Stochastic Dynamics of Evolutionary Multi-Agent Systems

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Abstract. The refined model for the biologically inspired agent-based computation system EMAS conformed to BDI standard is presented. The considerations are based on the model of the system dynamics as the stationary Markov chain already presented. In the course of paper space of the system states is modified in order assure state coherency and set of actions is simplified. Such a model allows for better understanding the behavior of the proposed complex systems as well as their limitations.

1 Introduction

Immunological systems are relatively new technique used for solving different problems i.a. intruder detection [1–3], or optimization [4]. Evolutionary Multi-Agent Systems (EMAS) proposed in 1996 by Cetnarowicz [5] and later researched in [6–9] try to enrich the classical evolutionary mechanisms using social inspirations [10]. These two techniques were merged and the first results were published in [6–8]. In order to conduct intensive further research, these techniques should be formalized, and the authors tend to perform some quantitative and qualitative analysis representing EMAS as the stationary Markov chains.

Agents in EMAS may be perceived as autonomous individuals. Every agent is capable of observing its environment by gathering information which it finds important, making decisions which affect its activity and performing actions which lead to changes in the overall state of the system (see e.g. [11, 12]).

We will focus on system that solves the global optimization problems which consist of finding all global minimizers $\arg\min\{\Phi(x)\}, x \in \mathcal{D}$ of the objective: $\Phi : \mathcal{D} \to \mathbb{R}_+$ where $\mathcal{D} \subset \mathbb{R}^N$ stands for the admissible set of solutions. Every EMAS agent contains an immutable genotype, which stands for the encoded solution of the problem. Genotypes belong to the binary or real-number based genotype universum U. Agents are assigned to locations (analogous of "islands", see e.g. [13]) and may migrate among them. Genetic operations performed on the agent's genotypes, such as crossover and mutation, are similar to those used in classical evolutionary algorithms.

Each agent is transformed asynchronously in the EMAS system. Selection mechanisms correspond to their prototype and are based on the existence of a non-renewable resource called *life energy*, which is gained and lost when agents perform actions [9]. Direct employment of different selection techniques (such

as proportional or tournament-based) is impossible because of the asynchronous nature of the system and decomposition of the population.

Some important optimization tasks have already been solved by EMAS and yield more effective results than certain classical approaches (e.g. optimization of neural-network architecture [6–8]). In contrast to the classical genetic approach in which the network is fully trained for each individual, the fully- and partially-trained as well as newly-introduced networks may exist at the same time in EMAS what may enhance the adaptivity of the computation.

We present further development of the model described first in the paper [14] and extended in [15]. The main novelty in this paper is updating the system space in order to assure coherency, what is followed by removing unnecessary action of death and simplifying the other actions. We also introduce the constrained locations capacities (limited number of agents). The results gathered in this paper prepare us for the further study of asymptotic behavior of EMAS.

2 EMAS definition

We propose the formal model for EMAS which follows results in this area already published (see e.g. [14, 8]).

2.1 EMAS structure

EMAS may be modeled as the following tuple

$$< U, Loc, Top, Ag, agsel, \omega, Act > . \tag{1}$$

In the course of the section all symbols mentioned above will be defined.

EMAS contains a dynamic collection of agents that belong to the predefined finite set Ag. Every agent $ag_{gen} \in Ag$ contains exactly one potential solution of the given problem or its encoded representation (genotype), so there exists the bijection $Ag \ni ag_{gen} \rightarrow gen \in U$. We restrict our considerations to the case of finite universa $\#U = r < +\infty$.

The state of a single agent is characterized by the tuple $Ag \ni ag_{gen} =< gen, e >$, where $e \in [0, 1]$ stands for the fraction of the total energy gathered by the agent.

Active EMAS agents are contained in locations described by a set of immutable integer labels $Loc = \{1, \ldots, s\}$. The locations are linked by the channels along which agents may migrate from one location to another. The topology of channels is determined by the symmetric relation $Top \subset Loc^2$. We assume that the connection graph $< Loc, Top >$ is coherent, and does not change during the system evolution.

