Seeking Open-Ended Evolution in Swarm Chemistry

Hiroki Sayama

Binghamton University, State University of New York Binghamton, New York 13902–6000, USA (sayama@binghamton.edu)

Abstract—This paper reports several new simulation results obtained with the revised Swarm Chemistry model. The model extensions included local transmission of recipes (kinetic rules) between particles, their stochastic differentiation, and competition and mutation of recipes. These extensions aimed to make the swarms capable of demonstrating open-ended evolution. The results indicated that "cooperation" among particles is essential for creating and maintaining macroscopic coherent structures, and that high mutation rates and dynamic environmental conditions may promote continuing evolutionary changes.

I. INTRODUCTION

In the closing session of ALIFE XII, Packard [1] pointed out that several subfields were reaching their maturity in the Artificial Life community, including (a) artificial chemistry/origin of life, (b) evolutionary dynamics/open-ended evolution, and (c) swarm robotics/collective behavior. Packard also claimed that integrating those subfields into unified research projects would be the next major challenge of Artificial Life research.

This paper presents an attempt to achieve such an ambitious goal by integrating evolutionary dynamics (topic (b) above) into Swarm Chemistry [2], [3], [4] which already integrated (a) and (c). A particular focus is on the endeavor toward demonstrating open-endedness in the evolutionary dynamics of artificial chemical systems. In what follows, several model extensions added to Swarm Chemistry, some preliminary simulation results, and future research plans will be discussed.

II. MODEL

Swarm Chemistry [2], [3], [4] is an artificial chemistry framework that can demonstrate self-organization of dynamic patterns of kinetically interacting heterogeneous particles. A swarm population in Swarm Chemistry consists of a number of simple self-propelled particles moving in a two-dimensional continuous space. Each particle can perceive average positions and velocities of other particles within its local perception range, and change its velocity in discrete time steps according to kinetic rules similar to those of Reynolds' Boids [5].

Each particle is assigned with its own kinetic parameter settings that specify preferred speed, local perception range, and strength of each kinetic rule (see [2] for details of the simulation algorithm and the use of these parameters in it). Particles that share the same set of kinetic parameter settings are considered of the same type. Particles do not have a capability to distinguish one type from another; all particles look exactly the same to themselves. For a given swarm, specifications for its macroscopic properties are indirectly and

implicitly woven into a list of different kinetic parameter settings for each swarm component, called a *recipe* (see Fig. 1), which would be hard to obtain through conventional design methods but can be obtained heuristically through interactive evolutionary methods [2], [6].

Several major modifications were recently implemented in the Swarm Chemistry model [3], [4], as follows:

- 1) There are now two categories of particles, active (moving and interacting kinetically) and passive (remaining still and inactive). An active particle holds a recipe of the swarm (a list of kinetic parameter sets) (Fig. 1(a)).
- 2) A recipe is transmitted from an active particle to a passive particle when they collide, making the latter active (Fig. 1(b)).
- 3) The activated particle differentiates randomly into one of the multiple types specified in the recipe, with probabilities proportional to their ratio in it (Fig. 1(c)).
- 4) Active particles randomly and independently redifferentiate with small probability, r, at every time step.
- 5) A recipe is transmitted even between two active particles of different types when they collide. The direction of recipe transmission is determined by a competition function that picks one of the two colliding particles as a source (and the other as a target) of transmission based on their properties (Fig. 1(d)).
- 6) The recipe can mutate when transmitted, as well as spontaneously at every time step, with small probabilities, p_t and p_s , respectively (Fig. 1(e)). In a single recipe mutation event, several mutation operators are applied, including duplication of a kinetic parameter set (5% per set), deletion of a kinetic parameter set (5% per set), addition of a random kinetic parameter set (10% per event in Exps. 1, 2, 3; increased to 50% per event in Exps. 4, 5), and a point mutation of kinetic parameter values (10% per parameter).

These extensions made the model capable of showing morphogenesis and self-repair [3] and autonomous ecological/evolutionary behaviors of self-organized "superorganisms" made of a number of swarming particles [4].

