Influence of Dynamic Environments on Agent Strategies

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***Abstract*—This paper presents Evolutionary Spatial Games in dynamic environments. This game is a concept based on Evolutionary Game Theory (EGT) and Evolutionary Algorithms (EAs). The main goal is to study the implicit influence of dynamic environments on the behavior of agents in EGT. The paper considers three different types of populations which interact using a modifiable and individualized payoff matrix for their agents. As each agent of a certain type can have a different payoff value than the rest of the population, the populations evolve towards a diverse set of agents. In order to study the diversity in each population, we propose a model based on EAs and study the impact of dynamic environments on the populations and their diversities. The main question to answer is that whether diversity can help to obtain a stable strategy and if the dynamics in a certain environment can influence the Spatial Game. The experiments on three different environments show that the stable strategies can contain a diverse set of agents particularly in dynamic environments.**

I. INTRODUCTION

Evolutionary Game Theory (EGT) has been used to analyze the stability of a certain strategy (population of agents playing a certain strategy) when interacting or playing against other strategies co-existing in the same environment [1] [2]. In fact, in this way we can analyze the behavior of individuals and observe if a cooperative behavior can develop in a world of several strategies [2]. In the field of spatial games the effects of the spatial distribution of agents on the development of cooperation has been studied [3].

The iterated prisoner's dilemma (IPD) game has been very often used to study the evolution of cooperative behaviors in evolutionary computation [4], [5]. The major aspects consider the payoff matrix, spatial relations among agents, representations and noisy games e.g., [6]–[9]. The choice of a representation scheme is known to be important. Ishibuchi et al. [8] studied various representations and introduced heterogeneous representation schemes in a single population in order to examine the evolution of cooperative behavior. The goal of our paper is to study the influence of the dynamic environments and representations on the behaviors in EGT. For this purpose, we combine the concepts of Evolutionary Algorithms (EAs) and EGT. The individuals contain genes which can adapt to the environments. From the other side they utilize a payoff matrix for interactions. In this context, the effect of the payoff has been studied in the literature e.g. in [6]. In our model each agent uses a global payoff matrix as a basis for his type of strategy for interaction purposes. However, the agent modifies the values of the payoff matrix according to his genes which are adapted to the environment over time. In other words, we do not define any explicit behaviors. Let us assume we have Hawks, Doves and Worms as agents. The payoff matrix from EGT defines that Hawks win against Doves. Nevertheless a Hawk located in a very poor area in the environment with less nutrition is not as powerful as a Hawk from a rich environment. This results in different behaviors of Hawks interacting with Doves. The question arises if stability is possible in the presented model and whether diverse sets of agents can develop under the given dynamic environments.

The focus of this work is on stability between three populations of agents and on diversity of the gene pool in dynamic environments. Instead of having an explicit fitness function and selection method as in EAs, our concept is close to natural selection. Every agent can accumulate or lose resources when executing behaviors. Agents with low resources will perish, while agents with many resources can reproduce. Thus, agents which fit into their local environment have a higher probability of passing their mutated genomes to the next generation. In our model, the behaviors depend both on the agent's local environment and the behaviors of other individuals. The results of the simulation indicate that diversity in one strategy can help to obtain a stable state for the population with that certain strategy. Furthermore we study the influence of the dynamic environments with various changing properties. Our results demonstrate the dynamics in the environment can help increase the diversity in the populations. In addition, the stability can be increased in environments with slow dynamics.

This paper is structured as follows. Section II includes the background. The main contribution of the paper is being presented in Section III. Section IV is dedicated to the experiments and Section V concludes the paper.

II. BACKGROUND

The field of EGT deals with the question how cooperation can arise in populations of selfish individuals [1]. Its applications cover a wide range of topics in the various fields such as sociology, economics and physics. The concept of evolution into the Game Theory (GT) was introduced by Maynard Smith and Price [1]. In their work "The logic in animal conflict" a repeated game with five fixed strategies is used and Evolutionary Stable Strategy (ESS) is introduced as one of the most important concepts in EGT. They analyzed the strategies which remain stable in a population over time. It means that if most members of a population adopt a certain strategy, there will be no other so-called mutant strategy that can give a higher payoff [1].

A more dynamic approach in ESS contains replicator dynamics [10], [11] which computes the mean fitness of a certain strategy by taking the frequency of the strategies into consideration. However, these equations require assumptions such as an infinite size for the population, a well-mixed strategy and no mutations. Considering a spatial component in EGT has been studied in the field of spatial games and Cellular Automata [12]. Nowak and May [3] experimented with a simple deterministic spatial implementation of the non-repeated prisoner's dilemma, resulting in complex chaotic spatial patterns. They concluded that "a deterministically generated spatial structure within populations may often be necessary for the evolution of cooperation".

