

Agent-Based Modeling and Simulation of Speciation and Ecosystem Diversity

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Abstract—The agent-based approach to modeling and simulation (ABMS) has recently become very popular, especially among researchers dealing with biological and social simulations. The ABMS approach allows for modeling complex phenomena, resulting from interactions between many individuals, in a very natural way. The agent-based approach is especially useful when it comes to simulating emergent phenomena, which usually arise from interactions between a large number of individuals, each of which acts according to some simple patterns or rules. In this paper, two agent-based models of species formation processes are presented and experimentally verified. The first one is a model in which speciation takes place as a result of geographic barriers that split the population. In the second the speciation results from existence and interactions between flocks of individuals, which presence restricts mating between individuals from the same species. During experiments, the ecosystem diversity and the number of existing species are measured using entropy-based indicators.

Keywords—agent-based modeling and simulation, speciation, population diversity, entropy-based diversity measures

I. INTRODUCTION

The agent-based approach to modeling and simulation (ABMS) has become popular among researchers dealing with models of complex, real-world phenomena [1]–[4]. The ABMS approach allows for relatively easy modeling of complex biological and social phenomena because it provides all the necessary notions and mechanisms like the environment, autonomously acting individuals (agents), passive objects and relations between agents, objects, and the environment. Thus, it allows modeling of complex biological and social phenomena in a very natural way, especially when it comes to investigating the emergent behavior [5]–[7].

Agent based approach is particularly useful when we want to model and simulate biological phenomena [1], [3], social mechanisms and relations [8], economic mechanisms [9], [10], political mechanisms and interactions [11], demographic phenomena [12], transportation systems and road traffic [13].

In this paper, the multi-agent system with biological and social mechanisms (BSMAS) [14] is used to model the speciation phenomena which occur in natural populations. BSMAS was developed as an extended and improved version of the co-evolutionary multi-agent system (CoEMAS) [15], which allowed for the development of computational agent-based systems with co-evolutionary and sexual selection mechanisms. CoEMAS was in turn inspired by the evolutionary multi-agent system (EMAS) proposed in [16], which allowed

for agent-based evolutionary computations. Co-evolutionary multi-agent systems were applied to multi-modal optimization [17], multi-objective optimization [18] and generating investment strategies [19].

The BSMAS approach allows for modeling all kinds of biological phenomena—including co-evolution, sexual selection and speciation—and social relations and structures. It also provides the possibilities of integrating within a single simulation system many different bio-inspired artificial intelligence techniques, like evolutionary algorithms, neural networks, and artificial immune algorithms. The BSMAS approach was successfully used for modeling and simulation of sexual selection and pair formation mechanisms and investigating their impact on speciation processes [20].

The speciation is a biological term to specify the processes of species formation caused by different factors [21], [22]. The most popular are *allopatric* models in which the speciation takes place as a result of splitting the population of a single species into several sub-populations caused by the appearance of geographical barriers between them. Such separation limits the flow of genes between sub-populations and ultimately may lead to the reproductive isolation and emergence of new species.

The second model of speciation is called *parapatric*. In this case, sub-populations of a single species live within partially overlapping habitats. Such conditions also limit the flow of genes between sub-populations and may lead to speciation.

And finally, the third model of speciation, which is called *sympatric*. Here, the speciation takes place as a result of co-evolution or sexual selection. In this model, the space factor does not play any role in the speciation. The only factor causing the speciation is the selective pressure caused by interactions between species or sexes. In some conditions, it may create the reproductive isolation of sub-populations and trigger the emergence of new species.

In this paper, the BSMAS approach is used to prepare simulation models of allopatric and parapatric speciation. The first one is caused by geographical barriers while the second one by flocking mechanism. As opposed to the previous work [14] the carried out simulation experiments will be aimed at verifying the impact of different speciation models on the course of speciation processes. The entropy-based indicators will be used to analyze the course of speciation and how it affects the diversity of the ecosystem.

II. THE AGENT-BASED SIMULATION MODELS

Both models presented in this section are based on BSMAS concept [14]. The model is composed of the environment, which has a graph structure. The agents are located within the environment and can interact with it and with each other. There is a resource in the system, which is needed by the agents for performing all of their actions, like reproduction and migration. The total amount of resource in the system is constant, so it serves as a mechanism of limiting the maximal number of agents that can live within the simulated ecosystem [23]. Each agent can obtain some amount of resource from the environment. An agent which runs out of resources dies and is removed from the system.