III. EXPERIMENTS

Several simulation experiments were conducted using the revised Swarm Chemistry model described above. The simulator codes were written in Java. In all simulation runs, 10000 particles were simulated for a fixed number of time

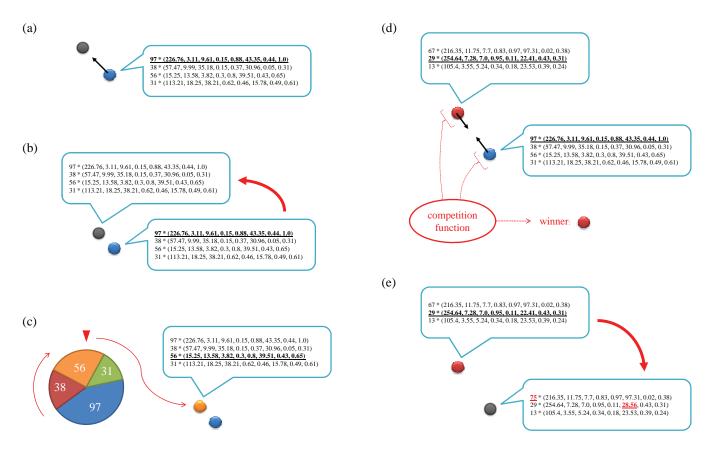


Fig. 1. How particle interactions work in the revised Swarm Chemistry (from [4]). (a) There are two categories of particles, active (blue) and passive (gray). An active particle holds a recipe of the swarm in it (shown in the call-out). Each row in the recipe represents one kinetic parameter set. The underline shows which kinetic parameter set the particle is currently using (i.e., which kinetic type it is differentiated into). (b) A recipe is transmitted from an active particle to a passive particle when they collide, making the latter active. (c) The activated particle differentiates randomly into a type specified by one of the kinetic parameter sets in the recipe given to it. (d) A recipe is transmitted between active particles of different types when they collide. The direction of recipe transmission is determined by a competition function that picks one of the two colliding particles as a source (and the other as a target) of transmission based on their properties. (e) The recipe can mutate when transmitted with small probability.

steps. In all the simulation results presented in this paper, the redifferentiation probability was set to r=0.005, while the mutation probabilities p_t and p_s were varied.

Two different kinds of initial conditions were used: a *random* initial condition made of 9900 inactive particles and 100 active particles with randomly generated one-type recipes distributed over the space, and a *designed* initial condition consisted of 9999 inactive particles distributed over the space, with just one active particle that holds a pre-designed recipe positioned in the center of the space. Specifically, recipes of "swinger", "rotary" and "walker-follower" patterns (Fig. 2) were taken from the project website¹ and used.

All the simulations were done in a finite, 5000×5000 square space (in arbitrary units; for reference, the maximal perception radius of a particle was 300). A "pseudo"-periodic boundary condition was applied to the boundaries of the space. Namely, particles that cross a boundary reappear from the other side of the space just like in conventional periodic boundary conditions, but they do not interact across boundaries with other particles sitting near the other side of the space.

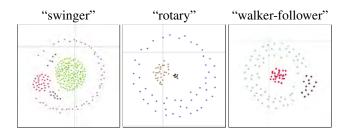


Fig. 2. Patterns generated by three recipes used for *designed* initial conditions in the experiments.

In other words, the periodic boundary condition applies only to particle positions, but not to their interaction forces. This specific choice of boundary treatment was initially made because of its simplicity of implementation, but it proved to be a useful boundary condition that introduces a moderate amount of perturbations to swarms while maintaining their structural coherence and confining them in a finite area.

