



Evolutionary stability for matrix games under time constraints



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ABSTRACT

Game theory focuses on payoffs and typically ignores time constraints that play an important role in evolutionary processes where the repetition of games can depend on the strategies, too. We introduce a matrix game under time constraints, where each pairwise interaction has two consequences: both players receive a payoff and they cannot play the next game for a specified time duration. Thus our model is defined by two matrices: a payoff matrix and an average time duration matrix. Maynard Smith's concept of evolutionary stability is extended to this class of games.

We illustrate the effect of time constraints by the well-known prisoner's dilemma game, where additional time constraints can ensure the existence of unique evolutionary stable strategies (ESS), both pure and mixed, or the coexistence of two pure ESS.

Our general results may be useful in several fields of biology where evolutionary game theory is applied, principally in ecological games, where time constraints play an inevitable role.

1. Introduction

Every interaction takes time. In classical economical and evolutionary game theory, the time durations of different interactions are not widely considered. However, in ecology, activity-dependent time constraints are important. For instance, Holling-type functional response (Holling, 1959) takes into account that the number of active predators is less than their total number, since after a successful attack predators have to handle and digest their prey before they continue hunting. Moreover, in optimal foraging theory (Charnov, 1976a,b), in ecological games on kleptoparasitism (Broom et al., 2008, 2009; Broom and Ruxton, 1998; Broom and Rychtář, 2013; Sirot, 2000), and in the dispersal-foraging game (Garay et al. 2015a,b), time constraints have an essential effect on optimal behavior. Thus our main question arises: What is the effect of time constraints on the concept of evolutionary stability in games within one species?

Our question is motivated by the following lines of research. Our primary motivation originates in ecological games with time constraints describing the complex phenomenon of kleptoparasitism (e.g., Broom et al., 2008, 2009; Broom and Ruxton, 1998; Broom and Rychtář, 2013; Sirot, 2000). The overwhelming majority of models on kleptoparasitism consider polymorphic populations (Hadjichrysanthou and Broom, 2012). The aim of this paper is to adapt Maynard Smith's standard concept of evolutionary stability to

matrix games with time constraints in a monomorphic population.

Our secondary motivation comes from the classical prisoner's dilemma (PD) game, where cooperation can be achieved by taking account of some extra specific mechanism (e.g., Nowak, 2006; Nowak and May, 1993; Santos et al., 2006; Szabó and Fátih, 2007; Szabó et al., 2005). Notice however that the original payoff matrix of the PD game is given by time (term of imprisonment, while the prisoner cannot go out to rob). It is natural to ask whether the evolutionary stability of cooperation can be achieved by suitable time constraints. According to our knowledge, this is the first attempt to investigate the effect of time constraint in the PD.

To answer our main question, we introduce matrix games under time constraints, in which the players must wait after each interaction before they engage in the next one, and these waiting times depend on the pure strategies followed by the players. Then we conceive the definition of ESS for this class of games. First, we derive formulas for the players' average payoff via heuristic calculation under two assumptions, then we introduce an exact mathematical model, where those requirements are met and the heuristic calculations get justified with rigorous proofs. For that we assume that the waiting times are exponentially distributed, thus we can use the standard method of continuous time Markov processes to describe the stationary state of the population (cf. Broom et al., 2010; Yates and Broom, 2007). However, we emphasize the possibility that other, non-Markovian

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models could also satisfy our assumptions, and the heuristic calculations would remain valid for them.

We were also motivated by the “dynamical linking” model by Pacheco et al. (2006a,b), where the number of repetitions of the interactions between two individuals depends on the payoff from the given interaction. That pair forming process modifies one of the basic assumptions of classical evolutionary games, namely, the randomness of interactions between players, since the connections between different phenotypes have different repetition numbers. In contrast, our model keeps the randomness of the pair forming process at each interaction, and after the interaction players have to wait before they get ready for the next interaction. We emphasize that both models have the same consequence: the average interaction rates between different phenotypes are not proportional to the relative frequencies of phenotypes, unlike in classical evolutionary games.

Finally, we apply our general results in the following two cases. In the introduced prisoner's sharing game, the time constraints are given by the matrix of the prisoner's dilemma and the payoff matrix defines how the fraternal sharing is distorted by a symmetric zero-sum component with a strength of s that favors mutual cooperation if $s > 0$. When increasing s , first the defector, then a mixed strategy, and finally the cooperator is the unique evolutionarily stable strategy. In the second case, the prisoners' dilemma occurs for the payoff matrix. As the average time duration of defector strategy increases, first the defector is the unique evolutionarily stable strategy, after that the game becomes bistable, and finally the cooperator is the unique evolutionarily stable strategy.

