to the wider notion of mutator phenomenon, assuming either the change of mutation rate or the fitness landscape.[23] In this work we propose a simple generalization of standard evolutionary games assuming switching of the system between two different regimes with different payoff matrices. Similar random switching between different games have been already considered in game theory, related with the Parrondo paradox.[24]

We investigate finite populations with instructions on how the agents act are probabilistic: the whole situation changes with some probability, similar to the model of gene self-regulation.[25] In this paper we follow our recent work,[26] where we solved a modification of the master equation using the Hamilton–Jacobi equation (HJE) method.[27–30]

Let us first consider a deterministic equation describing the dynamics of a large population in the context of ordinary evolutionary games. In our approach the population consists of m strategies with a total number of players N (N is a large number). The index i specifies the type of strategy and i-th population size equals X_i. This model is formulated as a system of ordinary differential equations (ODE):

$$\dot{x}_i = x_i((A\bar{x})_i - (\bar{x}, A\bar{x})) \qquad (1)$$

where $\bar{x} = (x_1, \ldots, x_m)$, $x_i = X_i/N$, $N = \sum_{k=1}^m X_k$, and A is an $m \times m$ payoff matrix.

The replicator equation (1) describes the deterministic situation with a definite strategy.

In this work we suggest a new version of evolutionary games with a payoff matrix that can be changed between two situations A and B, and give an analytical solution.

2. The Master Equation and Its Solution via Hamilton–Jacobi Equation

Let us consider the model with constant matrices: $A = \{a_{ij}\}$, $B = \{b_{ij}\}$, $i,j = 1, 2, \ldots, m$. The total population size is N; variable X represents the number of players in the first population category. As shown in Fig. 1, the whole system can exist in two versions: the upper chain with matrix A and the lower chain with matrix B, and there are transitions between the two chains.

Here we have the probability conservation condition at any moment of time τ:

$$\Sigma_{0 \le X \le N}(P(X, \tau) + Q(X, \tau)) = 1 \qquad (2)$$

where $P(X, \tau)$ is the probability that the system is in state A and there are X players with the first strategy, and $Q(X, \tau)$ is the probability that the system is in state B with X players with the first strategy.
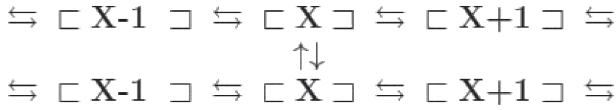
Fig. 1. The scheme of available transitions for the system states (arrows denote transitions). Upper chain corresponds to the game with matrix A, the lower — with matrix B.

We describe the dynamics of the distribution as

$$\frac{dP(X,t)}{N\,dt} = P(X-1,t)R^A_{+1}(X-1) + P(X+1,t)R^A_{-1}(X+1)$$
$$+ P(X,t)R^A_0(X) + Q(X,t)R^{BA}(X);$$

$$\frac{dQ(X,t)}{N\,dt} = Q(X-1,t)R^B_{+1}(X-1) + Q(X+1,t)R^B_{-1}(X+1)$$
$$+ Q(X,t)R^B_0(X) + P(X,t)R^{AB}(X). \qquad (3)$$

Here transitions inside the chains have non-negative rates R^A_{+1}, R^A_{-1} (R^B_{+1}, R^B_{-1}) for the chain A (chain B), and between the chains with rates R^{AB} and R^{BA}. All these rates are derived from the infinite population fitness described via matrices A and B, while different schemes are possible for the finite population version of the model (see Appendices A and B).

To construct our theory for the mutator gene,[21,22] we relate P to a population of replicators with normal allele of a mutator gene, while Q corresponds to a mutated gene, and the transitions between P and Q can be considered as mutations of the mutator gene.

There are two versions of the payoff matrix, each with two strategies. There are transitions between the two regimes, and any moment in time the system can exist in only one regime. Therefore, the concrete player can choose a strategy, but cannot choose a regime. The system moves together from one regime to another with some probability. The situation is like the annealed version of spin glass: first the spins (strategy choice) change according to the given couplings (payoff matrix), then the couplings themselves (payoff matrices) change slowly.

We assume:

$$R^A_{-1}(X) + R^A_{+1}(X) + R^A_0(X) + R^{AB}(X) = 0,$$
$$R^B_{-1}(X) + R^B_{+1}(X) + R^B_0(X) + R^{BA}(X) = 0. \qquad (4)$$

Equation (4) is a balance condition for a smooth population distribution, when the differences of P (Q) at $X-1$, X, and $X+1$ can be neglected.

The system (3) is modified at the boundaries: for $X = 0$ we hold only R^A_0, R^A_1 terms and for $X = N$ we hold only R^A_0, R^A_{-1} terms in Eq. (3). It is important to calculate both the dynamics of the maximum and the variance, and we can find them using the Hamilton–Jacobi equation approach.