A. Exp. 1: Spontaneous Evolution in Swarm Chemistry

The first experiment was to see the basic evolutionary dynamics of the model under low mutation rates ($p_t =$

¹http://bingweb.binghamton.edu/~sayama/SwarmChemistry/

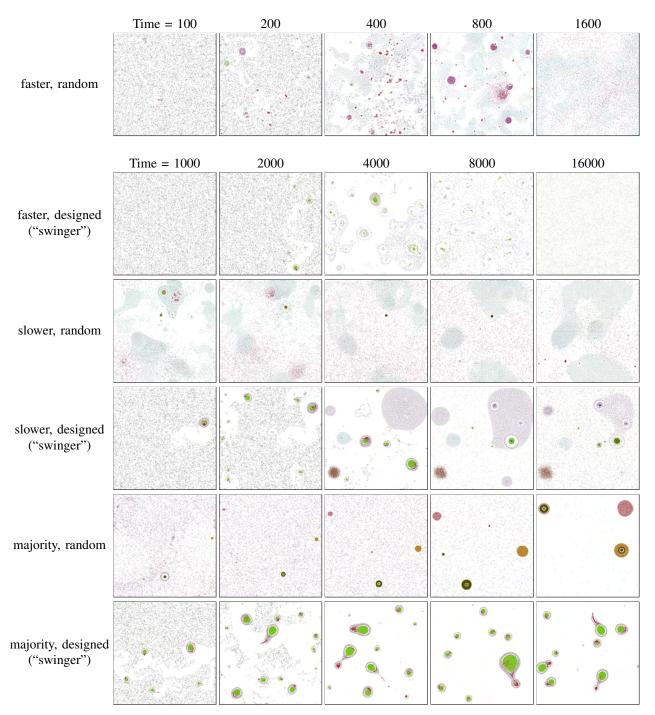


Fig. 3. Results of Exp. 1: Evolutionary processes observed in the revised Swarm Chemistry model. Each image shows a snapshot of the space in a simulation, where dots with different colors (or gray levels in print) represent particles of different types. Labels on the left indicates the competition function and the initial condition used in each case. Snapshots were taken at logarithmic time intervals.

 10^{-3} , $p_s=10^{-5}$). Random and designed ("swinger") initial conditions were used. The following four basic competition functions were implemented and tested:

- faster: The faster particle wins.
- slower: The slower particle wins.
- *behind*: The particle that hit the other one from behind wins. Specifically, if a particle exists within a 90-degree angle opposite to the other particle's velocity, the former

particle is considered a winner.

• *majority*: The particle surrounded by more of the same type wins. The local neighborhood radius used to count the number of particles of the same type was 30. The absolute counts were used for comparison.

Results are shown in Fig. 3. The results with the "behind" competition function were very similar to those with the "faster" competition function, and therefore omitted from the

figure. In general, growth and replication of macroscopic structures were observed at early stages of the simulations. The growth was accomplished by recruitment of inactive particles through collisions. Once a cluster of active particles outgrew maximal size beyond which they could not maintain a single coherent structure (typically determined by their perception range), the cluster spontaneously split into multiple smaller clusters, naturally resulting in the replication of those structures. These growth and replication dynamics were particularly visible in simulations with designed initial conditions. Once formed, the macroscopic structures began to show ecological interactions by themselves, such as chasing, predation and competition over finite resources (i.e., particles), and eventually the whole system tended to settle down in a static or dynamic state where only a small number of structures (or types of particles) were dominant. There were some evolutionary adaptations also observed (e.g., in faster & designed ("Swinger"); second row in Fig. 3) even with the low mutation rates used in this experiment.

It was also observed that the choice of competition functions had significant impacts on the system's evolutionary dynamics. Both the "faster" and "behind" competition functions always resulted in an evolutionary convergence to a homogeneous cloud of fast-moving, nearly independent particles. In contrast, the "slower" competition function tended to show very slow evolution, often leading to the emergence of crystallized patterns. The "majority" competition function turned out to be most successful in creating and maintaining dynamic behaviors of macroscopic coherent structures over a long period of time, yet it was quite limited regarding the capability of producing evolutionary changes. This was because any potentially innovative mutation appearing in a single particle would be lost in the presence of local majority already established around it.