2. A heuristic calculation of evolutionary stability

We consider pairwise interactions having different time durations. We have n pure strategies, and the phenotype is a probability distribution $p = (p_1, \dots, p_n)^T$ on these pure strategies. (Vectors are meant as columns; T stands for transpose.) A matrix game under time constraints is defined by the following parameters. If the focal individual uses the i -th pure strategy and its opponent the j -th one, the focal individual's payoff is a_{ij} , and the focal individual cannot play the next game during an average time duration $\tau_{ij} > 0$. Thus, each individual is either non-active or active; and only active individuals are ready to play the next game round. Hence our game is characterized by two matrices, the intake matrix $A = (a_{ij})_{n \times n}$ and the time constraint matrix $T = (\tau_{ij})_{n \times n}$.

In our heuristic calculation of evolutionary stability, we strictly follow Maynard Smith's (1982) monomorphic setup, as much as possible. The population is assumed to be sufficiently large and the generations do not overlap. All individuals can only differ in the strategy p and all individuals are the same from all other points of view of natural selection. Let us consider a resident population in which every individual has a resident phenotype p^* . Assume that mutation is rare enough and denote by ε the relative frequency of mutants. The rarity of mutation has two consequences: Firstly, the relative frequency of mutants is small; secondly, the time between two consecutive mutations is sufficiently long so that less fit phenotypes get selected out by natural selection. Thus only one mutant and one resident phenotype coexist at the same time. Then the relative frequency of residents is $\varepsilon^* = 1 - \varepsilon$. The interaction is well mixed: each active individual finds another active individual uniformly at random. Assume that the lifetime D of one generation is large enough and individuals play the above game during the whole D .

After an individual finishes an interaction, it looks for an opponent for the next interaction, which also takes time. The searching time depends on the searching process. For instance, if active individuals A and B are looking for opponents, and each of them covers the average distance between them during τ_0 , then the encounter only takes time $\tau_s = \tau_0/2$, since until the encounter both cover half the distance between them. The same is true if the random searching times are independent

and exponentially distributed with equal means. In this case the interaction can follow as a result of either participant's finding the other one, hence the waiting time in fact is the minimum of two exponentially distributed searching times with mean τ_0 , which is exponential with mean $\tau_0/2$. By symmetry, at every encounter both players must have the same probability to select and to be selected.

Of course, it can happen that a searching individual finds an inactive one; in this case the searching period starts over. We will term the time span between two searches (that is, τ_s plus the time of interaction, when the searching individual finds an active opponent) a *turn of activity*.

Our heuristic calculation is based on the following two assumptions.

Assumption 1. The population is in a stationary state, i.e., each individual having the same phenotype possesses the same activity distribution.

Assumption 2. The total intake of each phenotype is equal to the average intake in its stationary state (cf. Luther and Broom, 2004).

In order to calculate the fitness of mutant and resident phenotypes, we will consider a focal mutant, resp. a focal resident individual, who plays against the whole population. Since the interaction is well mixed, a focal individual (independent of its phenotype) has the following encounter distribution based on the stationary state of the whole population $(r, \varepsilon - r, r^*, \varepsilon^* - r^*)$, where r and r^* are the relative frequencies of active (interaction is possible) mutants and residents, resp., while $\varepsilon - r$ and $\varepsilon^* - r^*$ are the relative frequencies of inactive (interaction is not possible) mutants and residents, resp. We emphasize that these proportions are defined by the stationary distribution, thus $\varepsilon, \varepsilon^*, r, r^*$ do not vary with time: the main point is that the state of the population is aperiodic. Furthermore, the encounter distribution depends on the phenotypes of resident and mutant.

Now, the time average of an arbitrary activity turn of a focal mutant individual is

$$E_p = \tau_s + rp^T T p + r^* p^{*T} T p^*.$$

Indeed, τ_s is the time to find the next opponent to play the game against, r and r^* are the probabilities that the focal mutant meets an active mutant or an active resident individual in a stationary population, respectively. Finally, $p^T T p$ resp. $p^{*T} T p^*$ is the average time duration when the focal mutant plays the game with a mutant or a resident opponent. Similarly, the time average of one turn of activity of a focal resident is

$$E_{p^*} = \tau_s + rp^{*T} T p + r^* p^{*T} T p^*.$$

The time constraint on interactions determines the average number of interactions of individuals during the lifetime D of one generation, thus the number of games played by the mutant and that by the resident phenotype are defined as

$$G_p := \frac{D}{E_p} \quad \text{and} \quad G_{p^*} := \frac{D}{E_{p^*}},$$

respectively.

Since the interactions are well mixed during D (i.e., each individual interacts with mutant and resident with probability r and r^* , respectively), each mutant individual has the following total average payoff:

$$G_p(rp^T A p + r^* p^{*T} A p^*).$$

Indeed, here $rp^T A p + r^* p^{*T} A p^*$ is the average intake of the focal mutant individual from one turn of interaction. Similarly, the total average payoff of a resident individual is

$$G_{p^*}(rp^{*T} A p + r^* p^{*T} A p^*).$$

Based on classical Darwinism, supposing that the mutant is rare enough, the mutant phenotype is outperformed by the resident phenotype if the fitness of the resident phenotype is higher than that

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