

Chapter 13

Bacterial Foraging Optimization

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ABSTRACT

The bacterial foraging optimization (BFO) algorithm mimics how bacteria forage over a landscape of nutrients to perform parallel nongradient optimization. In this article, the author provides a tutorial on BFO, including an overview of the biology of bacterial foraging and the pseudo-code that models this process. The algorithms features are briefly compared to those in genetic algorithms, other bio-inspired methods, and nongradient optimization. The applications and future directions of BFO are also presented.

1. INTRODUCTION: BACTERIAL FORAGING: E. COLI

The *E. coli* bacterium has a plasma membrane, cell wall, and capsule that contain, for instance, the cytoplasm and nucleoid. The pili (singular, pilus) are used for a type of gene transfer to other *E. coli* bacteria, and flagella (singular, flagellum) are used for locomotion. The cell is about $1\mu\text{m}$ in diameter, and $2\mu\text{m}$ in length. The *E. coli* cell only weighs about 1 picogram, and is composed of about 70% water. *Salmonella typhimurium* is a similar type of bacterium.

The *E. coli* bacterium is probably the best understood microorganism. Its entire genome has been sequenced; it contains 4,639,221 of the A, C, G, and T “letters”—adenosine, cytosine, guanine, and thymine—arranged into a total of 4,288 genes. When *E. coli* grows, it gets longer, then divides in the middle into two “daughters.” Given sufficient food and held at the temperature of the human gut (one place where they live) of 37 deg. C, *E. coli* can synthesize and replicate everything it needs to make a copy of itself in about 20 min.; hence, growth of a population of bacteria is exponential with a relatively short “time to double” the population size. For instance,

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following (Berg, 2000), if at noon today you start with one cell and sufficient food, by noon tomorrow there will be $2^{72} = 4.7 \times 10^{21}$ cells, which is enough to pack a cube 17 meters on one side. (It should be clear that with enough food, at this reproduction rate, they could quickly cover the entire earth with a knee-deep layer!)

The *E. coli* bacterium has a control system that enables it to search for food and try to avoid noxious substances (the resulting motions are called “taxes”). For instance, it swims away from alkaline and acidic environments, and towards more neutral ones. To explain the motile behavior of *E. coli* bacteria, we will explain its actuator (the flagella), “decision-making,” sensors, and closed-loop behavior (i.e., how it moves in various environments—its “motile behavior”). You will see that *E. coli* perform a type of “saltatory search.”

1.1 Swimming and Tumbling via Flagella

Locomotion is achieved via a set of relatively rigid flagella that enable it to “swim” via each of them rotating in the same direction at about 100–200 revolutions per second (in control systems terms, we think of the flagella as providing for actuation). Each flagellum is a left-handed helix configured so that as the base of the flagellum (i.e., where it is connected to the cell) rotates counterclockwise, as viewed from the free end of the flagellum looking towards the cell, it produces a force against the bacterium so it pushes the cell. You may think of each flagellum as a type of propeller. If a flagellum rotates clockwise, then it will pull at the cell. From an engineering perspective, the rotating shaft at the base of the flagellum is quite an interesting contraption that seems to use what biologists call a “universal joint” (so the rigid flagellum can “point” in different directions, relative to the cell). In addition, the mechanism that creates the rotational forces to spin the flagellum in either direction is described

by biologists as being a biological “motor” (a relatively rare contraption in biology even though several types of bacteria use it). The motor is quite efficient in that it rotates a complete revolution using only about 1000 protons and thereby *E. coli* spends less than 1% of its energy budget for motility.

An *E. coli* bacterium can move in two different ways: it can “run” (swim for a period of time) or it can “tumble,” and it alternates between these two modes of operation its entire lifetime (i.e., it is rare that the flagella will stop rotating). First, we explain each of these two modes of operation. Following that, we will explain how it decides how long to swim before it tumbles.

If the flagella rotate clockwise, each flagellum pulls on the cell and the net effect is that each flagellum operates relatively independent of the others and so the bacterium “tumbles” about (i.e., the bacterium does not have a set direction of movement and there is little displacement). To tumble after a run, the cell slows down or stops first; since bacteria are so small they experience almost no inertia, only viscosity, so that when a bacterium stops swimming, it stops within the diameter of a proton. Call the time interval during which a tumble occurs a “tumble interval.” Under certain experimental conditions (an isotropic, homogeneous medium—one with no nutrient or noxious substance gradients) for a “wild type” cell (one found in nature), the mean tumble interval is about 0.14 ± 0.19 sec. (mean \pm standard deviation, and it is exponentially distributed) (Berg, 1972, 2000). After a tumble, the cell will generally be pointed in a random direction, but there is a slight bias toward being placed in a direction it was traveling before the tumble.

If the flagella move counterclockwise, their effects accumulate by forming a “bundle” (it is thought that the bundle is formed due to the viscous drag of the medium) and hence, they essentially make a “composite propeller” and push the bacterium so that it runs (swims) in one direction. On a run, bacteria swim at a rate of about

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