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A lifecycle model for simulating bacterial evolution

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A R T I C L E I N F O

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A B S T R A C T

This paper presents a lifecycle model (LCM) to simulate bacterial evolution from a finite population of *Escherichia coli* (*E. coli*) bacteria. The potential of this approach is in relating the microscopic behaviors of single bacterial cell to the macroscopic effects of bacterial colonies. This can be accomplished via use of an individual-based modeling method under the framework of agent–environment–rule (AER). Here, our study focuses on investigating the behaviors at different developmental stages in *E. coli* lifecycle and developing a new biologically inspired methodology for static or dynamic systems. The experimental results through a varying environment demonstrates that our model can be used to study under which circumstances a certain bacterial behaviors emerges, and also give an inspiration to design a new biological optimization algorithm being used for optimization problems.

1. Introduction

Escherichia coli, or *E. coli* is probably the best-understood microorganism, and well studied in various aspects of microbiology science [16,4,5,15]. Its entire genome has been sequenced into 4639221 A, C, G, and T "letters"—adenosine, cytosine, guanine, and thymine [14]. Understanding of these single-cell organisms is an essential step towards understanding more complex organisms.

In biology, the term lifecycle refers to the various phases an individual passes through from birth to maturity and reproduction. This process often leads to drastic transformations of the individuals with stage-specific adaptations to a particular environment. The lifecycle of *E. coli* has three major stages: a free swimming stage spent searching for prey in water of soil, a growth stage spent inside the periplasm of the prey bacterium, and a lysis stage spent when getting insufficient nutrition form environment [13].

The fundamental unit of bacterial life, encapsulating action and information interaction as well as variability, is the cell. Therefore, it seems appropriate to construct ecological models in terms of individual cells and their behaviors. The existing extensive literature on modeling cells and their behaviors is almost based on classical mathematical approaches [9,12]. Those approaches always restricted the minds of modelers. This paper presents a bio-inspired computational model, which simulates a population of individual *E. coli* bacteria during their whole lifecycle.

There are many bio-inspired computational models, such as genetic algorithm (GA) [10], particle swarm optimization (PSO) [8,11] and ant system (AS) [6]. GA is a model to mimic the behaviors of evolution process in natural system specifically those that follow Darwin's principle of survival of the fittest. PSO is a collaborative population-based stochastic optimization model, which is inspired by the social behaviors of organisms, such as bird flocks and fish schools. AS algorithm is inspired by the behaviors of real ants finding the shortest path between their nest and a food source.

In the above models, they are all established based on population-based modeling approach. In a population-based model, the individuals follow the same rules and take the same actions simultaneously (all individuals are identical). In addition, the behaviors of a certain individual cannot be controlled and tracked.

Unlike the population-based method, our proposed model—lifecycle model (LCM) is developed using an individual-based modeling (IBM) approach. Compared with the population-based modeling approach, IBM possesses a more flexible and robust capability for simulating bacterial system, where there are a large number of individuals (cells) which have their own behavior dynamics influenced by the other individuals and the environment. In LCM, each individual corresponds to an autonomous artificial bacterium in the simulated domain. They possess different properties and the behaviors of each individual can be controlled and tracked.

The primary objective of the study is to investigate the behaviors at different developmental stages in their lifecycle. The secondary objective is to construction of a biologically inspired artificial ecology being of interest in itself.

The experimental results through a varying environment demonstrates that our model can be used to study under which circumstances a certain bacterial behavior emerge, and also give

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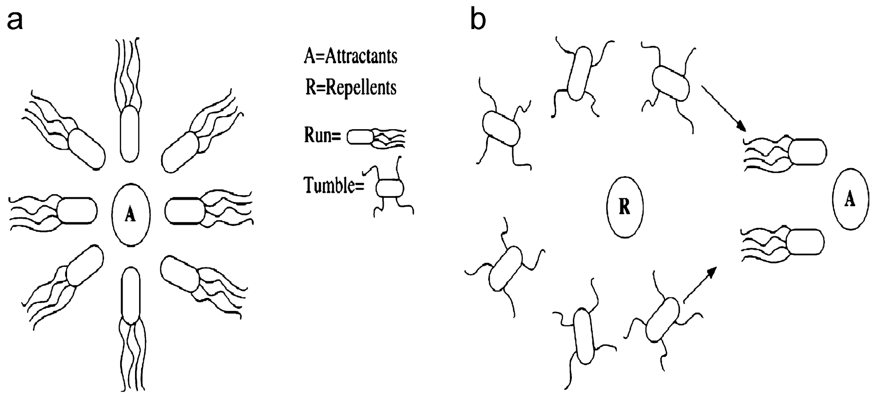

Fig. 1. Bacterial chemotaxis: (a) bacteria attracted to attractants and (b) bacteria repelled by repellents.

an inspiration to design a new biological optimization algorithm being used for optimization problems.