Let us consider the system (3) at the limit $N \gg 1$ with the following ansatz:

$$P(X,t) = v_1 \exp[Nu(x,t)]; \quad Q(X,t) = v_2 \exp[Nu(x,t)]. \quad (5)$$

Here we denote $x = X/N$ and define the functions $r^A_l(x)$, $r^B_l(x)$, $r^{AB}(x)$, $r^{BA}(x)$ of continuous variable x:

$$R^A_l(X) = r^A_l(x), \quad R^B_l(X) = r^B_l(x); \quad l = -1, 0, 1;$$
$$R^{AB}(X) = r^{AB}(x), \quad R^{BA}(X) = r^{BA}(x). \qquad (6)$$

We assume that $r^A_l(x), r^B_l(x), r^{AB}(x), r^{BA}(x)$ are the smooth functions of x.

Equation (4) gives:

$$r^A_0(x) = -r^A_+(x) - r^A_-(x) - r^{AB}(x);$$
$$r^B_0(x) = -r^B_+(x) - r^B_-(x) - r^{BA}(x). \qquad (7)$$

Assuming the smoothness of the rate functions and dropping the terms dv_i/dt, $i = 1, 2$, we derive the following system of equations:

$$v_1 q = v_1(r^A_+(x)e^{-u'} + r^A_-(x)e^{u'} + r^A_0(x)) + v_2 r^{BA}(x),$$
$$v_2 q = v_2(r^B_+(x)e^{-u'} + r^B_-(x)e^{u'} + r^B_0(x)) + v_1 r^{AB}(x). \qquad (8)$$

Here we denoted

$$u' = \frac{\partial u(x,t)}{\partial x} \equiv p; \quad q \equiv \frac{\partial u(x,t)}{\partial t}.$$

The consistency condition for linear system of Eq. (8) for the variables v_1 and v_2 together with Eq. (7) gives the following condition:

$$\det[M_{ij}(x,p) - q\delta_{ij}(x)] = 0, \qquad (9)$$

where

$$M_{11} = r^A_+(e^{-p} - 1) + r^A_-(e^p - 1) - r^{AB};$$
$$M_{22} = r^B_+(e^{-p} - 1) + r^B_-(e^p - 1) - r^{BA};$$
$$M_{12} = r^{BA}, M_{21} = r^{AB}. \qquad (10)$$

Equations (9) and (10) imply that

$$\det[M_{ij}(x,0)] = 0. \qquad (11)$$

Expanding the left-hand side of Eq. (9) in the degrees of q, we get the equation:

$$H_0 - qH_1 + q^2 H_2 = 0, \qquad (12)$$

where H_0 and H_1 are defined by Eq. (16) below, and $H_2 = 1$.

Thus we have HJE $q = -H(x,p)$ with the Hamiltonian:

$$H = \frac{H_1 \pm \sqrt{H_1^2 - 4H_0 H_2}}{2H_2}. \qquad (13)$$

We take the "−" solution while considering the dynamics of the maximum. From Eq. (11) we have:

$$H_0(x,p)|_{p=0} = 0. \qquad (14)$$

Looking at the exact dynamics of the maximum or the variance of distribution, we can expand our solution (13) with the "−" sign to get:

$$H = \frac{H_1 - \sqrt{H_1^2 - 4H_0}}{2} \approx \frac{H_0}{H_1} + \frac{H_0^2}{H_1^3}, \qquad (15)$$

where

$$H_0 = \det[M_{ij}],$$
$$H_1 = -\frac{d}{dq}\det[M_{ij}(x,p) - q\delta_{ij}]|_{q=0}. \qquad (16)$$

To investigate the dynamics of the maximum, we assume the ansatz

$$u = -\frac{V(t)}{2}[x - y(t)]^2 + O([x - y(t)]^3), \qquad (17)$$

where $y(t)$ is the average number of players with the first strategy at time t. For our purposes (to calculate exactly the average number of players and the variance), it is enough to keep the $[x - y(t)]^2$ term. To calculate the higher order

correlation, we should consider the higher order expansion terms. These high order terms don't change the found bulk expressions for the $y(t)$ and the $V(t)$.

Let us differentiate (12) with respect to x at the point $x = y(t)$. Using an ansatz Eq. (17), we obtain:

$$\left[-V \frac{\partial H_0(x,p)}{\partial p} - q'_x H_1(x,p) \right]\bigg|_{p=0} = 0. \tag{18}$$

We have the Hamilton equation for the particle with the Hamiltonian given by Eq. (15). Using $H_0(x,0)$, we obtain:

$$\frac{dy(t)}{dt} = -\frac{H'_{0,p}(y,0)}{H_1(y,0)} \equiv b(y). \tag{19}$$

Using (10) and (16) we get:

$$H_0 = Z^A(x,p)Z^B(x,p) - r^{BA}(x)Z^A(x,p)$$
$$- r^{AB}(x)Z^B(x,p);$$

$$Z^\tau(x,p) = r^\tau_+(x)(e^{-p} - 1) + r^\tau_-(x)(e^p - 1); \quad \tau = A, B.$$