A more complex model by Lindgren and Nordahl [13] considers aspects such as repeated games, noise and genome for the individuals which acts as a memory for the strategies in repeated game. They found that even homogeneous environments can affect the evolutionary processes. Their extension of the model has shown that given the dynamics of the spatial model, diversity can be generated even in a homogeneous environment [13]. The influence of age of the individuals [14] and the spatial disorder with empty sites [15] have been recently studied in EGT.

III. EVOLUTIONARY SPATIAL GAMES

In this section, we describe our proposed model called Evolutionary Spatial Game. In the following we describe the agents, theirs behaviors and the environment.

A. Agents and Their Genes

An agent is defined as a 4-tuple $(\vec{x}, s, e, a)$. The vector $\vec{x}$ represents the genotype (with n genes). One fixed strategy denoted by s is assigned to every agent. We consider three strategies (types of agents) such as Hawk, Dove and Worm. The result from the interactions between two agents determines the received payoff for an agent and is added to the accumulated payoff denoted by e. The age a of an agent is being recorded in every time step. The maximum age is predefined. The age limits the life-span and influences the agent's behavior. In conclusion an agent is defined by:

- $\vec{x} \in \mathbb{R}^n$: Genome;
- $s \in \{Hawk, Dove, Worm\}$: Strategy or Type;
- $e \in \mathbb{R}$: Accumulated payoff;
- $a \in \mathbb{N}_0$: Age;
- $f(\vec{x}) : \mathbb{R}^n \rightarrow \mathbf{B}$: Mapping genes to behaviors in $\mathbf{B}$;
- $f_{consumption}(\vec{x}) : \mathbb{R}^n \rightarrow \mathbb{R}$: Mapping genes to payoff.

Every agent has a set of certain behaviors. The quality of these behaviors depends on the genes. The function $f(\vec{x})$ maps a genotype to a behavior. An agent can receive a payoff through the interaction behavior, which is based on the concepts from EGT and considers a certain strategy for an agent.

TABLE I: Payoff matrix

Payoff	Hawk	**Dove**	Worm
Hawk	-5	**10**	0
Dove	-10	2	5
Worm	0	-5	2

The genome of an agent is considered to include the following $n = 9$ genes: Move Threshold (x_1), Exist Threshold (x_2), Death Modifier (x_3), Reproduce Modifier (x_4), Age Modifier (x_5), Attack Modifier (x_6), Defense Modifier (x_7), Photo Efficiency (x_8) and Feeding Efficiency (x_9). Using real numbers as genes and an appropriate mapping from genes to behaviors, satisfies the condition of gradualism in the theory of evolution. The behaviors can only be active, if the gene value is greater than zero. Having such a mapping means that natural selection can favor even slight improvements and the following can hold: Agents with similar genotypes have a similar chance of survival (given a similar local environment) and agents with similar genotypes have similar behaviors (phenotypes).

The strategy of an agent is not affected by the genes and is important in terms of interaction. The interaction is based on a payoff matrix denoted by C. If an agent interacts with another agent, their strategies are used to perform a lookup in the payoff matrix shown in Table I. The Hawks are the predators, which ignore agents with the strategy Worm. The Doves get hunted by the Hawks and cooperate with each other. Doves hunt the Worms. The Worms cooperate with each other, while Hawks do not cooperate with each other. A payoff value is selected from the matrix by playing the column player against the row player i.e., the payoff value for a Hawk playing against a Dove (both shown in bold) is 10. We denote this by $C(s_i, s_j) = 10$. In our model, we use the payoff values for reproductions: The interaction using the payoff matrix results in either a positive or a negative payoff. If the accumulated payoff is too low, the agent will die, and if it is high enough it can reproduce. In each time step, we add a negative value to the accumulated payoff values of the agents. This value is called basic consumption and is calculated by using a weighted sum of the genes:

$$f_{consumption}(\vec{x}) = \sum_{i=0}^{n} \omega_i * x_i^2 \tag{1}$$

where the effective range of the genes is set to be $[0, 1]$ and the weights w_i are positive values. The input vector for $f_{consumption}(\vec{x})$ is clamped to $[0, \infty)$ so that it cannot return negative values.

The accumulated payoff e for each agent depends on the energy it gets from the environment (e.g., Photosynthesis and feeding) denoted by f_{energy}, the energy gained through interaction with other type of agents $f_{interaction}$ and the consumption energy. The payoff value can be calculated as follows:

$$e = f_{energy} + f_{interaction} - f_{consumption} + e \tag{2}$$

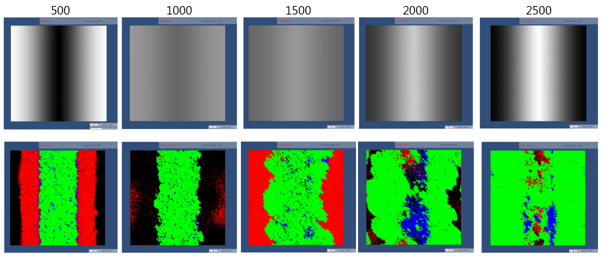

Fig. 1: Top - Property map for movement (white and black colors indicate the area on which it is hard or easy to move). Below - Worms (green) with the weakest movement genes, Doves (blue) slightly better genes than worms, Hawks (red) the strongest movement genes.