2.2 EMAS state

Let us introduce the set of incedence and energy matrices X with s columns (number of all locations) and r (number of all genotypes) rows. The columns

$ince(i) \in X$ will contain energies of agents in i-th location. In other words, if $ince(i,j) > 0$, it means that an agent denoted by gene $j \in U$ is active, its energy is $ince(i,j) = e(j)$ and it is located in i-th location.

We assume, that i-th column may contain at most $q_i \leq r$ values greater than zero, what denotes the maximum capacity of the i-th location, and j-th row may contain at most one value greater than zero, what expresses that j-th agent may be present in only one location at a time. Moreover $ince(i,j) \geq 0, \forall\ j = 1,\ldots,r, i = 1,\ldots,s$ and $\sum_{j=1}^{r}\sum_{i=1}^{s} ince(i,j) = 1$.

Gathering all these conditions, the set of incedence and energy matrices, that constitutes the EMAS space of states, may be described in the following way:

$$X = \left\{ ince \in [0,1]^{r\cdot s} : \sum_{j=1}^{r}\sum_{i=1}^{s} ince(i,j) = 1 \right.$$
$$\wedge\ \forall\ i = 1,\ldots,s \sum_{j=1}^{r} [ince(i,j) > 0] \leq q_i$$
$$\left. \wedge \forall\ j = 1,\ldots,r \sum_{i=1}^{s} [ince(i,j) > 0] \leq 1 \right\} \tag{2}$$

where $[\cdot]$ denotes the value of the logical expression contained in the parentheses.

2.3 EMAS behavior

Every agent starts its work in EMAS immediately after being activated. In every observable moment a certain agent gains the possibility of changing the state of the system by executing its action.

The following random function is used do determine, which agent will be the next one to interact with the system

$$agsel : X \to \mathcal{M}(Ag) \tag{3}$$

where here and later $\mathcal{M}(\cdot)$ stands for the space of probabilistic measures. The probability $agsel(x)(\{gen\})$ vanishes when the agent ag_{gen} is inactive in the state $x \in X$.

After being chosen, the agent chooses one of the possible actions, then it checks whether the associated condition is true, if so, the agent performs the action. The agent suspends its work in the system after performing the action which results in its death. The cycle of an agent's life is presented in Figure 1.

Every agent may perform actions contained in a predefined, finite set Act. The action, whose decision is to be evaluated by an agent, is chosen using the following function

$$\omega : U \times X \to \mathcal{M}(Act). \tag{4}$$

In the simplest case ω returns the uniform probability distribution over Act.

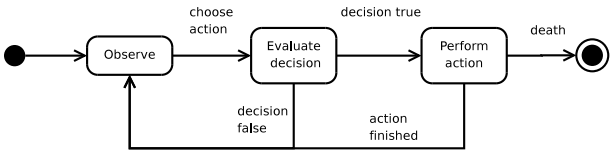

Fig. 1. Agent's state transition diagram

Every action $\alpha \in Act$ is the pair $(\delta_\alpha, \{\vartheta_\alpha^{gen}\}), gen \in U$ where

$$\delta_\alpha : U \times X \to \mathcal{M}(\{0,1\}) \tag{5}$$

will denote the decision. The action α is performed with the probability $\delta_\alpha(gen, x)(\{1\})$ by the agent ag_{gen} in the state $x \in X$. Moreover

$$\vartheta_\alpha^{gen} : X \to \mathcal{M}(X) \tag{6}$$

defines the non-deterministic state transition caused by the execution of the action α by the agent ag_{gen}. The trivial state transition

$$\vartheta_{null} : X \to \mathcal{M}(X) \tag{7}$$

such that for all A being the measurable set in X and all $x \in X$

$$\vartheta_{null}(x)(A) = \begin{cases} 1 & \text{if } x \in A \\ 0 & \text{otherwise} \end{cases} \tag{8}$$

is performed with the probability $\delta_\alpha(gen, x)(\{0\})$.

2.4 EMAS actions

Let us consider the following set of actions

$$Act = \{repr, get, migr\} \tag{9}$$

where *repr* activates an agent as the offspring agent in the system, *get* lets the better agent (better — in the means of predefined fitness function) to take the part of the life energy from the worse agent and may make the agent with low energy inactive, *migr* denotes migration of agents between two locations.