Note that $Z^\tau(y,0) = 0$, $H_0(y,0) = 0$. Let us denote $\Delta r^\tau(x) = r^\tau_+(x) - r^\tau_-(x)$. We have:

$$H'_{0,p}(y,0) = r^{BA}(y)\Delta r^A(y) + r^{AB}(y)\Delta r^B(y);$$

$$H_1(y,p) = -r^{AB}(y) - r^{BA}(y) + Z^A(y,p) + Z^B(y,p);$$

$$H_1(y,0) = -r^{AB}(y) - r^{BA}(y). \tag{20}$$

Then we derive

$$b(y) \equiv H'_{0,p}(y,0) = \sigma \Delta r^A(y) + (1-\sigma)\Delta r^B(y); \tag{21}$$

where $\sigma = \frac{r^{BA}(y)}{r^{BA}(y) + r^{AB}(y)}$.

Consider the dynamics of the variance[26] [we denote $Q = 1/V$ and use the equality $dQ/dt = dQ/dy\, b(y)$]. According to the recent work[26] we have for the variance:

$$Q(y) = b(y) \int_{y_0}^y \frac{c(x)dx}{b(x)^3}; \quad c(x) = -H''_{pp}(x,0) \tag{22}$$

Eq. (15) gives:

$$c(x) = -H''_{pp}(x,0) = -\frac{H''_0}{H_1} + 2\frac{H'_0 H'_1}{H_1^2} - 2\frac{(H'_0)^2}{H_1^2} \tag{23}$$

where

$$H'_{1p}(x,0) = -\Delta r^A - \Delta r^B$$

$$H''_{0pp}(x,0) = 2\Delta r^A \Delta r^B - r^{BA}(r^A_+ + r^A_-) - r^{AB}(r^B_+ + r^B_-).$$

For the finite population dynamics via Moran process (Appendix A) we get

$$\Delta r^A(x) = x\left(\frac{(A\bar{x})_1 - (A\bar{x})_2}{(\bar{x}, A\bar{x})} \right);$$

$$\Delta r^B(x) = x\left(\frac{(B\bar{x})_1 - (B\bar{x})_2}{(\bar{x}, B\bar{x})} \right). \tag{24}$$

For the local update law (Appendix B) we have

$$\Delta r^A(x) = x\kappa_1((A\bar{x})_1 - (A\bar{x})_2);$$

$$\Delta r^B(x) = x\kappa_2((B\bar{x})_1 - (B\bar{x})_2). \tag{25}$$

Using the formulas (A·2) and (A·3) in the master equation (3) and (A·8) in the maximum and variance dynamics equations (19), (21), (22), and (23), we can compare the analytical results with the numeric solutions as plotted in Figs. 2 and 3 which show that our analytical results are very reliable.
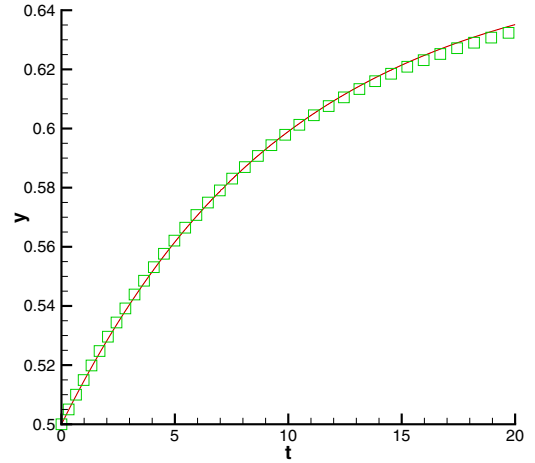
Fig. 2. (Color online) PD+PD: Maximum $y(t)$ as a function of time t via Moran process for $y = \sum_X [P(X,t) + Q(X,t)]\frac{X}{N}$. The numerical solution of y calculated by Eq. (3) with $N = 1000$ (smooth line) versus our analytical results by the HJE method Eq. (19) (squares). We take transition rates $r^{AB} = 0.5$; $r^{BA} = 1$; $A = [3 \quad 1; 3.2 \quad 1.5]$; $B = [7 \quad 0.1; 7.5 \quad 0.3]$.
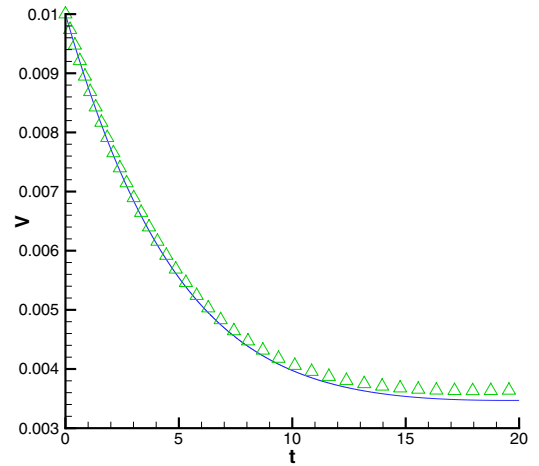
Fig. 3. (Color online) PD+PD: Variance $V = 1/Q$ as a function of t with $V = \sum_X [P(X,t) + Q(X,t)](\frac{X}{N} - 1)^2$. The numerical result for Q calculated using Eq. (3) (smooth line) with $N = 1000$ versus the analytical results by Eqs. (22) and (23) (triangles). Parameters are the same as those in Fig. 1.