The reproduction takes place when a given agent has enough resources and when it can find a partner, which is also ready for the reproduction. An agent searches for partners within the same node of the environment, so the number of agents that it can interact with is limited. Children are produced with the use of intermediate recombination [24] and mutation with self-adaptation [25]. Parents give some amount of their resource to their children during the reproduction.

In the following sections, two agent-based models are presented. The first one uses the mechanism of allopatric speciation, in which there exist geographical barriers separating sub-populations. In the second one, the speciation is caused by flocking mechanism, which limits the flow of genes between sub-populations.

A. The Model with Geographical Barriers

In the multi-agent system with geographical barriers (aBSMAS) the speciation takes place as a result of allopatric speciation [14]. In allopatric speciation model, a new species emerges as a result of evolving sub-populations separated by a geographical barrier. In such conditions, the flow of genes is reduced, and after some time the sub-populations become reproductively isolated and in fact, new species arise.

In the proposed aBSMAS model the geographical barriers are simulated by a very high cost of migration between nodes of the environment (see fig. 1). It causes that practically there are no such agents that can migrate because none of them has enough resources to do that. Migrations are theoretically possible but very rare. Thus sub-populations evolve separately, and gradually distinct species emerge.

The multi-agent system with geographical barriers (aBSMAS) is defined in the following way:

$$\begin{aligned} aBSMAS(t) = \langle EnvT(t) = \{et\}, Env(t) = \{env\}, \\ ElT(t) = VertT(t) \cup ObjT(t) \cup \\ AgT(t), ResT(t) = \{rt\}, InfT(t) = \emptyset, \\ Rel(t), Attr(t) = \{genotype\}, Act(t) \rangle \end{aligned} \quad (1)$$

$EnvT(t)$ is the set of environment types. $Env(t)$ is the set of environments. $ElT(t)$ is the set of system's element types. $VertT(t) = \{vt\}$ is the set of vertex types. $ObjT(t) = \emptyset$ is the set of object types. $AgT(t) = \{ind\}$ is the set of agent types. $ResT(t)$ is the set of resource types (the amount

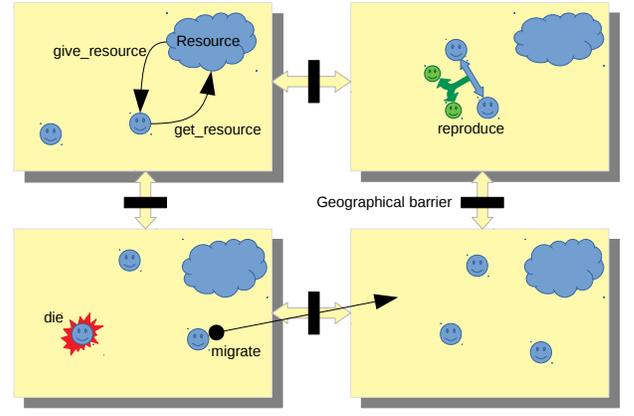


Fig. 1. Multi-Agent System with Geographical Barriers

of resource of type $rest(t) \in ResT(t)$ will be denoted as $r^{rest}(t)$). $InfT(t)$ is the set of information types (information of type $infT(t) \in InfT(t)$ will be denoted as $inf^{infT}(t)$). $Rel(t)$ is the set of relations between sets of agents, objects, and vertices. $Attr(t)$ is the set of attributes of agents, objects, and vertices (in the case of the aBSMAS system, there is only one attribute *genotype*). $Act(t)$ is the set of actions that can be executed by agents, objects, and vertices.

The set of actions is defined as follows:

$$Act = \{die, reproduce, get_resource, give_resource, migrate\} \quad (2)$$

Environment type et is defined as follows:

$$et = \langle EnvT^{et} = \emptyset, VertT^{et} = VertT, ResT^{et} = ResT, InfT^{et} = \emptyset \rangle \quad (3)$$

$EnvT^{et} \subseteq EnvT$ is the set of environment types that may be connected with the environment of type et . $VertT^{et} \subseteq VertT$ is the set of types of vertices that may exist within the environment of type et . $ResT^{et} \subseteq ResT$ is the set of resource types that may exist within the environment of type et . $InfT^{et} \subseteq InfT$ is the set of information types that may exist within the environment of type et .