Let us denote by l the location of the current active agent (indexed by the genotype *gen*) performing the action (i.e. $ince(l, gen) > 0$).

The decision of the of energy transfer action *get* is

$$\delta_{get}(gen, x)(\{1\}) = \begin{cases} 1 & \text{if } NBAG_{gen} \neq \emptyset \\ 0 & \text{otherwise} \end{cases} \tag{10}$$

where $NBAG_{gen} = \{\{U \setminus \{gen\}\} \ni gen' : ince(l, gen') > 0\}$ is the set of agents neighboring ag_{gen} (present in the same location), for an arbitrary $gen \in U$ and

$x \in X$. So, the agent decides to transfer the energy, when it has at least one neighboring agent. In this case the following state transition is performed:

$$\vartheta_{get}^{gen}(x)(A) = \frac{1}{\#NBAG_{gen}} \left(\sum_{gen' \in BET_{gen}} \chi_A(x'(x, gen, gen')) + \sum_{gen' \in NBAG_{gen} \setminus BET_{gen}} \chi_A(x'(x, gen', gen)) \right) \tag{11}$$

where

$$BET_{gen} = \{NBAG_{gen} \ni gen' : FITN(gen') \geq FITN(gen)\} \tag{12}$$

is the set of neighboring agents better than the active agent in the means of fitness function defined as follows $FITN : U \to \mathbb{R}$. The fitness function is related in some way to the objective Φ. In the simplest case $FITN(gen) = \Phi(code(gen))$, where $code : U \to \mathcal{D}$ is the encoding function. Moreover $\chi_A(\cdot)$ denotes the characteristic function of the set A.

During the meeting, better agent takes part of energy of the worse agent, then the following state transition is performed:

$$x'(x, a, b) = ince' :$$
$$ince'(i, j) = \begin{cases} ince(i, j) - \Delta e \text{ if } j = a \wedge \ i = l \\ ince(i, j) + \Delta e \text{ if } j = b \wedge \ i = l \\ ince(i) \qquad\qquad \text{otherwise} \end{cases} \tag{13}$$

Here $x = ince$ and $\Delta e = min\{ince(l, a), e_{tr}\}$ denotes the portion of energy that may be passed between agents during single *get* action (in both cases), $\Delta e > 0$ is the variable parameter that characterizes the action *get*.

The decision of the reproduction action *repr* gets for an arbitrary $gen \in U$ and $x \in X$

$$\delta_{repr}(gen, x)(\{1\}) = \begin{cases} 1 \ \text{ if } ince(l, gen) > e_{repr} \wedge RPAG_{gen} \neq \emptyset \\ \quad \wedge \sum_{j=1}^{r} [ince(l, j) > 0] < q_l \\ 0 \ \text{ otherwise} \end{cases}$$

where $RPAG_{gen} = \{NBAG_{gen} \ni gen' : ince(l, gen') > e_{repr}\}$ is the set of neighboring agents with higher energy than the variable threshold of reproduction e_{repr}. So, the agent decides to reproduce when its energy reaches or exceeds e_{repr} and when it has at least one neighbor with the proper energy When these conditions are satisfied, the following state transition is performed

$$\vartheta_{repr}^{gen}(x)(A) = \frac{1}{\#RPAG_{gen}}$$
$$\sum_{gen' \in RPAG_{gen}} \sum_{gen'' \in U} MIX(gen, gen')(\{gen''\}) \chi_A(x'(x, gen, gen', gen'')) \tag{14}$$

where $MIX : U \times U \to \mathcal{M}(U)$ is the family of probability distributions associated with genetic mixing (crossover followed by mutation, see e.g. [16]). In particular $MIX(gen, gen')(\{gen''\})$ denotes the probability that gen'' is born from the parents gen and gen'.