B. Exp. 2: Testing Various Competition Functions

Based on the results of the previous experiment, the following five more competition functions were implemented and tested. The last three functions that took recipe length into account were implemented in the hope that they might promote evolution of increasingly more complex recipes and therefore more complex patterns:

- majority (probabilistic): The particle surrounded by more
 of the same type wins. This is essentially the same
 function as the original "majority", except that the winner
 is determined probabilistically using the particle counts
 as relative probabilities of winning.
- majority (relative): The particle that perceives the higher density of the same type within its own perception range wins. The density was calculated by dividing the number of particles of the same type by the total number of particles of any kind, both counted within the perception range. The range may be different and asymmetric between the two colliding particles.
- recipe length: The particle with a recipe that has more kinetic parameter sets wins.

- recipe length then majority: The particle with a recipe that has more kinetic parameter sets wins. If the recipe length is equal between the two colliding particles, the winner is selected based on the "majority" competition function.
- recipe length × majority: A numerical score is calculated for each particle by multiplying its recipe length by the number of particles of the same type within its local neighborhood (radius = 30). Then the particle with a greater score wins.

Results are summarized in Fig. 4. As clearly seen in the figure, the majority-based rules are generally good at maintaining macroscopic coherent structures, regardless of minor variations in their implementations. This indicates that interaction between particles, or "cooperation" among particles of the same type to support one another, is the key to creating and maintaining macroscopic structures. Experimental observation of a number of simulation runs gave the author an impression that the "majority (relative)" competition function would be the best in this regard, therefore this function was used in all of the following experiments. Unfortunately, none of these majority-based functions showed notable evolutionary changes because of the reason discussed in the previous subsection.

In the meantime, the "recipe length" and "recipe length then majority" competition functions did not show any evolution toward more complex forms, despite the fact that they would strongly promote evolution of longer recipes. What was occurring in these conditions was an evolutionary increase of "garbage" kinetic parameter sets in a recipe, which did not show any interesting macroscopic structure. This is qualitatively similar to the well-known observation made in Tierra [7].

C. Exp. 3: Testing Different Recipes

A few other designed recipes were also used as initial conditions in order to explore the effects of recipe contents on evolutionary dynamics. Here the three recipes shown in Fig. 2 were used. Figure 5 shows three different simulation results, each starting with a different designed recipe. Their dynamics were remarkably different. Moreover, there were a couple of other interesting observations. Firstly, the macroscopic structures emerging from a designed recipe may be quite different from the target patten intended when it was designed (shown in Fig. 2; this was especially true for the "walkerfollower" example). This was because the number of available particles and spatial dimensions were much larger in these experiments. Secondly, the time scale of the initial growth and replication of those macroscopic structures may strongly depend on the nature of the recipe. The "rotary" example showed a very rapid proliferation of cellular structures over the space, while the "walker-follower" one showed a very slow growth process. This observation assures that different recipes (=genotypes) can cause different ecological properties of the resulting macroscopic structures (=phenotypes) in the Swarm Chemistry world.

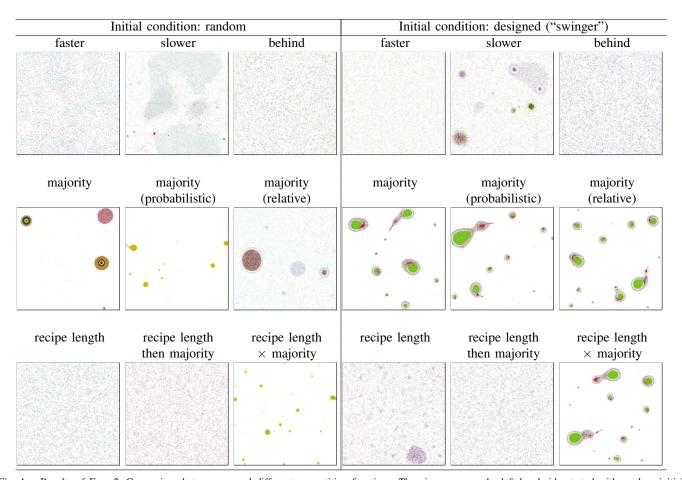


Fig. 4. Results of Exp. 2: Comparison between several different competition functions. The nine cases on the left hand side started with random initial conditions, while the other nine on the right hand side started with designed initial conditions with the "swinger" recipe. Snapshots were taken at time = 20000 for all cases.