Environment env of type et is defined as follows:

$$env = \langle gr^{env}, Env^{env} = \emptyset \rangle \quad (4)$$

The directed graph gr^{env} is defined as follows:

$$gr^{env} = \langle Vert, Arch, cost \rangle \quad (5)$$

$Vert$ is the set of vertices. $Arch$ is the set of arches. Function $cost$ computes an amount of resource, that an agent migrating between two nodes would lose.

Vertex type vt is defined in the following way:

$$\begin{aligned} vt = \langle Attr^{vt} = \emptyset, Act^{vt} = \{give_resource\}, \\ ResT^{vt} = ResT, InfT^{vt} = \emptyset, VertT^{vt} = \\ VertT, ObjT^{vt} = \emptyset, AgT^{vt} = AgT \rangle \end{aligned} \quad (6)$$

$Attr^{vt} \subseteq Attr$ is the set of attributes of vt type of vertex. $Act^{vt} \subseteq Act$ is the set of actions, which vertex type vt can execute. $ResT^{vt} \subseteq ResT$ is the set of resource types, which can exist within vertex type vt . $InfT^{vt} \subseteq InfT$ is the set of information, which can exist within vertex type vt . Vt^{vt} is the set of types of vertices that can be connected with vertex type vt . $ObjT^{vt} \subseteq ObjT$ is the set of types of objects that can be located within vertex type vt . $AgT^{vt} \subseteq AgT$ is the set of types of agents that can be located within vertex type vt at the beginning of its existence. *give_resource* is the action of giving a certain amount of resource to an agent.

Each vertex $vert \in Vert$ is defined as follows:

$$vert = \langle Attr^{vert} = \emptyset, Act^{vert} = Act^{vt}, Res^{vert} = \{res^{vert}\}, Inf^{vert} = \emptyset, Vert^{vert}, Obj^{vert} = \emptyset, Ag^{vert} \rangle \quad (7)$$

$Attr^{vert} \subseteq Attr$ is the set of attributes of vertex $vert$. $Act^{vert} \subseteq Act$ is the set of actions, which vertex $vert$ can execute. Res^{vert} is the set of resources of types from $ResT$ set. Inf^{vert} is the set of information of types from $InfT$ set. $Vert^{vert}$ is the set of types of vertices from $VertT$ set that are connected with vertex $vert$. Obj^{vert} is the set of objects of types from $ObjT$ set that are located within vertex $vert$. Ag^{vert} is the set of agents of types from AgT set that are located within vertex $vert$. res^{vert} is the amount of resource of type rt that is possessed by vertex $vert$. $Vert^{vert}$ is the set of sixteen vertices connected with the vertex $vert$. Ag^{vert} is the set of agents located within the vertex $vert$.

There is only one type of agents in the system:

$$ind = \langle Gl^{ind} = \{gl_1, gl_2, gl_3\}, Attr^{ind} = \{genotype\}, Act^{ind} = \{die, reproduce, get_resource, migrate\}, ResT^{ind} = ResT, InfT^{ind} = \emptyset, ObjT^{ind} = \emptyset, AgT^{ind} = \emptyset \rangle \quad (8)$$

Gl^{ind} is the set of goals of ind agent. $Attr^{ind} \subseteq Attr$ is the set of attributes of ind agent. *genotype* contains two independent variables and the parameters of mutation (standard deviations). $Act^{ind} \subseteq Act$ is the set of actions, which ind agent can execute. $ResT^{ind} \subseteq ResT$ is the set of types of resources, which can be used by ind agent. $InfT^{ind} \subseteq InfT$ is the set of information types, which can be used by ind agent. $ObjT^{ind} \subseteq ObjT$ is the set of types of objects that can be located within ind agent. $AgT^{ind} \subseteq AgT$ is the set of types of agents that can be located within ind agent.

gl_1 is the goal “get resource from the environment”, gl_2 is the goal “reproduce”, and gl_3 is the goal “migrate to another vertex”. *die* is the action of death (agent dies when it runs out of resources), *reproduce* is the action of reproducing (with the use of recombination and mutation operators), *get_resource* is the action of getting some amount of the resource from the environment, and *migrate* is the action of migrating to another vertex.

