Comment

Inspiration of the biological behavior of Physarum polycephalum on mathematical modeling
Comment on "Does being multi-headed make you better at solving problems? A survey of Physarum-based models and computations" by C. Gao et al.

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In recent years, biological behaviors such as foraging and adapting to dynamic environments have been very instructive for mathematical modeling. Gao et al. have studied the physiological mechanism behind the quasi-intelligent behavior of the Physarum polycephalum and its application to solve complex computational problems [1]. They summary the Physarum-based models from three aspects: morphology, taxis and positive feedback dynamics.

Physarum polycephalum is a multinucleated, a single-celled organism that grows in a dark, humid environment and feeds on bacteria and microorganisms, which has powerful computing and mobility capabilities to form complex network systems. Additionally, it could lead to improved technical systems, such as more powerful computers and mobile communications networks. What is more, it also has a powerful ability to solve mazes. As a result, physarum is an attractive modeling target. They study from two different perspectives: modeling and computing. In the process of research modeling, they focus on the foraging behavior of physarum, so that its core characteristics and potential mechanisms can be better captured. Its properties and physiological mechanisms can be used to solve complex computing problems such as travel salesman problems (TSPs) and community detection [2]. Due to advances in technology, sensing technology is becoming more and more common and data streams can be recorded in real time. Consequently, it is necessary to comprehensively review the studies on physarum from the perspective of modeling and calculation.

There are a cellular automata model based on morphology [3]. It replicates Physarum polycephalum morphological behavior. When there is a food source, physarum polycephalum moves its body mass to the food source through the

protuberance of the protoplasm, retracts it from elsewhere, and maintains connectivity. In the CELL model, cells at the food source location are defined as "active regions", and the initial organism is defined as "internal cells", and the active cells that simulate its dynamical behavior are generated in its potential routes. Active cells are randomly generated in the outer cells of the active region. The active cell then moves randomly to an internal cell until all the internal cells around the cell are accessed. Finally, the active cell will be replaced with the state of the final cell. The process of cell formation, movement, and replacement are repeated until a pathway to an active region emerges. The final pathway is composed entirely of internal cells, similar to the network produced by physarum polycephalum during foraging.

Relevant models can be used to design effective transport networks, such as VP-S model [4]. The VP-S model is similar to biological networks and more economical in calculation. The similarity rate between the VP-S design model and the real network is 75%, and it has been proved that the network generated by this model is more efficient, shorter in total length and more stable than the real transport networks. It suggests the strong ability of using biological behavior to design networks.

In addition, because of the ability of the Physarum to detect the nutrient concentration of food, researchers use this to analyze biological behavior from different perspectives [5]. In the top-down models, the oregonator-based model reveals how the model inhibits diffusion in the negative gradient direction of the chemical attractant. The gradient-based model use Physarum's plasmodium grows in the direction of the nearest food source to result spanning tree. In the down-top models, they proposed the form of multi-agent systems and cellular automata. MAS demonstrates the evolution of its behavior over time by using microscopic platforms to simulate the behavior of physarum polycephalum, which has been successfully applied to planning path. Amoeba-like cellular automaton model uses local effects to simulate the strategic behavior of expansion.

Computational applications of the taxis of protoplasmic extension include network planning, route planning (maze solving and optimal route selection), and graph mining. Using the ALCA model to design efficient transport networks, major cities and transportation hubs are regarded as food sources, and different population sizes represent different food concentrations. Most high-probability connections are generated by this model, which nicely illustrate the application of biological behavior. In addition to path planning and network planning, they also used convergence of protoplasm extension to design the graph mining algorithm.

Finally, current reinforcement (CR) models is a dynamical model with positive feedback. It can search for the shortest path in a maze. In the maze, the CR model randomly initializes the pipe conductivity to find the shortest path [6]. Then, the tubes with zero electrical conductivity gradually disappeared from the maze. If there are two or more paths to solve the maze, the longer paths will eventually disappear and the model will eventually converge to the shortest path. Researchers extends the CR model from maze solving to network. The generated network is similar to the protoplasmic network of Physarum polycephalum, showing good efficiency and fault tolerance. Furthermore, it has been successfully applied in the reconstruction project of Tokyo rail transit system.

Computational applications of the CR model are network and route planning, efficient networks in expanding domains, hybrid optimization algorithms with the current reinforcement model and community detection. Network planning based on the CR model has been successfully applied in the construction of efficient fault tolerant network, such as traffic network, Bayesian network, and so on. The path selection model can solve some optimization problems. More interestingly, the results show that the improved algorithm has faster convergence rate, higher stability and stronger searching ability than the original algorithm. In other words, CR model can improve the level of community detection.

Gao et al. have summarized many modeling methods that can simulate the behavior of physarum [1]. However, other aspects of the organism's decision are not well mentioned. In particular, how and where individual environmental information is produced remains unknown. If we can identify the mechanisms by which biological information is stored, we can find the most primitive forms of biological information storage and understand how organisms learn and store information based on reaction-diffusion equations [7–11]. It should be worth noting that if network structures are included [12,13], more information can be obtained. In this sense, the investigations of biological behavior are still research hotspots in the coming years.

Acknowledgements

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