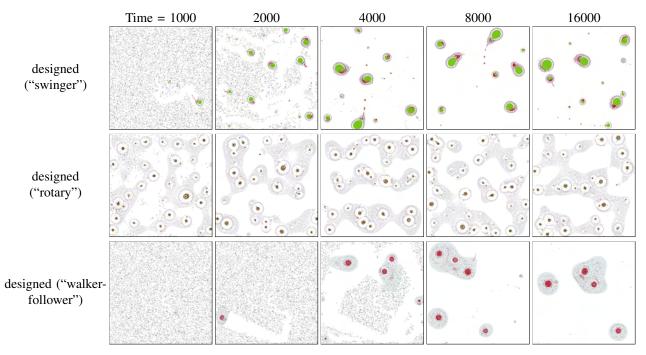


Fig. 5. Results of Exp. 3: Sample simulation runs with designed initial conditions using different recipes. All cases used the majority (relative) competition function. Snapshots were taken at logarithmic time intervals.

The experiments described above suggested the potential of Swarm Chemistry for producing more creative, continuous evolutionary processes, yet the results obtained up to this point were not quite satisfactory. Therefore two additional factors were examined in the following experiments in order to further promote continuous evolutionary changes.

D. Exp. 4: Increasing Mutation Rates

The first factor to be manipulated was the mutation rate. All of the above experiments showed the high robustness of macroscopic structures against mutations when a majority-based competition function was used. Therefore simulations were conducted with increased mutation rates that were 10 times (medium) or 100 times (high) greater than those in the original experiment. The probability of addition of a random kinetic parameter set in a single mutation event was also increased from 10% to 50% per event.

Results are shown in Fig. 6, where some major evolutionary changes emerged, e.g., in the "rotary" cases with both mutation rates and the random and "walker-follower" cases with high mutation rates. In these simulation runs, the dominant structures changed over time, which was not seen in earlier experiments (Figs. 4 and 5). The evolutionary changes halted, however, when most of the particles were absorbed in evolved dominant macroscopic structures. This may be understood in that the swarms were stagnated at a local optimum in the recipe possibility space after a relatively short period of adaptation. In the meantime, it was intriguing to see different levels of mutation tolerance among different recipes. The "swinger" recipe turned out to be tolerant to high volumes of mutations, while the "rotary" one was quite fragile.

E. Exp. 5: Introducing Exogenous Perturbations

The second factor considered was the exogenous perturbation in order to create a dynamically changing environment. Our earlier work on evolutionary cellular automata demonstrated that such dynamic environments may make evolutionary dynamics of a system more variation-driven, promoting long-term evolutionary changes [8], [9]. This experiment was to implement similar mechanisms in Swarm Chemistry. The following two exogenous perturbations were considered in the form of temporal variations of competition functions:

- perturbation I: The competition function was switched to either "faster" or "slower" temporarily for 50 time steps in every 5000 time steps. The choice of the competition function was randomly determined at the beginning of each perturbation period.
- perturbation II: The competition function was switched to either "faster" or "slower" temporarily for 50 time steps in every 2000 time steps only inside either left or right half of the space. The choices of the competition function and the spatial area to be affected were randomly determined at the beginning of each perturbation period.

With these exogenous perturbations, some simulation runs finally demonstrated continuous changes of dominant macroscopic structures over a long period of time. Figure 7 presents two examples of such processes. A fundamental difference between this and earlier experiments was that the perturbation introduced to the environment could break the "status quo" established in the swarm population, often making room for further evolutionary innovation to take place. It appeared that the perturbation II was slightly more effective in promoting evolutionary changes and maintaining diversity within the system due to the spatially heterogeneous nature of perturbations, though no statistical data is available to validate this speculation at this point. It should also be noted that such continuous evolutionary changes did not occur always; they were observed only in two out of four simulation runs conducted in this experiment so far. Nevertheless, these results were unique and promising, suggesting a possibility of creating a truly open-ended evolution in the Swarm Chemistry world through further model revisions.

