Inverse Bayesian Feedback Model of True Slime Mold

Iori Tani[1]

[1]Information Science and Technology Center, Kobe University, Kobe, Hyogo, Japan
iori_tani@penguin.kobe-u.ac.jp

Abstract

We propose asynchronous cellular automata fashioned model of true slime mold *Physarum polycephalum* plasmodium equipped with a dynamic feedback mechanism based on Bayesian and inverse Bayesian inference. These are implemented as feedback from dynamical protoplasmic flow into local tubular structures in slime mold. Because inverse Bayesian inference replaces conditional probabilities with empirical ones and relaxes the probability space, the model can behave robustly and adaptively. We describe a brief overview of our model in this paper.

Introduction

Modeling the behavior of natural organisms with simple mechanisms is essential in biology and the study of artificial life, especially in species with some intelligence. We propose asynchronous cellular automata fashioned model of true slime mold *Physarum polycephalum* plasmodium. *Physarum polycephalum* is one of the most widely studied species of true slime mold and is known to have a kind of information processing capability without any nervous system. For example, solving a maze with the shortest path (Nakagaki et al., 2000) and reproducing efficient inter-cities transport networks (Adamatzky and Jones, 2009) are well-known.

Plasmodium, a stage of the life cycle of slime molds, is a large amoeboid organism that crawls and explores to search for food sources. This unicellular, multinuclear amoeba shows high cell motility and forms a complex protoplasmic network consisting of fan-shaped, multi-headed front lines and subsequent tubular structures.

Since *Physarum* lacks a higher nervous system, it is considered that locally collected information is propagated by protoplasmic flow and integrated to make some decisions. In such information processing, feedback from actual cell movement has a significant role to self-organize cell shape and enhance motility. Implementing such a feedback mechanism as a model based only on local information and interaction is required. Our suggested model uses Bayesian and Inverse Bayesian inferences, defined as the inverse operation of Bayesian inference (Arecchi, 2003, 2011; Gunji et al., 2017), as a feedback mechanism and implements actual *Physarum*-like behavior by rewriting probability distributions spontaneously and adaptively.

Many types of the models of *Physarum* have already been proposed. Our model is a successor of the asynchronous cellular automata fashioned model (Gunji et al., 2008, 2011), and we extended the original model naturally. The asynchronous automata model has the advantage that amoeboid cell motility and protoplasmic network formation can be simulated with the same model (Tani et al., 2014).

An overview of the model is provided in the next section.

Overview of the Model

Our model is defined on a discrete lattice plane, and a point on the plane is represented by a pair of integers (i, j). A non-negative integer value $S(i, j)$ is defined for each point, representing the plasmodium's thickness. $S(i, j) = 0$ means the point is outside of the plasmodium, and $S(i, j) \geq 1$ means the protoplasm covers the point. If the points occupied by the plasmodium are adjacent to the Neumman neighborhood, these points belong to the same plasmodium.

The cell motility of the model is realized by alternately applying two types of asynchronous automaton rules: diffusion and flow. In the diffusion rule, the protoplasm diffuses to its neighborhood at the points where the thickness of the plasmodium exceeds a particular threshold. On the other hand, the flow rule changes the local thickness of the plasmodium through the protoplasmic flow. Therefore, the flow rule is applied multiple times after applying the diffusion rule one time.

In the diffusion rule, we scan the cell thickness at all intracellular points and check that it exceeds the threshold Th_{df}. If a point has a greater thickness than the Th_{df} and there are thinner points in the Neumann neighborhood, then the protoplasm moves from the center to the periphery with probability P_{df}. Although the thickness check is performed synchronously, the rule is asynchronous because individual diffusion occurs stochastically.

As in the original model, protoplasmic flow is described as the entry, movement, and arrest of the vacant particle (VP)

into the cell. VP moves inside the plasmodium by locally exchanging the position with neighbor protoplasm, resulting in a protoplasmic flow. Therefore, We represent the tendency of VP movement as a tuple of probability distributions and implement a dynamic feedback mechanism to them.

The latent tendency of the protoplasmic flow for each point is described as conditional probability $P_{(i,j)}(d|h)$. d means each direction in the Neumann neighborhood for each point. $k = 1 \cdots N_h$ is an index of latent tendency equivalent to the hypothesis in Bayesian inference, where N_h is the measure of local structural complexity allowed in the model. Whether each latent tendency is dominant or not is represented by another probability distribution $P_{(i,j)}(h)$. We set $P_{(i,j)}(d|h_k) = 0.25$ and $P_{(i,j)}(h_k) = 1/N_h$ for each d, k and (i, j) on the plane in the initial conditions.

A single application of the flow rule is divided into several subprocesses. First of all, scan all points on the plane and pick up the point such that $S(i, j) \geq 1$ and adjacent to the outside of the cell in the Neumann neighborhood, and randomly choose one of them. We set the probability weighting so that points adjacent to the unexplored area are selected more frequently.