3. Different 2×2 Game Classes

In this section we first discuss ordinary two strategy games, then in Sect. 3.1 consider the case of two payoff matrices, in Sect. 3.2 the Moran version of finite population model,[5] in Sect. 3.3 the local update mechanism[5] for the iteration loop of finite population evolutionary dynamics. Let us consider an ordinary two-strategy game with a single regime corresponding to 2×2 matrix denoted by

$$A = \begin{bmatrix} a & b \\ c & d \end{bmatrix}.$$

When the simplex is $S_2 = \{e_1, e_2\}$ the frequencies are denoted by $p = (p_1, p_2) \in S_2$. According to evolutionary game theory studies,[3] the dynamic is defined as

$$\dot{p}_1 = p_1(e_1 \cdot Ap - p \cdot Ap)$$
$$= p_1(1 - p_1)((a - c + d - b)p_1 + b - d) \tag{26}$$

since $p_2 = 1 - p_1$.

There are three qualitatively different classes of the phase portrait for standard replicator dynamics. The rest points of this dynamic (i.e., those $0 \leq p_1 \leq 1$ for which $\dot{p}_1 = 0$) are $p_1 = 0$ and $p_1 = 1$. The interior rest point (if it exists) is given by the solution

$$(a - c + d - b)p_1 = d - b.$$

In the theory of biological polymorphism with only two possible phenotypes of a species, the rest points $p = 0$ and $p = 1$ correspond to the existence of only one phenotype, while the interior rest point corresponds to the co-existence of two phenotypes.[17]

Depending on the constants a, b, c, d one can get:[3]

- Prisoner's dilemma (PD) class. The payoffs satisfy $(a - c)(d - b) \leq 0$. For this class every interior initial point evolves monotonically to 0 or 1, it means that the entire population will eventually consist of only one type of players.
- Coordination (CO) class. The payoffs satisfy $a > c$, $d > b$, $(a - c)(d - b) > 0$. Here different convergent trajectories may have different stable limit points, the interior rest point is unstable.
- Hawk–Dove (HD) class. The payoffs satisfy $a < c$, $d < b$, and every interior initial point evolves monotonically to the interior rest point. It can be understood as a coexistence of the two types of players.

3.1 Combinations of payoff matrices

We can analyze the maximum dynamics (19) using different types of matrices A and B ($B = \begin{bmatrix} e & f \\ g & k \end{bmatrix}$;). There are six different combinations of payoff matrices in (21).

(1) **PD+PD.** PD is a well-known paradigm of the game theory: individuals could either cooperate or defect. The payoff to a player is defined proportionally to the effect on its fitness (survival and fecundity),[31] these payoffs are also known as "temptation" (T), "reward" (R), "punishment" (P). We consider the situation when individuals can use either the A-payoff matrix or the B-matrix in a PD conflict. For example, the cooperation with some individuals can be more productive, but with a greater damage (with lower "sucker" payoff).

(2) **HD+HD.** In the case of HD game[1] two animals are contesting a resource of some value V (here we suppose that fitness of an individual obtaining a resource increases proportionally to this value). This resource could be, for example, a territory in a favorable habitat. The animals could suffer some injuries from the conflict, so the fitness could decrease by C. It is supposed that each animal in the population can play one of the two roles in this conflict: "Hawk" — when the animal escalates and continues until injured or until the opponent retreats, or "Dove" — the animal displays, retreats at once if opponent escalates. $A = \begin{bmatrix} \frac{V-C}{2} & V \\ 0 & \frac{V}{2} \end{bmatrix}$. In our case we consider the two different payoff matrices. We suppose that there is a population living in a specific geographic area. There are two different valuable resources (with values V_1 and V_2: $V_1 < V_2$). We can also interpret these resources as the preferable territories. The contest between two animals is one of the two types (corresponding to the different territories). Each animal chooses the habitat and is involved in only one conflict at the same time [with payoff matrix (2): $A_1(V_1)$ or $A_2(V_2)$].

(3) **CO+CO.** The most studied game in CO class is the Battle of the Sexes game,[3] when players have a mutual interest in cooperation, but different strategies are more preferable for each one. In the two-chain model we can suppose that there are two areas (with A and B payoff matrix) consisting of two alternative types of habitat.