IV. DISCUSSIONS AND FUTURE WORK

In this paper, a series of simulation experiments were presented to illustrate the recent progress in search for openended evolution in the computational universe of Swarm Chemistry. The key components of model revisions were the local transmission of recipe information from active to passive particles, as well as between two active particles, and the possibility of mutation and competition among different recipes. These model assumptions realized the three key ingredients of evolution—inheritance, variation and selection—all arising from local processes occurring at microscopic levels. Yet our simulation results successfully demonstrated that ecological and evolutionary dynamics of macroscopic structures can emerge in such systems.

This research is still work-in-progress, and there are a number of problems that need to be addressed. The single most crucial problem is the computational time and space needed to simulate a large-scale swarm, especially with a majority-based competition function that requires identification of local neighbors and their types. In a typical simulation run, simulating the system for one time step would take about 0.5 to 1 second on a single workstation. A drastic speed-up of simulation is of absolute necessity in order to conduct more systematic investigation of this model in the future. The application of General-Purpose Graphic Processing Units (GPGPUs) for large-scale particle simulation is currently planned. This will hopefully enable significant expansion of spatial as well as temporal scales of simulation, which may by itself have a huge impact on evolutionary dynamics of Swarm Chemistry.

The second major problem is the development of quantitative observation/analysis tools to characterize the evolutionary dynamics of Swarm Chemistry in a more systematic, objective way. In this paper, the experimental observation relied largely on visual inspection, but a more quantitative characterization would be necessary in order to confirm that the observed behavior is truly open-ended without falling into static or cyclic evolutionary attractors. Some measurement techniques are already available for this purpose [10], [11], [12], which should be directly applicable to the Swarm Chemistry world if

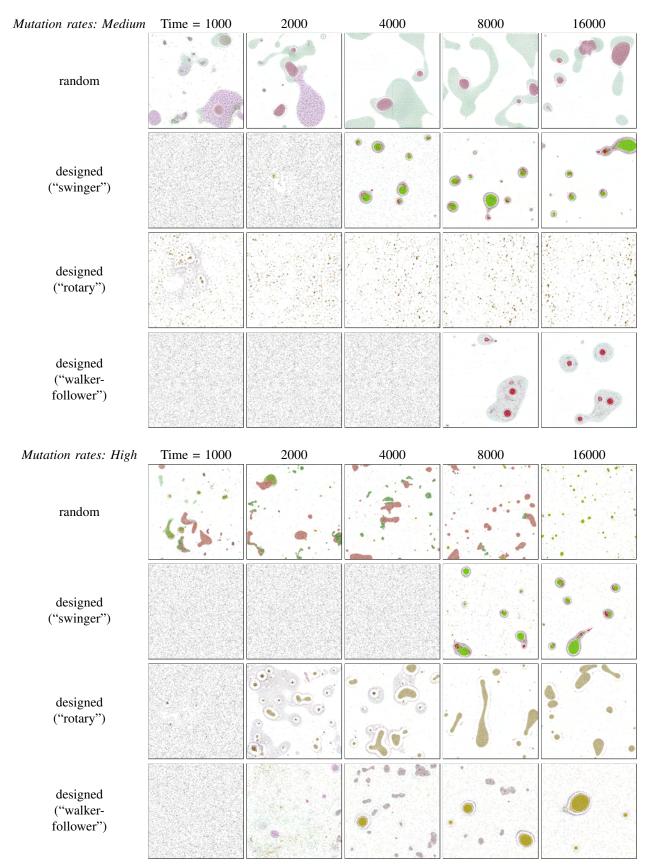
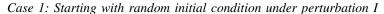
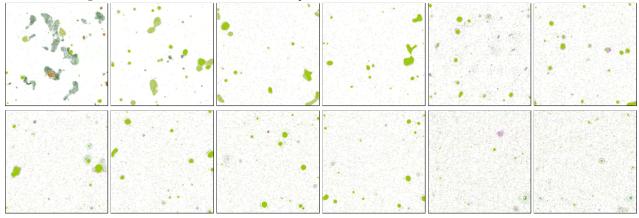


Fig. 6. Results of Exp. 4: Effects of increased mutation rates. The top four rows used medium mutation rates ($p_t = 10^{-2}$, $p_s = 10^{-4}$), while the bottom four used high mutation rates ($p_t = 10^{-1}$, $p_s = 10^{-3}$). See text for more details. All cases used the majority (relative) competition function. Snapshots were taken at logarithmic time intervals.





