

Non-Spatial Hash Chemistry

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There is an increasing level of interest in open-endedness in the recent literature of Artificial Life and Artificial Intelligence (Lehman and Stanley, 2008; Sayama, 2011; Taylor et al., 2016; Banzhaf et al., 2016; Taylor, 2018; Sayama, 2018; Stanley, 2019; Packard et al., 2019; Stepney, 2021; Borg et al., 2023; Stepney and Hickinbotham, 2023). As a promising mechanism to facilitate open-endedness in artificial evolutionary systems, we previously argued the importance of a “cardinality leap” of possibility spaces and demonstrated its effectiveness using Hash Chemistry, a simple artificial chemistry model that used a hash function as a universal fitness evaluator Sayama (2019). In Hash Chemistry, individual particles of various elements distribute in a two-dimensional finite space, and a group of spatially proximate particles are randomly selected and their replication/survival/death is determined based on the hash value of the group of those particles altogether. This extremely simple model exhibited a spontaneous increase of the complexity (size) of replicating higher-order entities and the number of novel higher-order entity types. However, the spatial nature of the original Hash Chemistry model came with extensive computational costs involved in its simulation (Sayama, 2019). Moreover, the particle density limit imposed to prevent explosion of computational costs prevented unbounded growth in complexity of higher-order entities.

To address these limitations, here we propose a simpler non-spatial variant of Hash Chemistry in which spatial proximity of particles is represented explicitly in the form of multisets (Sayama, 2024). More specifically, we treated multisets of individual entity types as the basic unit of replication (analogous to molecules) and defined the entire evolutionary system simply as a well-mixed population of such multisets, without any explicit spatial coordinates involved. The evolution of replicating entities is simulated via repeated pairwise competitions between two randomly chosen multisets followed by mutations (Fig. 1, top). This modification eliminated the need for neighbor detection in space and thus sped up numerical simulation substantially. Systematic numerical experiments showed that the non-spatial model achieved a 2.25 times speed-up compared to the original

model (Sayama, 2019). More details of the proposed non-spatial Hash Chemistry model and the numerical experiments can be found in (Sayama, 2024).

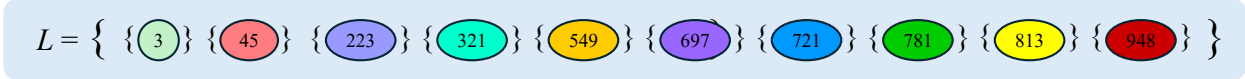
Results of numerical simulations showed much more significant unbounded growth in the sizes of replicating higher-order entities than the original model. Such size increase was caused by occasional mutations that duplicated the content of multisets. Figure 1 (bottom) shows the maximum (left) and average (right) numbers of individual entities involved in each replication event. It was clearly observed that the dominant multisets became larger over time in both measurements, demonstrating the evolutionary appearance of higher-order structures that was also confirmed in the original Hash Chemistry model (Sayama, 2019). The fact that this key behavior, *ongoing growth of complexity* (Taylor et al., 2016), is also obtained in our non-spatial model means that spatial extension is not an essential factor needed to induce cardinality leap and open-ended complexity increase in an evolutionary system.

To quantitatively evaluate the trend of the complexity increase, two different mathematical models of growth curves, bounded and unbounded ones, were fitted to the average behaviors during the time period 100–2,000 in logarithmic time scales, following the same analysis as in (Sayama, 2019). In both the maximum number (Fig. 1, bottom left) and the average number (Fig. 1, bottom right) of individual entities, the unbounded growth model was a significantly better fit to the data (details of the statistical analysis can be found in (Sayama, 2024)). This result is different from what was reported for the original model (Sayama, 2019) in which only the average number was inferred to be unbounded. Our result indicates that the removal of spatial extension and local density limit has made unbounded growth of higher-order entity size more natural and more manifested in the simulations.

These results demonstrate the effectiveness of the proposed non-spatial Hash Chemistry model as a minimalistic example of open-ended evolutionary systems. It also serves as concrete evidence that spatial extension is not a necessary ingredient for open-endedness in evolutionary systems.