(4) **PD+HD or PD+CO.** We consider the PD game with the following matrix $A_{PD} = \begin{bmatrix} R & S \\ T & P \end{bmatrix}$; where $T > R > P > S$. We suppose that the payoff S could increase: $S_1 > P$, so the fist strategy (cooperation) could become a dominant strategy. The matrix $B_{HD} = \begin{bmatrix} R & S_1 \\ T & P \end{bmatrix}$ represents the HD-case.

If the S-payoff remains the same and R increases ($R_2 > T$), we will have a CO-type interaction: $C_{CO} = \begin{bmatrix} R_2 & S \\ T & P \end{bmatrix}$.

(5) **HD+CO.** Let us consider the HD-HD case with (2) type of matrices and profit values V_1, V_2. If we change the set of strategies in the second payoff matrix and put "Choose V_1/V_2" instead of "Hawk/Dove", it will be the CO-type: $A_2 = \begin{bmatrix} V_1 & 0 \\ 0 & V_2 \end{bmatrix}$. So the individuals either conflict for the territories or coordinate.

3.2 Moran process

Consider the Moran process,[5] which is a way to describe simply the finite population dynamics in population genetics.[32] To organize iteration loop we need to describe the growth of different types according to their fitness functions, then organize the dilution of population to hold the constant population size, we need complete information about the system. We use (A·9) in (21). In general, there are trivial rest points in the maximum equation: $y = 0$ and $y = 1$ satisfy $b(y) = 0$ (except the case with the baseline fitness $w = 1$ and special type of matrices, which we analyze separately). For some matrices A and B, there is a rest point $y^* \in (0, 1]$. Note, that in the following sections we consider constant transition rate between chains ($r^{AB}, r^{BA} = const$). Let p^* be the rest point for A-dynamics and q^* for the B.

Let us consider the type of the rest point, depending on the type of matrix.

(1) A, B are zero-diagonal. In this case $\dot{y} = b(y)$ takes the form

$$b(y) = \frac{1}{y - 1}\left(\sigma \frac{c}{b + c} + (1 - \sigma)\frac{g}{f + g}\right) + 1.$$

a. **PD+PD.** Either there is no rest point or there is only an interior rest point. $A = \begin{bmatrix} 0 & -3 \\ 1 & 0 \end{bmatrix}$; $B = \begin{bmatrix} 0 & -1 \\ 2 & 0 \end{bmatrix}$; We get $y^* = 0.25$.

b. **HD+HD or CO+CO.** There is always an interior rest point.

c. **PD+HD or PD+CO.** There is no interior rest point in this case. For example, A is a PD-type matrix, B — HD-type. If $A = \begin{bmatrix} 0 & -3 \\ 1 & 0 \end{bmatrix}$; $B = \begin{bmatrix} 0 & -1 \\ -2 & 0 \end{bmatrix}$; then $y^* \approx 0.41$. But when $B = \begin{bmatrix} 0 & -4 \\ -1 & 0 \end{bmatrix}$; there is no rest point in $(0, 1)$.

d. **HD+CO.** It is easy to show, that there is always an interior rest point.

(2) A and B have a general form. Now $y = 0$ and $y = 1$ are always rest points, when $a_{22} \neq 0$; $b_{22} \neq 0$. For any combination of chain types it is possible to find such matrices A, B that there is only one or there is no interior point.

3.3 Local update mechanism

Consider now the local update mechanism.[5] Contrary to

Moran scheme we just choose a couple of replicators to organize the iteration loop. We have:

$$b(y) = \sigma y \kappa_1 ((A\bar{y})_1 - (A\bar{y})_2)$$

$$+ (1 - \sigma) y \kappa_2 ((B\bar{y})_1 - (B\bar{y})_2) \tag{27}$$

Equation (27) implies that $y = 0$ (and $y = 1$) is always a rest point. As it has a quadratic form, it either has no interior point or has an interior rest point.

(1) **PD+PD.** There is no interior rest point, when A and B matrices have the same dominant strategy (rest points for the replicator equation are both in 1 or in 0). We can consider the situation, when A and B represent PD-type, but with different stable states.

$$A = \begin{bmatrix} -1 & -2 \\ -0.9 & -1.5 \end{bmatrix}; \quad B = \begin{bmatrix} -2 & -7 \\ -2.5 & -7.1 \end{bmatrix}.$$

For A; the second strategy is dominant, for B — the first; the interior rest point we get is $y^* = 0.5$.

To illustrate the new behaviour of the system with transitions, we present Figs. 4, 5, and 6 for three situations: for $\sigma = 1$ — pure A-matrix game, for $\sigma = 0$ — pure B-matrix game and for $\sigma = 0.5$, the latter being the case under consideration here. In each figure we show the evolution of $y(t) = \sum_X [P(X,t) + Q(X,t)] \frac{X}{N}$ (fraction of first strategy playing agents) for different initial conditions.