The rest of paper is organized as follows: some typical bacterial behaviors during their whole lifecycle are provided in Section 2. A framework of LCM and the mathematical model of bacterial behaviors are described in Section 3. Experimental settings and experimental results are given in Section 4. Finally, Section 5 concludes the paper.

2. Bacterial behaviors during their whole lifecycle

2.1. Chemotaxis

A fascinating property of *E. coli* is their chemotactic behaviors. Chemotaxis (or more accurately, chemokinesis), the process by which a cell alters its speed or frequency of turning in response to an extracellular chemical signal, has been most thoroughly studied in the peritrichous bacterium *E. coli* [1,3]. The response to a chemical stimulus in their vicinity helps bacteria find sources of nutrients which are essential for their survival. Bacterial cells will migrate towards environment conditions it deems attractive (we call this chemo-attractants) and or away from surroundings it finds repellent (we call this chemo-repellents) by sensing chemical concentration using their receptors.

Flagellated bacteria *E. coli* produce motion by the movement of their flagellum. A counter-clockwise flagellar rotation results in a smooth swim motion in a straight line in a particular direction (we call this a run), while a clockwise rotation of the flagellum causes the bacterium to randomly reorient itself in a new direction (we call this a tumble). Motion alternates between these two modes of operation in its entire lifetime. The phenomenon of bacterial chemotaxis is illustrated in Fig. 1.

2.2. Reproduction, extinction and migration

E. coli grows by taking nutrients directly from the environment through its cell wall. Within the cell wall, the bacteria's cell contents are very simple: from one to four identical molecules of DNA and 15,000–30,000 ribosomes [14].

After taking up sufficient nutrients, it converts them into energy which allows it to make copies of its DNA. *E. coli* reproduction is almost always by simple division, i.e., when it *E. coli* grows, it gets longer, then divides in the middle into two identical *E. coli* cells. Under favorable conditions, this can occur once every 30 min, growing exponentially [7].

Meanwhile the bacteria living under a dislike environment for a long time or with poor foraging ability will be eliminated from environments, i.e., extinction occurs.

Migration is also usual phenomena in bacterial colonies. It may be that water or some animals will move populations of bacteria from one place to another in the environment.

3. Lifecycle model of *E. coli* bacteria

LCM consists of a number of fundamental elements, which work together to construct an artificial biological ecology system. The framework of this model is based on an agent–environment–rule (AER) schema, i.e., there are three fundamental elements: agent, environment, and rules. The detailed description of it is listed below

- *A*: artificial bacteria
- *E*: artificial environment
- *R*: the environment/organism interaction mechanisms.

$LCM = \langle A, E, R \rangle$ where $A = \{A_1, A_2, \ldots, A_N\}$ comprise N artificial bacteria. The artificial environment E is presented by an n-dimensional grid with distributed nutrient, in which the artificial bacteria are left to survive, interact, multiply, and evolve. R defines the interaction rules between bacteria–bacteria or environment and organism. The whole architecture is shown in Fig. 2. In following subsection gives the detailed description of each fundamental element.

LCM model is different from the original population-based model in which all the individuals[1] share the same state properties. LCM is a philosophy that embraces the uniqueness of the individuals in a system with multiple individuals that have its own properties (state variables and parameters). The overwhelming advantage of this approach is that bacterial evolution becomes open-ended. LCM brings together the macro- and the micro-scale. Thus, during the simulation, a bacterium can be monitored so that its movements, interaction with other bacterium are known. The reasons for the behaviors of that bacterium can then be determined.

3.1. Environmental complexity

Artificial environmental design is a key element in our model which is used to specify a series of artificial bacteria environment of graduated complexity. To accomplish this, the environment should be covered by some finite nutrients (food). The interaction between bacteria happens via the food source. Since all bacteria eat from the same food source, macroscopic behaviors might arise.

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[1] Hereafter individual also means a single bacterium.