

Learning from Bacteria about Natural Information Processing

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Under natural growth conditions, bacteria live in complex hierarchical communities. To conduct complex cooperative behaviors, bacteria utilize sophisticated communication to the extent that their chemical language includes semantic and even pragmatic aspects. I describe how complex colony forms (patterns) emerge through the communication-based interplay between individual bacteria and the colony. Individual cells assume newly co-generated traits and abilities that are not prestored in the genetic information of the cells, that is, not all the information required for efficient responses to all environmental conditions is stored. To solve newly encountered problems, they assess the problem via collective sensing, recall stored information of past experience, and then execute distributed information processing of the 10^9 – 10^{12} bacteria in the colony—transforming the colony into a “super-brain.” I show illuminating examples of swarming intelligence of live bacteria in which they solve optimization problems that are beyond what human beings can solve. This will lead to a discussion about the special nature of bacterial computational principles compared to Turing algorithm computational principles, in particular about the role of distributed information processing.

Key words: bacteria intelligence; natural computation; social intelligence; gene networks; social bacteria; bacteria language; cooperation; bacteria swarming

Introduction

This chapter presents new clues, drawn from the morphogenesis of bacterial colonies, about natural information processing, natural intelligence, and social intelligence. Some exciting observations of complex cooperative behavior of bacteria in colonies are presented, guided by the assumption that they might shed new light on the foundations of biocomplexity, natural computations, and the foundations of cog-

nitition. The chapter is aimed at researchers of different disciplines: microbiology, biology, chemistry, physics, mathematics, and computer science. To make it comprehensible to all I avoided the use of specialized terminology and limited the presented details.

Bacteria are not the simple, solitary creatures of limited capabilities they were long believed to be. The impression that bacteria act as unsophisticated, solitary creatures stems from years of laboratory experiments in which they were grown under artificial conditions. However, under the harsh conditions in the wild, or in the lab under growth conditions that mimic natural environments, these versatile organisms work as a team and employ chemical communication to form highly complex colonies, 10^9 – 10^{12} bacteria each.^{1–11} Such colonies behave much like a multicellular organism with cell differentiation, distribution of tasks, and in some

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cases, even modules that act like reproduction organs.

One aspect of these behaviors has to do with collective engineering of complex spatial organization of the colony, with the bacteria forming different patterns to better cope with the environment.^{8–11} To form such multicellular superorganisms, new functional features appear at every level, from the internal cellular gel and genome states to the growth of the colony as a whole—thus facilitating a high level of functional complexity. Bacteria cannot store in their genes all the relevant information required for creating colonial patterns. In a new scenario that I propose they need not, because the respective units (the individual bacteria) assume newly co-generated traits and faculties that are not explicitly stored in the genetic information of the individuals.^{8–13} The required contextual information is cooperatively generated by using internally stored information, as well as new information extracted from the environment. Thus, these bacteria only require genetically stored information on how to build information processing faculties and how these capabilities, along with the guidelines for using them, may be employed to generate new knowledge as required.^{8–13}

Focusing on the energy, matter, and thermodynamic imbalances provided by the environment, Schrödinger proposed that life required the consumption of negative entropy, that is, the use of thermodynamic imbalances in the environment. From the perspective of thermodynamics, each bacterium can be viewed as a complex system that is composed of an “engine” that uses imbalances in the environment to do work, and a “machine” that uses this energy (to act against the natural course of entropy increase) for the synthesis of organic substances.¹³ A third information-processing system is also needed for the coordination and synchronization of the functioning of the engine and the machine. Namely, a living cell is analogous to a complex man-made cybernetic system, or a “chimera,” composed of information-processing systems and of at least two thermo-

dynamic elements. In addition, using the outer membrane, cells sense the environment.

We proposed that, besides “negative entropy,” organisms sense the environment to extract latent embedded information.¹³ By *latent information* we refer to data embedded in the environment that, once processed cognitively, initiates change in the organism’s function or behavior. Information induces changes; hence it can be used to generate an internal condensed description (model or usable information) of the environment, which guides the organism’s functioning.

While individual bacteria (that are a few microns in size) can sense only a limited area between replications, a colony that is composed of billions of bacteria can sense a large area and over long time periods. For that degree of coherence, the bacteria exchange information about the myriad individual environmental detections and epigenetic adjustments that must then be stored as newly acquired information. In other words, as a member of a complex superorganism—the colony—each unit (bacterium) must possess the ability to sense and communicate with the other units comprising the collective and perform its task within a coordinated distribution of tasks.

These bacteria faculties represent the origins of cognition.^{8,12,13} I do not imply that bacteria possess human capabilities, but that the precursors, or the fundamental elements of cognition, originated at this level of evolutionary history. From a practical perspective, this realization can shed light on the evolution of cognition and the basic requirement for facilitation of cognition in all organisms as well as in man-made computing machines.

Mathematical Skills of the *Paenibacillus dendritiformis* Bacteria

Problem Solving

To study the mechanisms and principles by which the bacteria regulate (engineer) the