(2) **HD+HD or CO+CO.** There is always an interior rest point, and it is either stable or unstable for both chains.

(3) **PD+HD or PD+CO.** It can be no or one interior rest point in this case. For example, A is a PD-type matrix, B — HD-type. $A = \begin{bmatrix} 0 & -3 \\ 6 & 0 \end{bmatrix}$; $B = \begin{bmatrix} 0 & 1 \\ 6 & 0 \end{bmatrix}$; we have no rest point in the interval $(0, 1)$.

But for the following matrices $A = \begin{bmatrix} -1 & -2 \\ -1.1 & -2.5 \end{bmatrix}$; $B = \begin{bmatrix} -3 & -3 \\ -3.5 & -2 \end{bmatrix}$; We have the rest point $y^* = 0.4545$.

(4) **HD+CO.** We observe two cases (there is only one or no interior point). $A = \begin{bmatrix} 8 & 0 \\ 1 & 1 \end{bmatrix}$; $B = \begin{bmatrix} 0 & 5 \\ 3 & 1 \end{bmatrix}$; we have no rest point in the interval $(0, 1)$.

Taking $A = \begin{bmatrix} -1 & -2 \\ -2 & -0.5 \end{bmatrix}$; $B = \begin{bmatrix} -2 & -9 \\ -1.5 & -10 \end{bmatrix}$; gives the rest point $y^* = 0.5$.

4. Conclusion and Discussion

In conclusion, we suggested a new finite population version of evolutionary games. There are two regimes for the whole system with their corresponding payoff matrices and there is a possibility of random transitions between these two regimes. Such transitions between different games has been already considered in the game theory, related with Parrondo paradox.[24] We consider the annealed version of disorder in the payoff matrix with a realistic case of two strategies, versus the quenched disorder of payoff matrix with infinite number of strategies,[10] and our version of stochastic choice of strategies is much simpler than those in Ref. 9. The investigation of cooperation between cancer cell is a very important area of research, as the cooperation can be a target of therapy without selection pressure of individual cancer cells, often initiating the metastasis.[19] Recently the games have been applied to the bacteria and cancer as a simplest mathematical tool describing the cooperation, and one of the central ideas in cancer biology is the idea of the mutator gene. Our model just describes the combination of these two ideas: for the un-mutated gene we have the matrix A, for the mutated gene the matrix B.
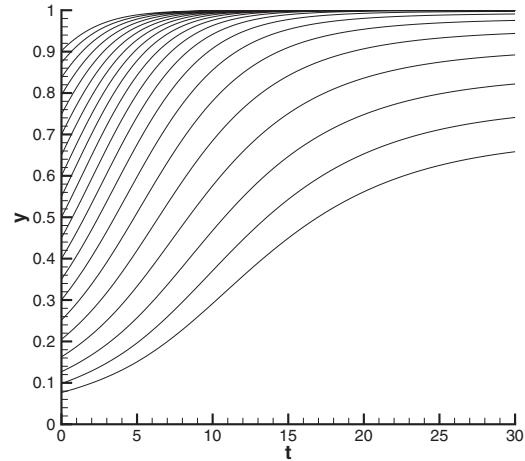

Fig. 4. The case PD+PD, see Sect. 3.3, (1). Maximum $y(t)$ as a function of time t via Local update mechanism for different initial distributions. The numerical solutions obtained for $N = 1000$ and $\sigma = 1$. First strategy is dominant, no interior rest points.
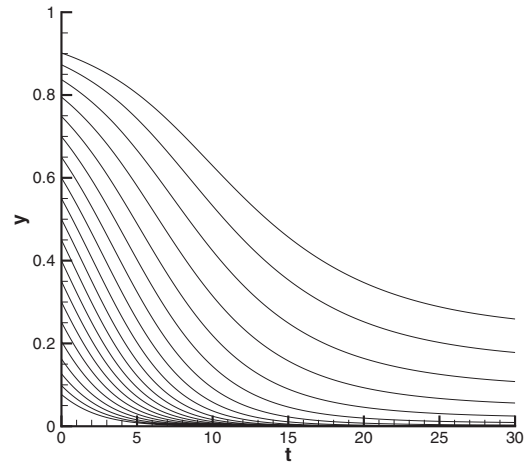

Fig. 5. The case PD+PD, see Sect. 3.3, (1). Maximum $y(t)$ as a function of time t via Local update mechanism for different initial distributions. The numerical solutions obtained for $N = 1000$ and $\sigma = 0$. Second strategy is dominant, no interior rest points.
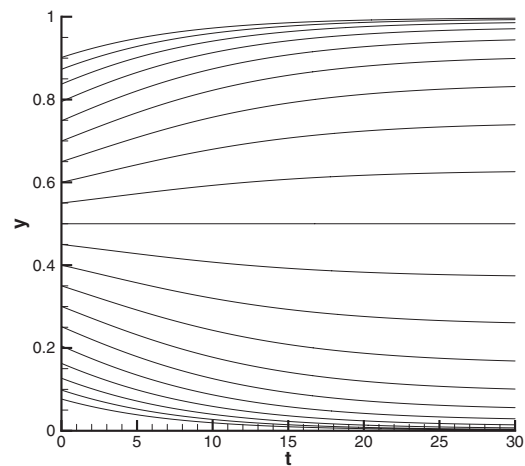

Fig. 6. The case PD+PD, see Sect. 3.3, (1). Maximum $y(t)$ as a function of time t via Local update mechanism for different initial distributions. The numerical solutions obtained for $N = 1000$ and $\sigma = 0.5$. Additional interior rest point at $y = 0.5$.