B. Environment

The environment, in which the agents live, is defined as a discrete 2D lattice, using a torus topology, of the size $N \times M$. Each cell on this lattice has a coordinate of c_x and c_y and can have two states, agent present or empty. The cell properties are defined as vector $\vec{p} \in \mathbb{R}^m$ which represents

- p_1 (Movement): terrain difficulty which affects movement and reproduction
- p_2 (Light): resource, which agents can use to generate energy
- p_3 (Nutrient): similar to light, but here the resource is consumed by agents

The cell properties can change over time and are dynamic. For instance nutrient can disappear, if an agent is located on the corresponding cell and consumes a portion of it. For a dynamic environment a sequence of property maps over a sequence of time-steps must be defined. Given these two sequences, the property maps are interpolated between the time-steps. An example for the property map for movement (p_1) is illustrated in Figure 1 for time-steps 500 to 2500 on the top row. The bottom row shows the agents and their locations on the environment. Worms are more distributed on the cells which are easy to move (black areas), where Hawks can move over the white cells indicating the hard area for moving.

Both the definition of agents and environment allow an alternative view on the data. The agents can be represented as vectors combining the agent properties and the cell property vector. In this case, we have a set of multivariate data, which is sampled on a discrete grid. This means that the data related to each cell with coordinates of c_x and c_y, can be described by $env(c_x, c_y) = z \in \mathbb{R}^{m+n}$ with m as the number of the cell properties and n as the number of genes. Thus, including the agents themselves as part of the environment definition. The advantage of this definition is that the data can be seen like in Figure 2, as a set of layered gray-scale textures. Here it becomes evident that this model has a different concept than the CA. Instead of having a finite set of states per cell, we have a vector of real values at each cell.

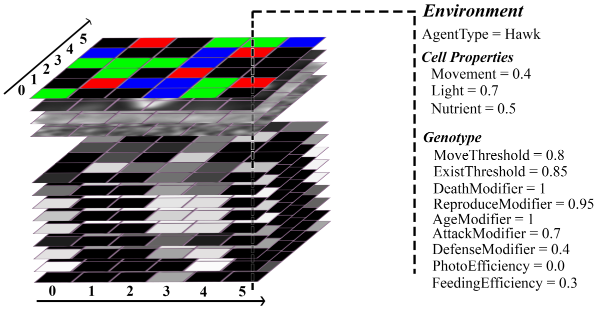

Fig. 2: The top layer shows a set of agents with the default color coding (red: Hawk, blue: Dove and green: Worm). The three layers below represent the cell properties and the following layers represent the genotype of the agents. On the right an example for the cell with coordinates (5,1) is shown.

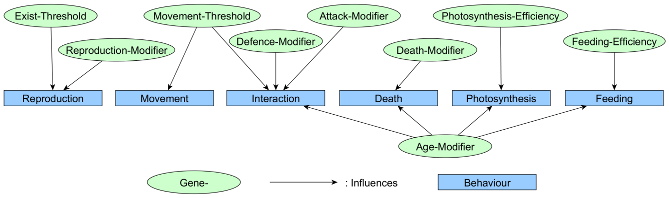

Fig. 3: An overview of the genotype to behavior mapping.

C. Behaviours

For each agent we define six different behaviors such as Reproduction, Movement, Interaction, Death, Photosynthesis and Feeding. Figure 3 gives an overview of a mapping between genes and the behaviors (genotype-phenotype mapping). Some of the behaviors need to perceive the neighboring cells according to the Moore-Neighborhood. The behaviors are described below:

Movement: Each agent decides to move to a neighboring cell by considering two conditions:

1) if the cell is empty
2) if p_1 at (c_x, c_y) is smaller or equal to Movement Threshold of the agent x_1

The agent selects a random neighboring cell fulfilling both of the above conditions and then moves to that cell as shown in an example in Figure 4.