Let (i, j) coordinate the selected point, and (i', j') means a Neumann neighborhood of (i, j). VP enters into the plasmodium, and plasmodial thickness increases at this point by 1. Protoplasm used to increase thickness is supplied from the neighborhood because we require the total amount of plasmodium to be unchangeable. We now introduce a value H_{VP} that indicates the vertical position of the VP. When VP enters the cell, H_{VP} is set to 1. Then, randomly select one of the neighboring points of VP such that $S(i', j') \geq H_{VP}$ using the conditional probability mentioned above. First, randomly choose a hypothesis based on $P_{(i,j)}(h)$. Next, the direction VP will move is determined based on the selected hypothesis h_k's conditional probability $P(d|h_k)$. However, because the directions in which VP can move have restriction $S(i', j') \geq H_{VP}$, the weight of the random selection is normalized for the movable directions.

When the VP moves, update the probability $P_{(i,j)}(h)$ by $P_{(i,j)}(d|h)P_{(i,j)}(h)$. This feedback is based on Bayesian inference. At the same time, count the direction of VP movement at each point VP passed through. After VP move from (i, j) to (i', j'), update H_{VP} with $S(i', j')$. Therefore, VP moves only toward the area of greater thickness.

In addition, there is a constraint on VP movement derived from the original model. VP cannot pass through the point that it has passed through again in the same flow rule application. This restriction means that protoplasmic flow cannot flow backward, allowing the plasmodium to continue its cell motion without splitting. The VP repeats the moves based on the above rules, but due to the constraints for movable directions, it eventually loses its movable neighborhood and stops. At this point, VP is ejected out of the cell, and thickness at the point is reduced by 1. We regard these sequential processes as a protoplasmic flow in which the protoplasm moves from the stop point to the entry point of VP.

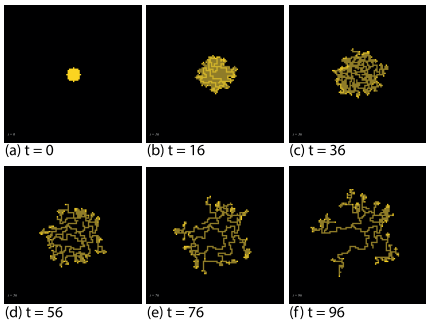

Figure 1: The time evolution of our model. t means the number of diffusion rule applications. The areas covered with protoplasm are colored yellow, while those with thicker protoplasm are colored brighter.

Next, we describe the essential mechanism in our model, namely the dynamical rewriting of conditional probability using inverse Bayesian inference. Our model applies the flow rule several times after applying the diffusion rule once. Furthermore, before the next diffusion rule application, apply the inverse Bayesian process for all points of the plasmodium. Let a point (i, j) be a part of plasmodium.Then, randomly select a hypothesis h_k to be rewritten based on weighting $1 - P_{(i,j)}(h)$. The conditional probabilities $P_{(i,j)}(d|h_k)$ for the selected hypotheses h_k are replaced by empirical probabilities $P_{(i,j)}(d)$ based on the actual movement of VPs counted when the flow rule is applied. This process is feedback from actual protoplasmic flow to latent flow tendency and has long time scale than Bayesian inference feedback. Note that $P_{(i,j)}(d|h)$ and $P_{(i,j)}(h)$ are set to uniform under the initial condition, so if there is no inverse Bayesian feedback, weights for selections do not change and do not affect random selection.

Behavior of the Model

The behavior of the model with each parameter set as $N_h = 10$, $P_{df} = .90$, and $Th_{df} = 5$ is shown in Figure 1. For each application of the diffusion rule, the flow rule was applied 200 times.

The plasmodium was initially placed thick at the center of the field and spread in a homogeneous circular pattern, gradually forming a dendritic heterogeneous network structure. This observation is consistent with the time evolution of the actual exploratory behavior of slime mold foraging on an agar plane without any attractant or repellent.

By implementing these two feedback mechanisms with different time scales, the protoplasmic flow's latent tendency self-organizes, reproducing real *Physarum*-like cell motility and diverse protoplasmic networks.

References

Adamatzky, A. I. and Jones, J. D. (2009). Road planning with slime mould: if physarum built motorways it would route m6/m74 through newcastle. *Int. J. Bifurc. Chaos*, 20:3065–3084.

Arecchi, F. T. (2003). Chaotic neuron dynamics, synchronization, and feature binding: Quantum aspects. *Mind and Matter*, 1(1):15–43.

Arecchi, F. T. (2011). Phenomenology of consciousness: From apprehension to judgment. *Nonlinear Dynamics, Psychology, and Life Sciences*, 15(3):359–375.

Gunji, Y.-P., Shinohara, S., Haruna, T., and Basios, V. (2017). Inverse bayesian inference as a key of consciousness featuring a macroscopic quantum logical structure. *Biosystems*, 152:44–65.

Gunji, Y.-P., Shirakawa, T., Niizato, T., and Haruna, T. (2008). Minimal model of a cell connecting amoebic motion and adaptive transport networks. *Journal of Theoretical Biology*, 253(4):659–667.

Gunji, Y.-P., Shirakawa, T., Niizato, T., Yamachiyo, M., and Tani, I. (2011). An adaptive and robust biological network based on the vacant-particle transportation model. *Journal of Theoretical Biology*, 272(1):187–200.

Nakagaki, T., Yamada, H., and Tóth, Á. (2000). Maze-solving by an amoeboid organism. *Nature*, 407(6803):470–470.

Tani, I., Yamachiyo, M., Shirakawa, T., and Gunji, Y.-P. (2014). Kanizsa illusory contours appearing in the plasmodium pattern of physarum polycephalum. *Front Cell Infect Microbiol*, 4:10.