The next state of the system x' is now defined as

$$x'(x, a, b, c) = ince'. \tag{15}$$

When child agent indexed by gen'' does not exist ($\forall i : ince(i, gen'') = 0$) then

$$ince'(i,j) = \begin{cases} ince(i,j) - \frac{e_0}{2} & \text{if } j \in \{a,b\} \wedge \ i = l \\ e_0 & \text{if } j = c \wedge \ i = l \\ ince(i,j) & \text{otherwise} \end{cases} \tag{16}$$

so, two agents identified by a and b create an offspring agent c and put it into their location. When the offspring agent already exists in the system ($\exists j : ince(j, c) > 0$) then

$$ince'(i,j) = \begin{cases} ince(i,j) - \frac{e_0}{2} & \text{if } j \in \{a,b\} \wedge \ i = l \\ ince(i,j) + e_0 & \text{if } j = c \wedge i = l \\ ince(i,j) & \text{otherwise} \end{cases} \tag{17}$$

where e_0 is the start energy of single agent, while $x = ince$. Thus energy of the already active offspring agent is raised by $e_0 < e_{repr}$.

The decision of the migration action $migr$ is given by

$$\delta_{migr}(gen, x)(\{1\}) = \begin{cases} 1 & \text{if } ince(l, gen) > e_{migr} \\ 0 & \text{otherwise} \end{cases} \tag{18}$$

for all $gen \in U$ and $x \in X$, where $e_{migr} \geq e_{repr}$ is a general energy threshold for migration. So, the agent decides to migrate when its energy reaches sufficient level. Let $l \in Loc$ be the label of the current location of the active agent, $ACCLOC_l = \{Loc \setminus \{l\} \ni l' : ((l, l') \in Top) \wedge (\sum_{j=1}^{r} [ince(l', j) > 0] < q_{l'})\}$ is the set of neighboring locations with the number of agents lower than maximum. The state transition for the migration action has following form

$$\vartheta^{gen}_{migr}(x)(A) = \frac{1}{\#ACCLOC_l} \sum_{loc' \in ACCLOC_l} \chi_A(x'(x, gen, loc')) \tag{19}$$

where

$$x'(x, a, k) = ince' : ince'(i,j) = \begin{cases} 0 & \text{if } j = a \wedge i = l \\ ince(l, a) & \text{if } j = a \wedge i = k \\ ince(i,j) & \text{otherwise} \end{cases} \tag{20}$$

while $x = ince$. The agent migrates to the one of uniformly chosen neighboring locations and the incidence matrix is changed.

2.5 EMAS dynamics

We intend to present the EMAS as the stationary Markov chain with the set of states X. The function of the stochastic state transition may be obtained in the following steps.

Let us denote by $\{\rho_{\alpha}^{gen}\}_{\alpha \in Act, gen \in U}$ the transition functions for all actions and all agents. The probability of passage from the state x to the state belonging the measurable subset $A \subset X$ caused by the action α invoked by the agent ag_{gen} is then

$$\rho_{\alpha}^{gen}(x)(A) = \delta_{\alpha}(gen, x)(\{0\}) * \vartheta_{null}(x)(A) + \delta_{\alpha}(gen, x)(\{1\}) * \vartheta_{\alpha}^{gen}(x)(A). \tag{21}$$

Let $\{\rho_{gen}\}_{gen \in U}$ be the set of transition function which are related to the activity of the agent ag_{gen}, then

$$\rho_{gen}(x)(A) = \sum_{\alpha \in Act} \omega(gen, x)(\{\alpha\}) \rho_{\alpha}^{gen}(x)(A). \tag{22}$$

Finally, the transition function for a single EMAS step is given by

$$\tau(x)(A) = \sum_{gen \in U} agsel(x)(\{gen\}) \rho_{gen}(x)(A). \tag{23}$$

3 Conclusions

In the course of paper, EMAS system was formally described according to the standard of BDI architecture (see e.g. [12]). The space of states of both systems and the transition functions allowing for uniform Markov chain modeling of the systems were proposed. The quantity of agents in the localizations was also limited.

In the opinion of authors, modelling of the system with use of Markov chains allows for better understanding of the behavior of the proposed complex systems as well as their constraints.

However the general form of the Marcovian kernels of the system state transition functions were identified, we intend to study the asymptotic behavior with respect to the probability distributions of mixing operator MIX, agent selection functions $agsel, \omega$ and energy thresholds of agents and lymphocytes. One of the most challenging task will be to investigate, if there exists certain configurations of agent's energy thresholds, for which every possible energetic state will be reachable after finite sequence of steps. This would prove the global search capabilities of the proposed systems.

Modelling and analysis of concurrent behavior of the system is also envisaged.

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