Multiple World Genetic Algorithm to Analyze Individually Advantageous Behaviors in Complex Networks

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ABSTRACT

We propose a novel method for evolutionary network analysis that uses the genetic algorithm (GA), called the *multiple world genetic algorithm*, to coevolve appropriate individual behaviors of many agents on complex networks without sacrificing diversity. We conducted the experiments using simulated games of social networking services to evaluate the proposed method. The results indicate that it could effectively evolve the diverse strategy for each agent and the resulting fitness values were almost always larger than those derived through evolution using the conventional evolutionary network analysis using the GA.

CCS CONCEPTS

• **Computing methodologies → Genetic algorithms**; *Multi-agent systems*;

KEYWORDS

Genetic algorithm, evolutionary network, coevolution, social network analysis, complex networks, diversity, social behavior

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1 INTRODUCTION

The genetic algorithm (GA) is used in many domains, such as sociology [2], bioinformatics/medical sciences [3], and social behaviors in the Internet [5] to find the interaction strategies on networks of agents. In *evolutionary network analysis* (ENA) [1] using GA, parents for reproduction are often selected among their neighbors under the assumption that neighbors' better strategies are useful. However, if they are on complex networks, agents exist in distinctive and diverse situations, and thus, they have their appropriate strategies. This property of diversity is somewhat inconsistent with the assumption mentioned above. Therefore, we propose the evolutionary computation method called *multiple-world GA* that uses a GA on fixed networks to achieve coevolution without neglecting diversity of individual agents.

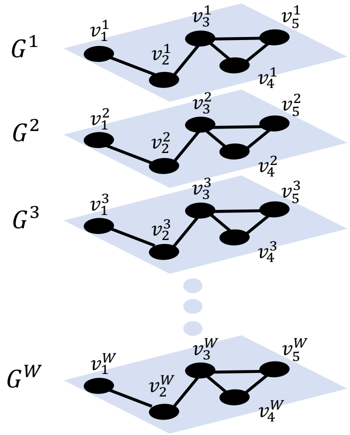

Figure 1: Conceptual structure of multiple-world GA.

2 MULTIPLE WORLD GA

Let $G = (V, E)$ be a graph representing the underlying network whose nodes $V = \{v_1, \dots, v_n\}$ are the set of agents and E the set of links between agents. G is called the *master network*, and each node $v_i \in V$ is called the *original agent*. We define N_i ($\subset V$) for all $\forall v_i \in V$ as the set of neighboring agents in G.

In the *multiple-world GA*, we make W copies of the master network G, each of which is denoted by $G^l = (V^l, E^l)$ for $1 \leq l \leq W$, where W is a positive integer called the *multiple-world number*. We represent the agents in the l-th world as $V^l = \{v_1^l, \dots, v_n^l\}$. An example of a *multiple-world GA* structure is illustrated in Fig. 1. Furthermore, we denote the set of agents at the same location in each network in the multiple worlds by $A_i = \{v_i^1, \dots, v_i^W\}$ for $1 \leq i \leq n$ and further assume that the agents in A_i are fully connected (so they form a complete graph). The set of agents A_i corresponds to an original agent v_i in G. Initially, agents in $V^1 \cup \dots \cup V^W$ decide their genes randomly. This means that agents in A_i are copies of the same original agent v_i but have different genes; thereby, they

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behave differently. Therefore, the elements in A_i are called the *sibling agents* of v_i.

In a social simulation using the multiple-world GA, all agents interact with their neighbor agents in each copy of graph G^l for $1 \le \forall l \le W$ and get certain rewards or signals that will be reflected in the values of the fitness function f. Because the neighboring agents have different genes in each copy of G, all sibling agents in A_i will have different values of the fitness function. Therefore, $v_i^l \in A_i$ lives in its own local environment that is different from those of other sibling agents in $A_i \setminus \{v_i^l\}$.

Each agent then generates the offspring agent for the next generation as follows. After a certain number of interactions with neighbors, agent $v_i^l \in V^l$ selects two appropriate agents (as parents) from the set of the sibling agents in the other worlds A_i on the basis of their values of the fitness function $f(v_i^l)$, by using a certain selection method such as roulette wheel selection. Then, crossover and mutation are applied in the same way as in the conventional GA, and the resulting gene is the one for v_i^l in the next generation. After the end of the interaction in the final generation defined in advance, the agent v_i^l with the highest fitness value in A_i is selected, and its gene is assumed to be the one for original agent $v_i \in V$.