Interaction: The interaction between the agents is based on the payoff matrix C and the strategies (types) of the agents. Each agent interacts with one of its neighbors, which it selects randomly. In contrast to the classical EGT [1] or GT approaches, we modify the values of the payoff matrix for each agent in every iteration. This modification is based on the genes of both involved agents. The value for modifying the payoffs depends on the role of the agents during the interaction. The agent who initiates the interaction is the attacker (s_i), the other one is defending (s_j). In this case the

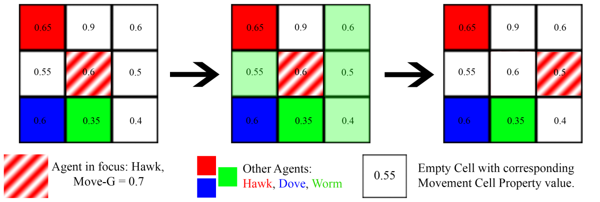

Fig. 4: Movement behavior of a Hawk located in the middle cell (left). Valid cells fulfilling the conditions are marked with green (middle). Hawk moves to the right cell (right).

modifier value α_i is:

$$\alpha_i = \frac{1 + k_1 a^i + k_2 x_6^i + k_3 x_1^i}{1 + k_1 a^j + k_2 x_7^j + k_3 x_1^j} \tag{3}$$

where i and j indicate the genes for attacker and defender strategies s_i and s_j. k_i is a weight factor with $\sum_{i=0}^{3} k_i = 1$ and weights three factors:

- the influence of the agents age a
- the influence of the Attack Modifier gene x_6^i for attacker with strategy s_i and Defense Modifier gene x_7^j for defender with strategy s_j
- the influence of the Move Threshold gene x_1 for both attacker and defender

In interactions between predator and prey, the ability to attack or defend determines the outcome. This concept is modeled with the two genes related to the Attack Modifier gene x_6 and Defense Modifier gene x_7. In such a situation the ability to move influences the interaction, for instance prey that can run faster than the predator is more likely to escape. Therefore, we additionally consider the Move Threshold gene x_1 of the agents.

The maximum age for every agent is a global constant (called default age) which is scaled by the gene x_5. By dividing the age of an agent by this maximum age, its normalized age $a_{normalized}$ can be calculated. This value is used for a lookup on a curve (Figure 5) to determine the efficiency of interaction $f_{age}(a_{normalized})$. Figure 5 models the concept, that individuals reach their maximum efficiency at a young age and lose it when getting old. The agents start with a value below 1 meaning that every agent has a short phase of vulnerability after it spawns.

The agents of type s_i use a modified value for a payoff for interacting with another agent of type s_j:

$$f_{interaction}(s_i) = C(s_i, s_j) * \alpha_i \tag{4}$$

This modification indicates that a Dove can now attack a Hawk. This case only occurs due to the lack of intelligent decision making. Hence, the agents can be considered as underdeveloped, such that prey will even attack its predators for no reason. In addition the interaction between agents of the same type is influenced, which has fortunate effects on the genes selection pressure. For example a Hawk with a high attack but small defense modifier will get a large payoffs on interaction with Doves with a small values of defense modifier. However, if the Hawks modifiers differs in a large extent, then the Hawk will get a disadvantage on interaction with another Hawk, because of the high ratio both will get a high negative payoff. This also works the other way around. If a Dove has a high defense modifier it will receive not as much negative payoff when it interacts with a Hawk. However, the more fortunate cooperative interaction with another Dove results in a smaller payoff, if the attack modifier of the Dove is small. Such a system does not favor a single superior solution, instead it requires to be balanced among the population, like the payoff matrix itself.

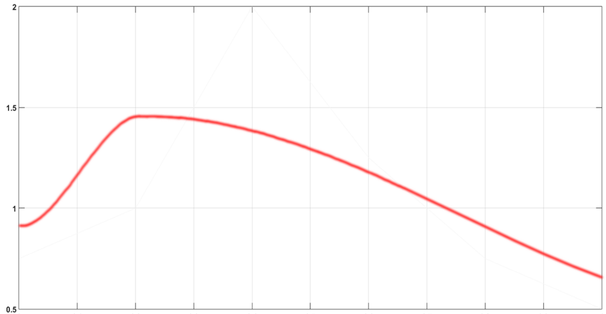

Fig. 5: $f_{age}(a_{normalized})$: The agents reach their maximum interaction efficiency at a young age.

Reproduction and Death: Agents can accumulate or lose energy through interactions. Depending on this energy value which is the accumulated payoff e, agents can either reproduce or perish. The reproduction behavior of an agent depends on its Reproduction Threshold gene x_4: The agent can reproduce if $e_{agent} \geq x_4 * \text{GRepro}$. An agent initiates the reproduction process if its energy exceeds the reproduction threshold, which is scaled by the Gene-Reproduction-Modifier (GRepro).

The reproduction itself is a single parent clonal operation, which includes a mutation operator. The mutation operator is implemented as follows: a vector of the same length as the genotype is created, every entry is randomly generated by using a Gaussian distribution with expected value of zero and a small standard deviation. This vector is added to the genotype vector. When an agent intends to spawn an offspring, empty cells have to be present in the neighborhood. Similar to the movement behavior these cells have to fulfill a second condition, this time the cell property is checked against the existence threshold x_2. If the agent's accumulated energy drops below the death threshold it will die. This threshold is scaled by the Death Modifier x_3. A dead agent is removed from the environment.