Agent ag^{ind} (of type ind) is defined as follows:

$$ag^{ind} = \langle Gl^{ag,ind} = Gl^{ind}, Attr^{ag,ind} = Attr^{ind}, Act^{ag,ind} = Act^{ind}, Res^{ag,ind} = \{r^{ag,ind}\}, Inf^{ag,ind} = \emptyset, Obj^{ag,ind} = \emptyset, Ag^{ag,ind} = \emptyset \rangle \quad (9)$$

Gl^{ind} is the set of goals, which ind agent tries to realize. $Attr^{ind} \subseteq Attr$ is the set of attributes of ind agent. $Act^{ind} \subseteq Act$ is the set of actions, which ind agent can execute in order to realize its goals. Res^{ind} is the set of resources (of types from $ResT$ set) which are used by ind agent. Inf^{ind} is the set of information (of types from the $InfT$ set), which ind agent can possess and use. Obj^{ind} is the set of objects (of types from $ObjT$ set), that are located within ind agent. Ag^{ind} is the set of agents (of types from the AgT set), that are located within ind agent.

Notation $Gl^{ag,ind}$ means “the set of goals of agent ag of type ind ”. $r^{ag,ind}$ is the amount of resource of type rt that is possessed by ag^{ind} agent.

The set of relations is defined as follows:

$$Rel = \left\{ \frac{\{get_resource\}}{\{get_resource\}} \right\} \quad (10)$$

The relation $\frac{\{get_resource\}}{\{get_resource\}}$ is defined as follows:

$$\frac{\{get_resource\}}{\{get_resource\}} = \left\{ \langle Ag^{ind,\{get_resource\}}, Ag^{ind,\{get_resource\}} \rangle \right\} \quad (11)$$

$Ag^{ind,\{get_resource\}}$ is the set of agents of type ind capable of performing action *get_resource*. This relation represents competition for limited resources between ind agents.

B. The Model with Flock Formation Mechanism

In the multi-agent system with flock formation mechanism (fBSMAS) [14] the speciation takes place as a result of flock formation, which restricts mating and causes that the flow of genes within the population is limited (see fig. 2). A ready-for-reproduction agent searches for a partner among the individuals that are members of the same flock. An agent can migrate between flocks, trying to find the one that is located within the same ecological niche.

Flocks can merge and split. Two flocks merge when they are located within the same ecological niche. A flock can also be divided into two flocks when some of the agents from the given flock are situated within different niche than the majority of the flock. An agent that is located outside the niche, within which majority of the individuals is located, tries to migrate to another flock, which is situated in its niche or creates its flock.

Flocks compete for limited resources that are located within the environment. At the same time, members of the given flock compete for limited resources between themselves. Flocks can migrate within the environment, and they lose some of their resources for such activity.

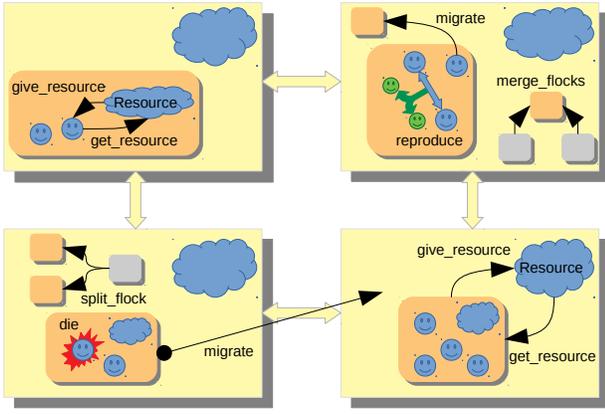


Fig. 2. Multi-Agent System with Flock Formation Mechanisms

The meaning of all symbols in the following equations is exactly the same as in the case of the aBSMAS model presented in Section II-A.

The multi-agent system with flocks $fBSMAS$ is defined in the same way as the $aBSMAS$ system (compare Equation (1)). Only AgT and Act sets are defined in a different way. The set $AgT = \{flock, ind\}$ and the set of actions is defined as follows:

$$Act = \{die, reproduce, get_resource, give_resource, migrate, search_flock, merge_flocks, split_flock\} \quad (12)$$

Environment type et and environment env are defined in the same way as in the case of $aBSMAS$ system (compare Equations (3) and (4)).