We formulated the finite population dynamics using both the Moran and the local update schemes and carefully analyzed all the possible situations. We solved the model mapping the large system of differential equations, the chains of equations with some transitions between them, into a single partial differential equation, HJE. According to Eq. (26), the switching between the two regimes is described via a very simple law. While deriving Eq. (8), we missed the terms $(dv_1/dt)/N, (dv_2/dt)/N$. The dropped terms don't affect the maximum or the variance for the full distribution $P(X,t) + Q(X,t)$, while can affect the distributions $P(X,t)$ or (X,t) for the small transition rates. One can consider analytically the switching between the three payoff matrices as well. In case of games the three strategies allow an oscillating dynamics. We assume that the new "dimension", allows a very rich physics, a similar system of two chains of equation reveals an algebraic structure, close to the one in strings.[33] A very interesting is to look the ratchet like phenomena[24] in this case in our HJE approach. While considering the dynamics of the maximum and variance, we used only one branch of the Hamiltonian (13). It is highly interesting look the situations, when both branches of Hamiltonian are relevant for the dynamics.

From numerical simulations[34] or analytic calculations,[35] statistical physics has been applied to understand scaling[36] and universal[37] behaviors of critical physical systems very successfully (for a recent review, see[38]), e.g., critical exponents of a Lennard–Jones system obtained by molecular dynamics simulations[39] are consistent very well those of the gas–liquid critical systems obtained by experiments.[40] Statistical physics has been applied to understand relaxation, folding, and aggregation of proteins,[41,42] biological evolution[43–45] and the origin of life[46,47] from the molecular level. Following this trend, the two-chain model of Fig. 1 can be used to represent interesting biological problems, such as the static and the mutator gene problem, in which the mutator gene can be either normal or abnormal. In the later case, the mutator rate of alleles will increase. One can use the upper chain of Fig. 1 to represent alleles with normal mutation rate and the lower chain to represent alleles with higher mutation rate. One can use Crow–Kimura model[43–45] on such chains to calculate the phase diagram of cancer[48] and dynamic behavior of a mutator gene model.[49]

Appendix A: The Finite Population Dynamics via Moran Process

There are different ways to define the rate functions R_m^τ ($\tau = A, B$; $m = \pm 1$) in the master equation (3) and r_m^τ ($\tau = A, B$; $m = \pm 1$) in our HJE. Here we analyze the selection dynamics of the game with two players and two different situations with matrices A and B. So we interpret each chain in (3) as a frequency-dependent Moran process in the case of finite population (which provides a stochastic microscopic description of a birth–death process).

We consider the 2×2 constant matrices $A = \begin{bmatrix} a & b \\ c & d \end{bmatrix}$; $B = \begin{bmatrix} e & f \\ g & k \end{bmatrix}$. Let indices 1 and 2 represent the number of chosen strategy. N_A, N_B describe the total number of species (here we assume $N_A = N_B = N$). Suppose that at the time t there are X players with type A, playing their first strategy, or X players with type B and the same strategy. In this model we have the following payoffs (we consider only intra-specific interconnections):

$$\pi_1^A(X) = \frac{a(X-1) + b(N-X)}{N-1},$$
$$\pi_2^A(X) = \frac{cX + d(N-X-1)}{N-1},$$
$$\pi_1^B(X) = \frac{e(X-1) + f(N-X)}{N-1},$$
$$\pi_2^B(X) = \frac{gX + k(N-X-1)}{N-1}. \tag{A·1}$$

The probability that the number of A-type individuals playing the first strategy increases from X to $X+1$ (here $1 - w + w\pi_i^\tau$ determines the relative contributions of the baseline fitness, normalized to one[5]):

$$R_+^A(X) = \frac{1 - w + w\pi_1^A(X)}{1 - w + w\langle \pi^A(X) \rangle} \cdot \frac{X}{N} \cdot \frac{N-X}{N}, \tag{A·2}$$

where w is the selection coefficient.

To describe the decrease of the same number, we can use the analogous equation

$$R_-^A(X) = \frac{1 - w + w\pi_2^A(X)}{1 - w + w\langle \pi^A(X) \rangle} \cdot \frac{X}{N} \cdot \frac{N-X}{N}. \tag{A·3}$$

In both cases

$$\langle \pi^A(X) \rangle = \frac{\pi_1^A(X)X + \pi_2^A(X)(N-X)}{N}; \tag{A·4}$$

represents the average payoff in the population.