Photosynthesis and Feeding: The agents consume energy in every simulation step. This leads to a fast death for agents in sparsely populated locations of the environment due to the lack of interaction. However, in nature individuals also use resources from their physical environment to survive. This is modeled by the two behaviors photosynthesis and feeding.

These two behaviors base their energy output on the cell

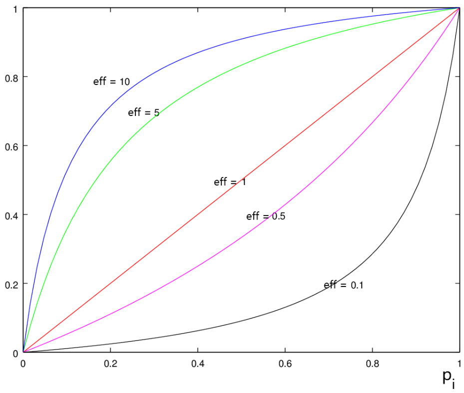

Fig. 6: Energy (f_{light} or $f_{nutrient}$) from the environment for different values of eff vs. light (p_2) or nutrient (p_3)

property of the agent's location. The output depends on both of the resources light p_2 and p_3. Furthermore, it depends on the corresponding genes for Photo Efficiency x_8 and Feeding Efficiency x_9:

$$f_{energy} = f_{light} + f_{nutrient} \tag{5}$$

$$f_{light} = f_{age}(a_{normalized}) \cdot \left(\frac{x_8 * p_2}{x_8 * p_2 - p_2 + 1}\right) \tag{6}$$

$$f_{nutrient} = f_{age}(a_{normalized}) \cdot \left(\frac{x_9 * p_3}{x_9 * p_3 - p_3 + 1}\right) \tag{7}$$

One possible mapping for f_{light} and $f_{nutrient}$ is depicted in Figure 6. The benefit of this function is the parameter eff (eff indicates x_8 and x_9 for p_2 and p_3, respectively) which allows a smooth control of the curves shape. We observe that with a resource value of 1, even a poor efficiency value results in maximum energy payoff. This models the fact that individuals in fortunate spots with many resources do not have to put the same effort in energy allocation like the same individual in a less fortunate spot. This configuration forces selection pressure on individuals with high efficiency genes in good spots, because they are wasting energy in the resulting higher basic consumption costs. In addition, the age of the agents has an impact on the final value.

The difference between the photosynthesis and the feeding behavior is that feeding consumes the local resource. This is done by decreasing the nutrient cell property value by a global consumption value, which is scaled by the efficiency value.

IV. EXPERIMENTS

The goal of our experiments is to analyze the behavior of the agents in a dynamic environment. We measure both stability and diversity as explained in the following. For the experiments, we have selected three different scenarios including various dynamic environments.

A. Metrics

For measuring the behavior of the agents, we record the stability and diversity. Similar to the concepts in ESS, we define a population to be stable if all the strategies (i. e. Hawk, Dove and Worm) survive to the last simulation step. Here we ignore the ratio between the sub-populations.

TABLE II: Parameters for the environments

parameters	Scenario 1	Scenario 2	Scenario 3
$N \times M$	200 × 200	200 × 200	200 × 200
Max. light	5	6	6
Max. nutrient	5	5	5.25
Reproduct. threshold	100	75	75
Death threshold	-100	-50	-100
Default Age	200	200	250
Nutrient increase	0.05	0.06	0.06

The diversity of the agents is measured independent from the pure strategies. Here, we aim to observe the diversity of agents in terms of their genes. The goal is to evaluate if diversity can develop or not. In order to measure the diversity for a given time-step, we build clusters of similar genes. These clusters are created independently from the spatial distribution of the agents. Each genotype is interpreted as a location in a nine-dimensional space. An agglomerative hierarchical clustering algorithm with Euclidean distance and the centroid method is used to receive a binary cluster tree from the data [16]. A cutoff distance of 2.0 is applied to the tree to find the final clusters which can be interpreted as species in the population. It is worth noting, that this method is not intended to receive data that states something about the quality of diversity. Therefore, this high cutoff distance, with respect to the mutations standard deviation of 0.01 for every gene, is chosen. This means, if the number of clusters increases over time, some agents have developed in a different direction than the others. To decide if diversity was developed, a threshold of 30 clusters is defined. Every experiment starts with 3 types of agents (3 clusters), this means that ten times more species have to develop than the start configuration, for a population to be considered diverse. Using the number of clusters as indicator for diversity hides the information about the long-time development of genes. For example the fact that the number of clusters both in an early stage and in an advanced stage of the simulation is n does not mean that the gene pool has not changed.