Vertex type vt is also defined as in the case of $aBSMAS$ system (compare Equation (6)). However, the meaning of $give_resource$ action from the $Act^{vt} = \{give_resource\}$ set is now different. It is the action of giving the resource to a flock. Also, the definition of $AgT^{vt} = \{flock\}$ set is different. Now the set includes only $flock$ type of agents.

Vertex $vert \in Vert$ is defined as in the case of $aBSMAS$ system (compare Equation (7)). However, there are two differences. The set $Vert^{vert}$ contains four vertices connected with the vertex $vert$ (compare Figure 2). Ag^{vert} is the set of agents of type $flock$ located within the vertex $vert$.

There are two types of agents in the system: $flock$ and ind . $flock$ type of agent is defined in the following way:

$$\begin{aligned} flock &= \langle Gl^{flock} = \{gl_1, gl_2, gl_3\}, Attr^{flock} = \emptyset, \\ Act^{flock} &= \{get_resource, give_resource, \\ migrate, merge_flocks\}, ResT^{flock} &= \\ ResT, InfT^{flock} &= \emptyset, ObjT^{flock} = \emptyset, \\ AgT^{flock} &= \{ind\} \rangle \end{aligned} \quad (13)$$

gl_1 is the goal “get resource from the environment”, gl_2 is the goal “merge with another flock”, and gl_3 is the goal “migrate to another vertex”. $get_resource$ is the action of

getting resource from the environment, $give_resource$ is the action of giving the resource to ind type agent, $migrate$ is the action of migrating to another vertex, and $merge_flocks$ is the action of merging with another flock.

ind type of agent is defined in the following way:

$$\begin{aligned} ind &= \langle Gl^{ind} = \{gl_4, gl_5, gl_6, gl_7\}, Attr^{ind} = \\ &\{genotype\}, Act^{ind} = \{die, reproduce, \\ &get_resource, migrate, search_flock, \\ &split_flock\}, ResT^{ind} = ResT, InfT^{ind} = \\ &\emptyset, ObjT^{ind} = \emptyset, AgT^{ind} = \emptyset \rangle \end{aligned} \quad (14)$$

gl_4 is the goal “get resource from the flock agent”, gl_5 is the goal “reproduce”, gl_6 is the goal “migrate to another flock”, and gl_7 is the goal “split flock”. die is the action of death—agent dies when it runs out of resources; $reproduce$ is the action of reproducing with the use of recombination and mutation operators; $get_resource$ is the action of getting the resource from $flock$ type agent; $migrate$ is the action of migrating to another flock; $search_flock$ is the action of searching for another flock, which is located within the same ecological niche; $split_flock$ is the action of creating a new flock.

Agent ag^{flock} (of type $flock$) is defined as follows:

$$\begin{aligned} ag^{flock} &= \langle Gl^{ag,flock} = Gl^{flock}, Attr^{ag,flock} = \emptyset, \\ Act^{ag,flock} &= Act^{flock}, Res^{ag,flock} = \\ &\{r^{ag,flock}\}, Inf^{ag,flock} = \emptyset, \\ &Obj^{ag,flock} = \emptyset, Ag^{ag,flock} \rangle \end{aligned} \quad (15)$$

Notation $Gl^{ag,flock}$ means “the set of goals of agent ag of type $flock$ ”. $r^{ag,flock}$ is the amount of resource of type rt that is possessed by the agent ag^{flock} . $Ag^{ag,flock}$ is the set of agents of type ind that currently belong to the flock agent.

Agent ag^{ind} (of type ind) is defined as follows:

$$\begin{aligned} ag^{ind} &= \langle Gl^{ag,ind} = Gl^{ind}, Attr^{ag,ind} = Attr^{ind}, \\ Act^{ag,ind} &= Act^{ind}, Res^{ag,ind} = \{r^{ag,ind}\}, \\ Inf^{ag,ind} &= \emptyset, Obj^{ag,ind} = \emptyset, Ag^{ag,ind} = \emptyset \rangle \end{aligned} \quad (16)$$

$r^{ag,ind}$ is the amount of resource of type rt that is possessed by the agent ag^{ind} .