Case 2: Starting with designed ("swinger") initial condition under perturbation II

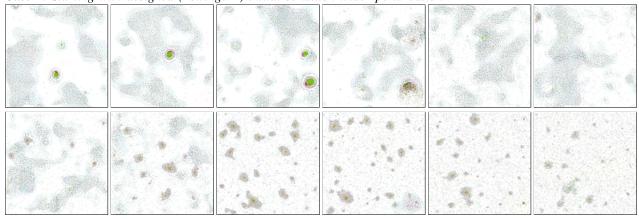


Fig. 7. Results of Exp. 5: Long-term evolutionary behaviors seen in simulation runs under dynamic environmental conditions with high mutation rates and the majority (relative) competition function. Snapshots were taken at constant time intervals (2500 steps) to show continuous evolutionary changes.

one measures the evolutionary activity at recipe (=genotype) levels within a swarm population. However, it would be more challenging to characterize the evolutionary activity at macroscopic structure (=phenotype) levels observed in Swarm Chemistry. It is expected that different approaches that utilize image processing, topological analysis, and/or information theoretic/entropic methods would be necessary for automating the observation tasks, including automatic detection and dynamic tracking of macroscopic coherent structures and their motions.

One relatively minor technical issue that should also be noted is in the collision detection algorithm in Swarm Chemistry. In its current implementation, collision detection depends on perception ranges of particles; if a perception range of a particle is close to zero, its recipe will be hardly overwritten by other recipes, and therefore, the near-zero perception range works as a genotypic attractor under the current model assumptions. This issue must have affected substantially the simulation results presented in this paper, which will be corrected in future experiments.

Some of the presented simulation results can be watched online at http://youtube.com/complexsystem.

REFERENCES

- N. H. Packard, A closing talk of Artificial Life XII, Odense, Denmark, 2010, unpublished.
- [2] H. Sayama, "Swarm chemistry," Artif. Life, 15:105-114, 2009.
- [3] H. Sayama, "Robust morphogenesis of robotic swarms," *IEEE Comput. Intel. Mag.*, 5(3):43-49, 2010.
- [4] H. Sayama, "Swarm chemistry evolving," Artificial Life XII, 2010, MIT Press, pp.32-33.
- [5] C. W. Reynolds, "Flocks, herds, and schools: A distributed behavioral model," *Comput. Graph.* 21(4):25-34, 1987.
- [6] H. Sayama, S. Dionne, C. Laramee and D. S. Wilson, "Enhancing the architecture of interactive evolutionary design for exploring heterogeneous particle swarm dynamics: An in-class experiment," *Proc. 2nd IEEE ALIFE*, 2009, IEEE, pp.85-91.
- [7] T. S. Ray, "An Approach to the Synthesis of Life," *Artificial Life II*, 1992, Addison-Wesley, pp.371-408.
- [8] C. Salzberg, A. Antony and H. Sayama, "Evolutionary dynamics of cellular automata-based self-replicators in hostile environments," *BioSystems* 78:119-134, 2004.
- [9] C. Salzberg and H. Sayama, "Complex genetic evolution of artificial self-replicators in cellular automata," *Complexity* 10(2):33-39, 2004.
- [10] M. A. Bedau and N. H. Packard, "Measurement of evolutionary activity, teleology, and life," *Artificial Life II*, 1992, Addison-Wesley, pp.431-461.
- [11] M. A. Bedau and C. T. Brown, "Visualizing evolutionary activity of genotypes," *Artif. Life*, 5:17-35, 1999.
- [12] C. L. Nehaniv, "Measuring evolvability as the rate of complexity increase," Artif. Life VII Workshop Proceedings, C. C. Maley and E. Boudreau, eds., 2000, pp.55-57.