B. Parameter Settings and Scenarios

To evaluate the described model, three different scenarios are selected. Each scenario consists of a unique environment with corresponding parameter sets shown in Table II. The values are selected from a large set of preliminary experiments we have performed. The setup was measured for 30000 time-steps. Each experiment is run for 10 times and the average number of agent and diversities are calculated. For measuring the diversity of the populations, the mean value of clusters and the standard error are calculated. The weights for the modifier of the payoff matrix are selected to be: $k_1 = 0.35$, $k_2 = 0.35$ and $k_3 = 0.3$. Here symmetric payoff matrices are chosen. If a Dove loses energy in the interaction with a Hawk, the Hawk cannot receive more energy than the Dove was losing. Tables I and III show the selected payoff matrix and the parameters for

TABLE III: Agent initial configuration

Agents	Hawk	Dove	Worm	w_i
Number	1000	1000	1000	-
x_1	0.8	0.55	0.4	1.25
x_2	0.8	0.55	0.4	0.5
x_3	1	1	1	0.25
x_4	0.6	0.8	1	0
x_5	2	2	5	0
x_6	0.75	0.5	0	1.25
x_7	0.25	0.4	0.1	1.25
x_8	0	0	0.8	1.5
x_9	0.0	0.7	0	1

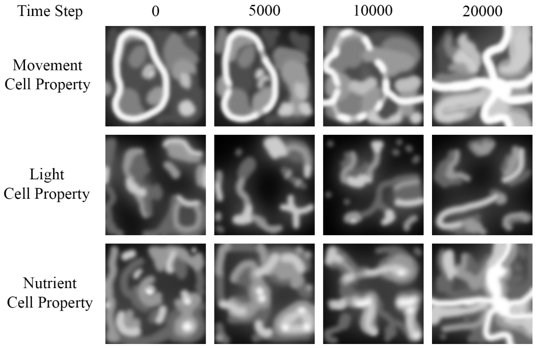

Fig. 7: Scenario 2 - Dynamic environment with slow changing cell properties in terms of movement, light and nutrient

the three populations. The size of the environment is selected to be 200×200 resulting in a maximum of 40.000 agents.

Scenario 1: The first scenario is designed to measure the behavior of the agents in a simple homogeneous environment. The goal of these experiments is to replicate the simple conditions of spatial games and to observe if stability can occur and especially if diversity can develop in such an environment. Therefore, the property of each cell in the environment is set to be 0.5.

Scenario 2: The goal of the this scenario is to evaluate and analyze the behavior of the agents in dynamic environments with slow changes. We select gradual changing values for the environment as shown in Figure 7.

Scenario 3: In the third scenario, we select a simple but a fast changing environment as shown in Figure 8. The environment is one pattern which rotates over time.

C. Results

Figures 9 and 10 show the results related to the diversity and stability (Average count of each population) for the three scenarios. We observe that while in the dynamic environments, the populations contain very diverse sets of individuals, in the static environment there is no diversity. By observing the average count of the individuals, we conclude that no population could be able to survive in Scenario 1. One reason for this phenomenon is the parameter settings for the environment and the agents initial values. This will be studied further into details later in this section. Comparing the rate of dynamics in the environments, we conclude that in Scenario 2 with slow changes, we have a very diverse set of populations.

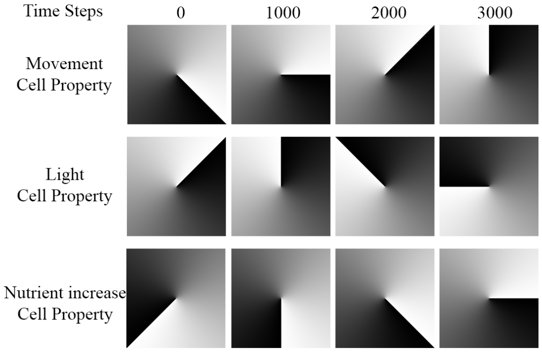

Fig. 8: Scenario 3 - Dynamic environment with fast changing cell properties in terms of movement, light and nutrient

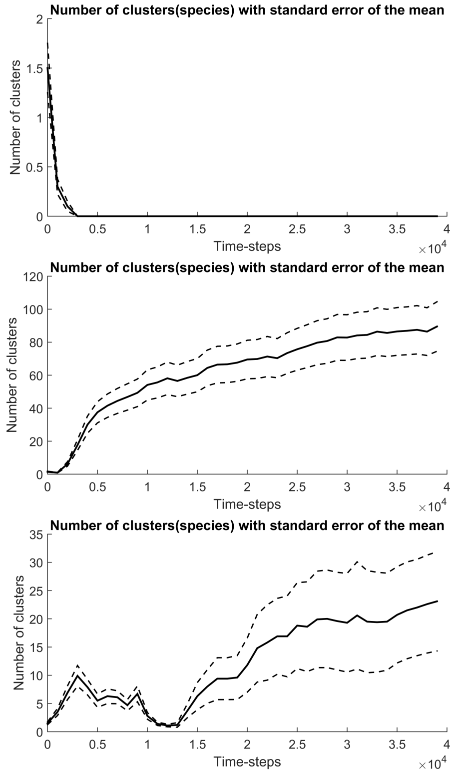

Fig. 9: Diversity for Scenario 1 (top), Scenario 2 (middle), Scenario 3 (bottom)

Considering the average number of agents in the populations, the agents with restricted movement values in their genes, were the most stable ones for both dynamic environments. We observe that even in the fast dynamic environment the Hawks could not increase their number when comparing them to Doves and Worms. The figure show a small number of agents in the Hawk population, but this small value stays stable.