The set of relations is defined in the same way as in the case of aBSMAS system (compare Equation (10)).

The relation $\frac{\{get_resource\}}{\{get_resource\}}$ is defined as follows:

$$\begin{aligned} \frac{\{get_resource\}}{\{get_resource\}} &= \left\{ \langle Ag^{flock, \{get_resource\}}, \\ &Ag^{flock, \{get_resource\}} \rangle, \right. \\ &\langle Ag^{ind, \{get_resource\}}, \\ &Ag^{ind, \{get_resource\}} \rangle \left. \right\} \end{aligned} \quad (17)$$

$Ag^{flock, \{get_resource\}}$ is the set of agents of type $flock$ capable of performing action $get_resource$. $Ag^{ind, \{get_resource\}}$

is the set of agents of type *ind* capable of performing action *get_resource*. This relation represents competition for limited resources between agents of the same type.

III. EXPERIMENTAL RESULTS

In this section, the results of experiments with the proposed agent-based models of speciation are presented. During the experiments, Waves fitness landscape was used. The entropy-based indicators were used to assess the ecosystem diversity.

Waves fitness landscape is given by the following equation [26]:

$$\begin{aligned}
 f_4(\vec{x}) = & -((0.3 * x_1)^3 - (x_2^2 - 4.5 * x_2) * x_1 * x_2 - \\
 & 4.7 * \cos(3 * x_1 - x_2^2 * (2 + x_1)) * \\
 & \sin(2.5 * \pi * x_1)) \\
 & x_1 \in [-0.9; 1.2], x_2 \in [-1.2; 1.2]
 \end{aligned} \tag{18}$$

Waves fitness landscape has many irregularly spaced local optima (see Fig. 3).

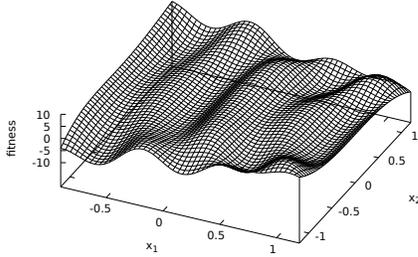


Fig. 3. Waves fitness landscape

The entropy-based indicator of ecosystem diversity [27] (the so called “true diversity” or “Hill numbers”) is defined as follows $D \equiv \left(\sum_{i=1}^S p_i^q \right)^{1/(1-q)}$. Variable q is the order of diversity, and it affects the sensitivity of the above indicator to common and rare species. For $q = 0$, the indicator is insensitive to species commonness, and we obtain the species richness indicator [27]: $D_0 = \sum_{i=1}^S p_i^0$. For $q = 0.5$ rare species are preferred [27]: $D_{0.5} = \left(\sum_{i=1}^S \sqrt{p_i} \right)^2$. For $q = 1$ neither rare nor common species are preferred. In this case, equation for D is undefined, but there exist its limit, which is the exponential of Shannon entropy [27]: $D_1 = \exp \left(- \sum_{i=1}^S p_i \ln(p_i) \right)$. For $q = 2$ common species are preferred [27]: $D_2 = 1 / \left(\sum_{i=1}^S p_i^2 \right)$.

The results of experiments with the allopatric model are shown in Figure 4. As it can be seen, there is only one species in the ecosystem in step 0 (Figure 4(a)). In the following steps, the speciation processes can be observed. The values of entropy-based indicators show that neither rare nor common species dominate in the ecosystem. It can also be observed that from step 2500 (Figure 4(c)) the number of distinct species in the ecosystem stabilizes at the level of 6. So, in the case of allopatric speciation, the speciation takes place as expected, and the diversity within species that emerged is quite balanced.