Possibility set of individual entities: $S = \{ \textcircled{1} \textcircled{2} \textcircled{3} \textcircled{4} \textcircled{5} \dots \textcircled{10} \dots \textcircled{100} \dots \textcircled{1000} \}$

Initial configuration:



Simulation procedure in each time step (this was iterated for 2,000 times in this study):

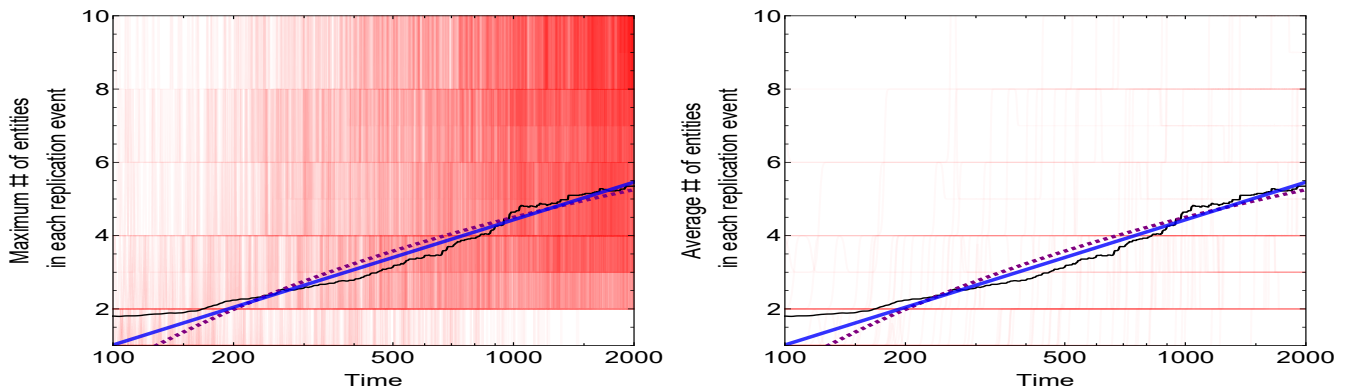
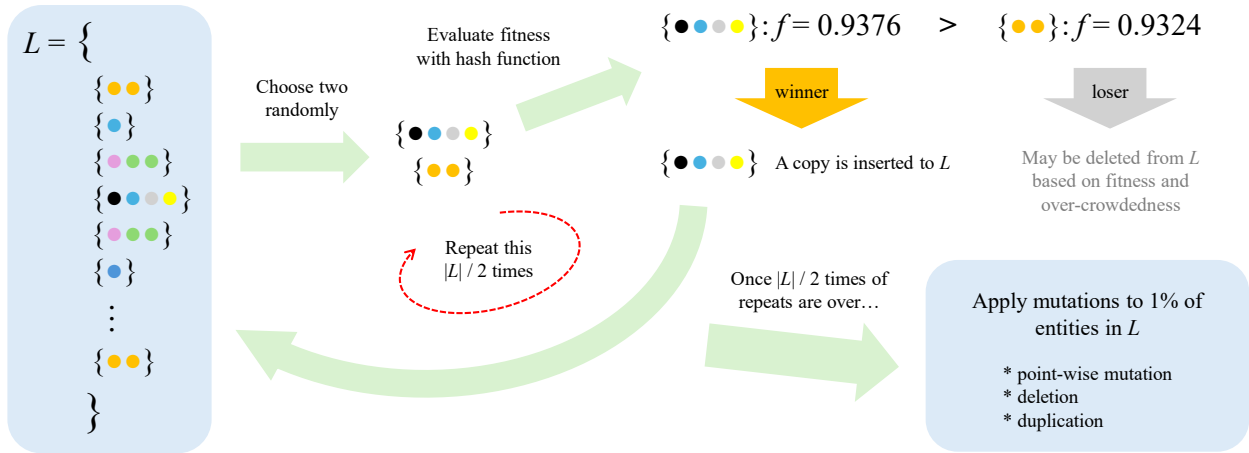


Figure 1: Top: Schematic illustration of the outline of the proposed non-spatial Hash Chemistry model. Bottom: Maximum (left) and average (right) numbers of individual entities in replicating multisets. The red curves show results of 100 independent simulation runs, while the black solid curve shows their average. Purple (dashed) and blue (solid) curves are two different growth models (purple: bounded growth, blue: unbounded growth) fitted to the average behaviors. In both plots, the unbounded growth model (blue curve) was a significantly better fit, presenting a better demonstration of open-endedness than in (Sayama, 2019).

Meanwhile, it was also observed in this study that the diversities of replicating entities (either individual or higher-order ones) were substantially lower in the non-spatial model than in the original one (Sayama, 2024). This indicates that, while not essential for open-endedness, spatial extension still has strong positive effects on diversification of evolving entities.

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