In all our experiments we observe that the interaction between individuals has a heavy and unpredictable influence on the resulting gene-pool and diversity. Figure 11 shows screenshots of the simulation on Scenario 2. We notice that

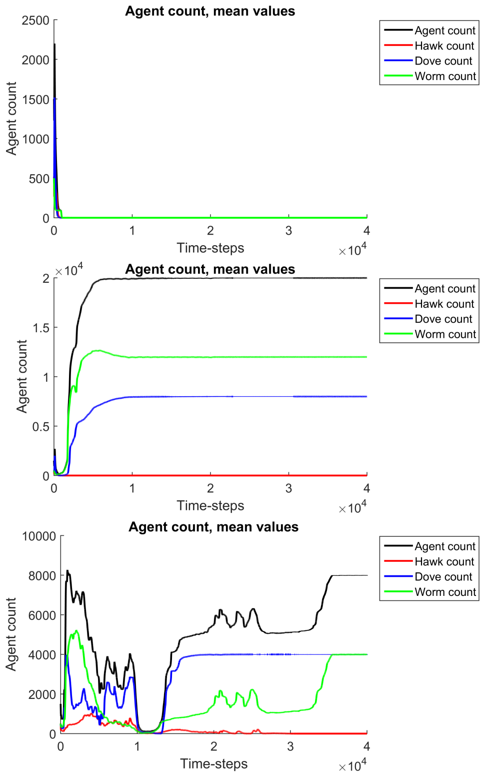

Fig. 10: Average count for Scenario 1 (top), Scenario 2 (middle), Scenario 3 (bottom)

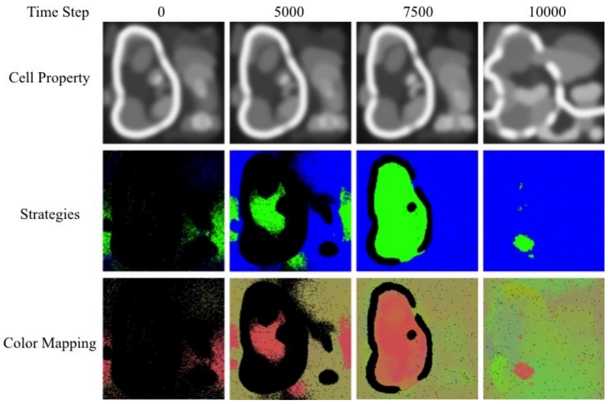

Fig. 11: Scenario 2 - Populations over time in a dynamic environment

TABLE IV: Scenario 1 - Agent new initial configuration

Agents	Hawk	Dove	Worm	Weights
Number	1000	1500	15000	-
x_1	0.7	0.55	0.55	1.25
x_2	0.7	0.55	0.55	0.5
x_3	1	1	1	0.25
x_4	1	1	1	0
x_5	1.5	1.75	3	0
x_6	0.75	0.5	0	1
x_7	0.25	0.4	0.1	1
x_8	0	0	0.8	1
x_9	0.2	0.7	0	1

the genes adapt quickly to the given environment, both to the cell properties and the other agents. This adaptation can be observed in gradual changing environments, since the mutation range is very small, even small changes increase the reproduction probability, so that a gene evolves in a certain direction. We observe that the white areas (difficult to move terrain) separates the agents into two sub-populations. These two populations require time to develop the ability to pass this difficult terrain. At the time-step 7500, there are two locations where the agents start to interact with each other, as at this time step due to the dynamics in the environment the difficult area turned to get simpler for movements. After this step the doves fully invade the worm population. Nevertheless, the doves evolve very diverse genes as shown by the color mapping.

As for evaluating the stability, we calculate the number of different types of agents over the simulations. Figure 10 show the results for the three scenarios. We could record one run out of 30 in which all three strategy can survive. This raises the question about the robustness of our proposed model. Furthermore, only considering the number of agents of each type for analyzing the stability seems not to be applicable for our model, as we have very high diverse genes in one type of agents. Therefore, it seems that the separation of genes and the strategies is not very useful. In our model, a Hawk can develop the same genes as a Worm of the start configuration. It remains for future works to experiment with an appropriate mapping from genes to strategies.