3 EXPERIMENTS AND RESULTS

We evaluated the multiple-world GA on the *meta-rewards game with diminishing marginal utility (dMRG)* proposed by Miura, Toriumi, and Sugawara [4], which is a social simulation model of users in social networking services, such as Facebook and LinkedIn and is a dual part of Axelrod's meta-norms game [2]. The details of dMRG are described in [4]. This game is aimed at finding the agents' reasonable strategies by searching the values for B_i which represents the probability of posting article, and L_i which represents the probability of comment. The networks used in our experiments were generated using the BA model, wherein the number of agents was one thousand ($n = |V| = 1000$) and the minimal degrees were set 10. We set $W = 30$. Note that the fitness value of each agent is the sum of the rewards received as the result of dMRG in every generation.

In the first experiment, we compared the fitness values obtained by the conventional ENA using GA and the *multiple-world GA*. Figure 2 plots the improvement in fitness values had by our method, which was defined as the difference in average fitness values of agent v_i. A positive value means that the agents of the multiple-world GA found better behavioral strategies with their neighbors. Figure 2 indicates that 97% of the agents' fitness values improved regardless of their degrees. Although approximately 3% of agents decreased their fitness values; we think that this was mainly caused by mutation.

We conducted the second experiment to investigate how multiple-world GA brought diversity to the strategies of agents in the complex networks by coevolution. Figure 3 is a 3D scatter graph in which the resulting B_i, L_i and degree for all $\forall v_i \in V$ are for the conventional ENA using GA and multiple-world GA. In the result of the conventional ENA, most agents had similar B_i and L_i for all $\forall v_i \in V$ (B_i and L_i were approximately 0.7 and 0.8, respectively). On the other hand, the result of multiple-world GA shows that the values of B_i and L_i were diverse and dependent on the characteristics of the agents' degrees and network locations.

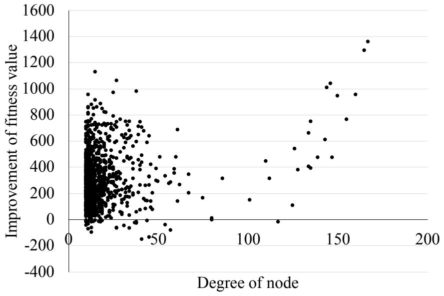
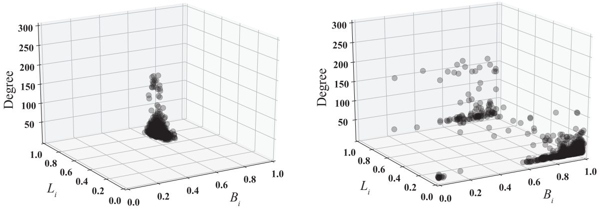


Figure 2: Improvement of fitness value in BA networks.



conventional ENA with GA multiple world GA

Figure 3: Distribution of B_i and L_i

4 CONCLUSION

We proposed a novel coevolutionary computation methodology for evolutionary network analysis based on GA, called *multiple-world GA*, in which agents can identify, through the process of coevolution, their own appropriate solutions/behaviors according to their own standpoints in complex social networks. Our experimental results indicate that it could actually evolve diversity in strategic behaviors and the resulting fitness values were almost always larger than those evolved using the conventional evolutionary network analysis using GA.

REFERENCES

[1] Charu Aggarwal and Karthik Subbian. 2014. Evolutionary Network Analysis: A Survey. *ACM Comput. Surv.* 47, 1, Article 10 (May 2014), 36 pages. https://doi.org/10.1145/2601412

[2] Robert Axelrod. 1986. An evolutionary approach to norms. *American political science review* 80, 4 (1986), 1095–1111.

[3] Payel Ghosh and Melanie Mitchell. 2006. Segmentation of medical images using a genetic algorithm. In *Proc. of the 8th Ann. Conf. on Genetic and Evolutionary Computation.* ACM, 1171–1178.

[4] Yutaro Miura, Fujio Toriumi, and Toshiharu Sugawara. 2018. Evolutionary Learning Model of Social Networking Services with Diminishing Marginal Utility. In *Companion Proceedings of the The Web Conference 2018 (WWW '18).* 1323–1329. https://doi.org/10.1145/3184558.3191573

[5] Fujio Toriumi, Hitoshi Yamamoto, and Isamu Okada. 2012. Why do people use social media? Agent-based simulation and population dynamics analysis of the evolution of cooperation in social media. In *Proc. of the IEEE/WIC/ACM Int. J. Conf. on Web Intelligence and Intelligent Agent Technology-Volume 02.* 43–50.