We consider this model in the case of two strategies, so the increase of the number of A individuals playing the 1 strategy means the decrease of the number of the same species playing the 2 strategy (if there is no switching between A and B type). For the B-type player we can use (A·2) and (A·3) equations substituting B in upper-indexes instead of A.

For the $N \to \infty$ we have ($x = \frac{X}{N}$):
$$\pi_1^A(x) = ax + b(1-x); \pi_2^A(x) = cx + d(1-x)$$
$$\pi_1^B(x) = ex + f(1-x); \pi_2^B(x) = gx + k(1-x). \tag{A·5}$$

Here we can derive the equations for densities of both players ($\tau = A, B$):

$$r_+^\tau(x) = \lim N \to \infty \left(\frac{\pi_1^\tau(Y) - \pi_2^\tau(Y)}{\Gamma + \langle \pi^\tau(x) \rangle} \cdot \frac{X}{N} \cdot \frac{N-X}{N} \right)$$
$$= \frac{x}{\Gamma + \langle \pi^\tau(x) \rangle} (\pi_1^\tau(x) - \langle \pi^\tau(x) \rangle); \tag{A·6}$$

where $\langle \pi^\tau(x) \rangle = x\pi_1^\tau(x) + \pi_2^\tau(x)(1-x)$; $\Gamma = \frac{1-w}{w}$ — the baseline fitness.

$$r_-^\tau(x) = \frac{x}{\Gamma + \langle \pi^\tau(x) \rangle} (\pi_2^\tau(x) - \langle \pi^\tau(x) \rangle). \tag{A·7}$$

It yields to the adjusted replicator dynamics[5]

$$r_+^A(x) = x\left(\frac{(A\bar{x})_1}{(\bar{x}, A\bar{x})} - 1\right); \quad r_-^A(x) = x\left(\frac{(A\bar{x})_2}{(\bar{x}, A\bar{x})} - 1\right) \quad (A\cdot 8)$$

here braces $(\bar{x}, A\bar{x})$ represent simple scalar product. For the B matrix rates r_+^B and r_-^B take the same form as (A·8). Therefore

$$\Delta r^A(x) = x\left(\frac{(A\bar{x})_1 - (A\bar{x})_2}{(\bar{x}, A\bar{x})}\right);$$

$$\Delta r^B(x) = x\left(\frac{(B\bar{x})_1 - (B\bar{x})_2}{(\bar{x}, B\bar{x})}\right). \quad (A\cdot 9)$$

Appendix B: The Population Dynamics via Local Update Mechanism

The second approach to analyze each chain is a local update mechanism.

We consider the same 2×2 constant matrices as in the Moran process with the same fitness π_i^τ, $i = 1, 2$; $\tau = A, B$. But for the probabilities of changing the number of the fist strategy players (A type) we have:

$$R_+^A(X) = \left(\frac{1}{2} + \frac{w}{2}\frac{\pi_1^A(X) - \pi_2^A}{\Delta\pi_{\max}^A} \cdot \frac{X}{N} \cdot \frac{N-X}{N}\right); \quad (B\cdot 1)$$

$$R_-^A(X) = \left(\frac{1}{2} + \frac{w}{2}\frac{\pi_2^A(X) - \pi_1^A}{\Delta\pi_{\max}^A} \cdot \frac{X}{N} \cdot \frac{N-X}{N}\right). \quad (B\cdot 2)$$

When we consider the limit $N \to \infty$ in this case ($\tau = A, B$):

$$r_+^\tau(x) = \lim N \to \infty \left(\frac{1}{2} + \frac{w}{2}\frac{\pi_1^\tau(X) - \pi_2^\tau}{\Delta\pi_{\max}^{A\tau}}\right) \cdot \frac{X}{N} \cdot \frac{N-X}{N}$$

$$= \kappa x(\pi_1^\tau - \langle\pi^\tau(x)\rangle); \quad (B\cdot 3)$$

where $\kappa = \frac{w}{\Delta\pi_{\max}}$.

$$r_-^\tau(x) = \kappa x(\pi_2^\tau - \langle\pi^\tau(x)\rangle); \quad (B\cdot 4)$$

For the 2×2 matrices it takes the form

$$r_+^A(x) = \kappa x((A\bar{x})_1 - (\bar{x}, A\bar{x}));$$

$$r_-^A(x) = \kappa x((A\bar{x})_2 - (\bar{x}, A\bar{x})); \quad (B\cdot 5)$$

So

$$\Delta r^A(x) = x\kappa_1((A\bar{x})_1 - (A\bar{x})_2);$$

$$\Delta r^B(x) = x\kappa_2((B\bar{x})_1 - (B\bar{x})_2). \quad (B\cdot 6)$$

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