As the results from Scenario 1 illustrate a non-stable behavior, we change the parameters for the environment and the agents as in Table IV. As the results for the two other scenarios remain unchanged (we do not observe drastic changes), we only report the results for Scenario 1 as in Figure 12. We observe that for a homogeneous environment, we are in fact able to obtain a high diversity among the genes. After 10^4 time-steps, we achieve 100 clusters, where in dynamic environments this value can be smaller. We conclude that this can only be achieved by certain parameter setting, while the behavior in dynamic environments is not so sensitive to the parameter settings.

From the experiments we can conclude that it is very difficult to define an environment in which a well-balanced and stable population can develop. Evolving advanced behaviors in environments with dynamically changing local resources adds to the difficulty of balancing the strategies. Furthermore, we observe that the most valuable resource for the agents is an empty space in the environment rather than the resources. Figure 13 illustrates a set of screenshots from Scenario 1, taken from simulation-step 1 to 4500. The first and second row from above show the initial collapse of the population and the following populations. This event happens, due to the difficulty of finding a well-balanced start configuration. The third row shows how the nearly extinct Hawks benefit from the vast number of Doves. They increase very quickly in numbers, killing most of the Doves resulting in an increase in the number of Worms, shown in the fourth row. The last

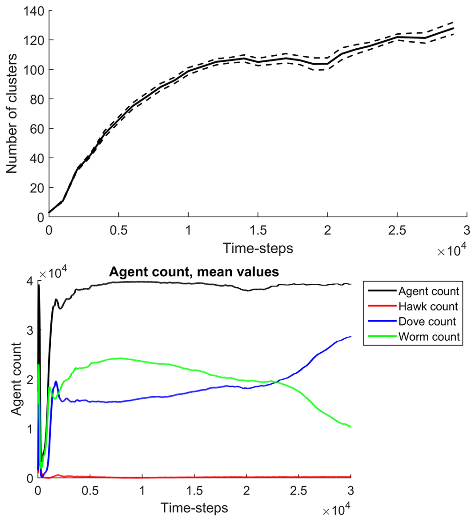

Fig. 12: Diversity and average number of agents for Scenario 1 with parameters from Table IV

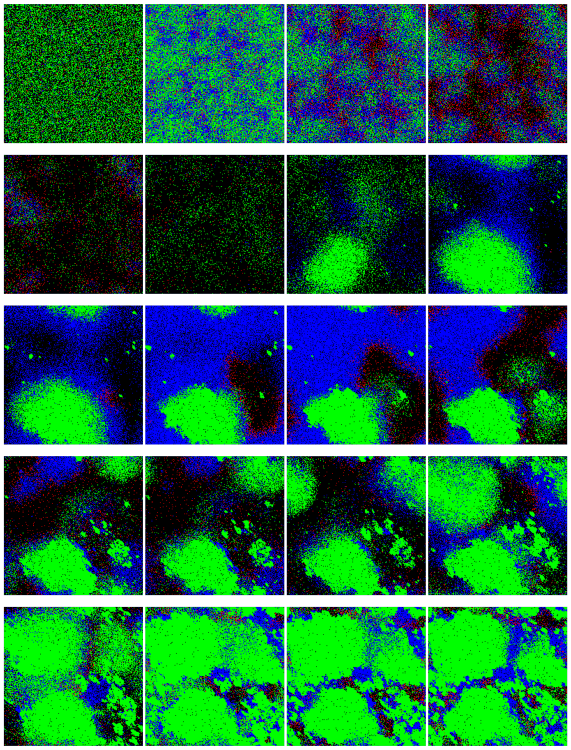

Fig. 13: Evolution of three populations over time in Scenario 1. Green, red and blue represent Worms, Hawks and Doves.

row shows a state of equilibrium between the three strategies, which was stable until 30.000 simulation steps.

V. CONCLUSION AND FUTURE WORK

In this paper, we have introduced and analyzed a new model called Evolutionary Spatial Games in dynamic environments. One of the major contributions of this work is that the agent can modify the values of the payoff matrix depending on the factors from the dynamic environment. Additionally, the genes of the agents can help them to change their strategies in the payoff matrix. We have tested our model in three different scenarios on populations of three different agents (strategies). We measure the number of agents and the their diversity in terms of their evolved genes. The results show that in very especial situations, the stability between three strategies can remain. Diversity can be developed in dynamic environments, particularly in environments with slow changes. It was observed that agents made full use of the given environment opportunities, by evolving into appropriate forms.

The results from this paper concern strategies in games with populations of agents co-existing in dynamic environments. Nevertheless, the findings can be interpreted in other contexts such as finance, economics, social and other complex simulations. Our approach has still room for improvements in future. There must be more experiments with different payoff values and other number of species. In addition we can improve the interactions between the agents by adding a decision making capability. For instance, the ability to interact can be included in the genes of the agents. More work need to be done in the evaluations of the results.

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