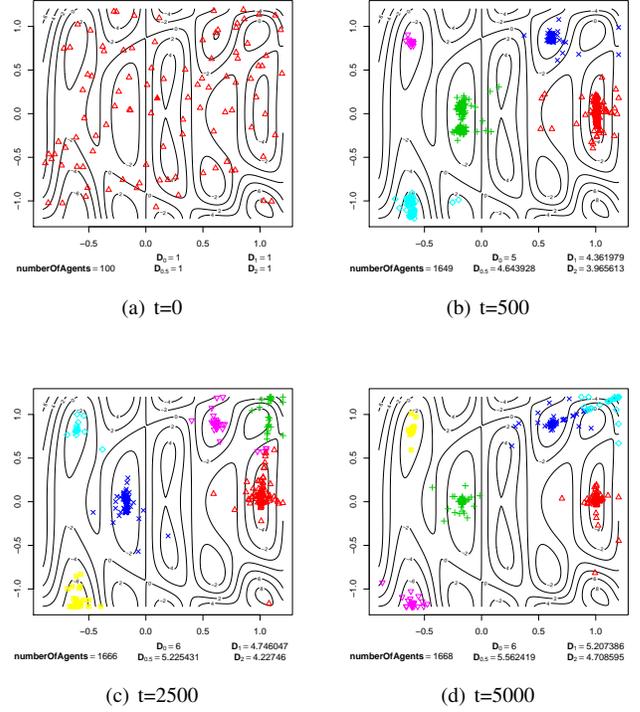


Fig. 4. The processes of species formation for allopatric mechanism

In the case of parapatric speciation model with flocking mechanism species also emerge during simulation (Figure 5). In step 0, there is only one species in the ecosystem (Figure 5(a)). It can be observed that in step 500 there are twelve distinct species (Figure 5(b)). In step 2500 the number of species drops to seven (Figure 5(c)) and then it raises again to twelve (Figure 5(d)). Such fluctuations in the number of distinct species result from the splitting and merging of flocks. It shows that ecosystem diversity measured as the number of distinct species is quite unstable when flocks are formed. However, finally, the ecosystem diversity is quite high with rare species slightly dominating in the ecosystem.

IV. SUMMARY AND CONCLUSIONS

In this paper, the bio-social multi-agent system (BS-MAS) [14] was used to develop two speciation models. The first one was the agent-based model of allopatric speciation. The second one was the agent-based model of parapatric speciation caused by the existence of flocks within the population.

The experiments showed that in both cases the speciation took place. However, the course of the processes taking place in the ecosystem was different in each case. In the case of allopatric speciation, six distinct species were formed. The population diversity within each species was kept at an average level. The values of entropy-based indicators showed that neither rare nor common species dominated the ecosystem.

In the case of the parapatric model with flocking mechanism the speciation also took place. It could be observed that a larger

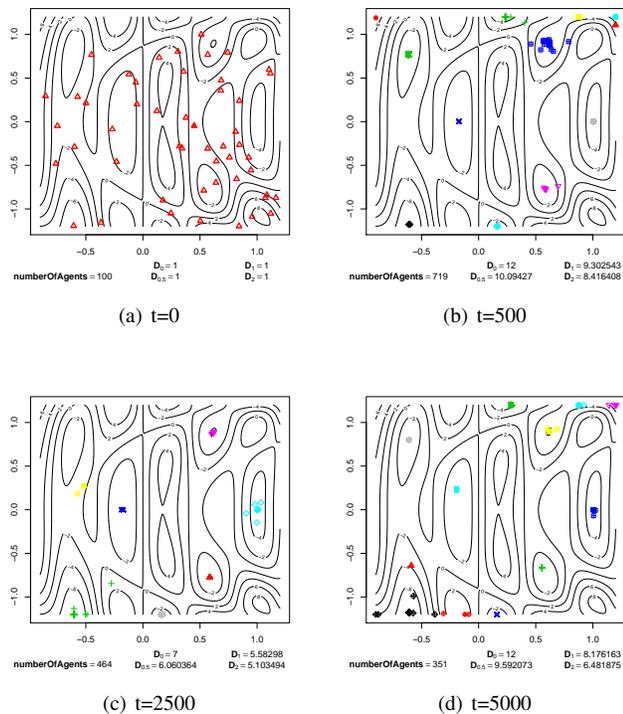


Fig. 5. The processes of species formation for flocking mechanism

number of species emerged in the ecosystem than in the case of the allopatric model. The entropy-based indicators show that twelve distinct species emerged and rare species prevailed in the ecosystem.

The carried out experiments have proven that agent-based models can provide useful information about emergent biological phenomena, and in-depth analyzes are possible in the case of phenomena that are difficult to explore differently.

The future research will include the further application of BSMAS approach in the area of evolutionary biology. Mainly, other models of speciation will be examined with the use of agent-based simulation models.

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