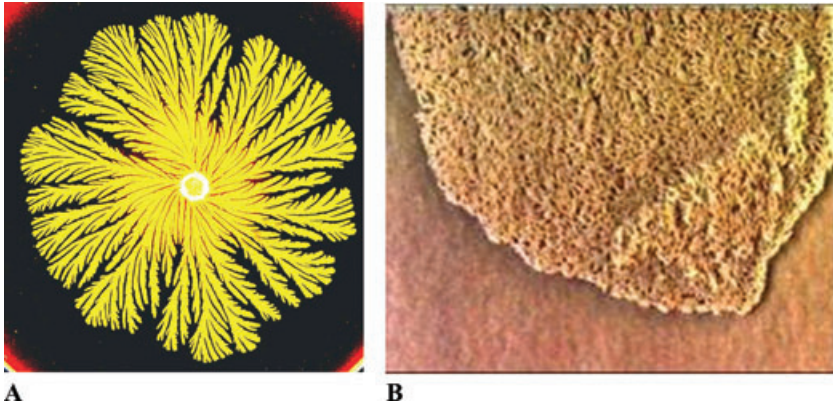


Figure 1. Colonial morphogenesis of the *Paenibacillus dendritiformis* bacteria when grown on hard and food depleted substrate. The colony starts from a droplet ($5\ \mu\text{l}$) inoculation at the center of the petri dish (the darker dot). After inoculation, the bacteria go through an “embryonic” colonial stage for several hours (presumably of assessment of the environmental conditions) and only then does the colony start to expand outward on the surface.^{8–11} **(A)** It takes the colony about 2 days to reach the observed size of about 8.8 cm in diameter shown here. **(B)** A snapshot from a video clip taken through an optical microscope with $500\times$ magnification. The video clip observations reveal bacteria swimming—segments of straight motion for about 1–3 sec at a speed of about 1 micron per second interrupted by bacterial tumbling terminating in a random new direction. That is why the bacterial movement is usually modeled as random walk.

complexity of colonial patterns, we developed a new strain of lubricating bacteria, *Paenibacillus dendritiformis*.⁸ The patterns shown in Figure 1 are generated during colony development of these bacteria in response to growth on nutrient-poor and hard surfaces. To cope with this situation, the bacteria collectively produce a lubricating layer of fluid that allows them to swim on the hard surface. The engineering capabilities of the bacteria are reflected by their ability to perform collective sensing of the level of nutrients and the hardness of the surface. And consequently, they regulate the genome level to adjust the secretion of lubrication and its viscosity to generate colonies whose structure matches the growth conditions. Although it sounds simple, this adjustment presents most challenging mathematical/computational tasks as I explain in the next section.

Bacteria Mathematical Skills—Functional Solvability

It is possible to model bacterial growth and obtain good quantitative agreements between

the simulated and observed colony patterns for different growth conditions (see Refs. 7 and 8 for more details). For that, we select the lubrication parameters (lubricant viscosity, rate of secretion, and degradation) for each growth condition (food level and substrate hardness). The question that comes to mind is how the bacteria select these parameters so that the branch width and the distance between branches fit the two requirements of sufficient lubrication for swimming within the branches and average cell density (determined by the branch width and distances between branches) appropriate for the food level. From a mathematics perspective, the requirement poses a functional solvability problem or functional self-consistency problem. In the past, when I studied pattern formation of nonliving systems (see concise review and references in Ref. 8), we discovered that it poses a microscopic solvability problem (interplay between macroscopic diffusion and microscopic dynamic at the interface) that we could solve using the singular perturbation methods. Albeit highly challenging, the snowflake problem is far simpler than the problem posed by the bacteria:

while in the former the water molecules do not change, in the latter the bacteria that constitute the colony change as they can secrete lubrication with different parameters. This is why I refer to the problem as functional solvability. To the best of my knowledge, this problem is beyond our current mathematical “tool kit.”

I also do not know how bacteria solve the problem, and the question is still open. Yet there are known mechanisms that are probably involved that might provide important clues and at the same time help clarify the notion of distributed information processing. For example, bacteria can secrete a variety of scissor-like proteins (proteases) that cut other proteins outside the cells.^{14,15} The proteases are known to be regulated by starvation of the cell (the level of food), the cell density (the level of quorum sensing signaling molecules), and the stress of other cells (level of the pheromone signaling molecules). Such regulatory mechanisms can hypothetically lead to distributed information processing and functional solvability. First, I assume that the rate of secretion of the lubricant is adjusted to the substrate hardness and its viscosity is regulated by some protease (which cuts the polysaccharides). Next, let’s also assume that *P. dendritiformis* secretes two types of quorum sensing messages, short range QS1 (sends information about the cell density within branches) and long range QS2 (sends information about the global density averaged over branches). This is a reasonable assumption; for example, we know that the attractive/repulsive chemotactic agents are short/long range, respectively.⁸ Put together, subtilisin secretion is regulated by QS1, QS2, the local food level measured by the cell, and the information it receives about the stress of the other cells. We can now envision how these mechanisms, when put together, can adjust the lubricant to satisfy the aforementioned requirements. I used the term *envision* to emphasize that a “true” understanding will require modeling of the regulatory pathways of these genes and checking that they can indeed solve the functional solvability problem.

Cognitive and Engineering Skills of *P. dendritiformis*

Chemotaxis—Rudimentary Cognitive Function

To achieve even greater engineering efficiency, bacteria employ the mechanism of chemotactic signaling. Chemotaxis is cell movement in response to gradients in the concentration of a chemical agent.⁸⁻¹¹ The movement can be biased either toward higher concentrations (attractive) or away from high concentrations (repulsive). Bacteria are too short to detect chemical gradients, yet swimming bacteria found a smart solution to detect gradients and bias their movement accordingly. In attractive chemotactic movement, the cells detect the concentration as they swim, and if the concentration increases they delay their tumbling. I emphasize that this process involves sensing (of the chemical level), memory (of the measured concentration) and information processing—evaluation of the change in concentration between measurements. Consequently, in accordance with the result of the computation (increase or decrease in the concentration), the cell decides whether to extend the forward movement or to tumble. The result is a biased random walk with longer excursions toward high concentrations. In the case of repulsive chemotactic, the tumbling is delayed when the concentration decreases.

The aforementioned description of chemotaxis can be executed by a robot equipped with a sensor and information-processing unit that is preprogrammed to control the taxis according to concentration gradients. The reason that I use the term *rudimentary cognitive function* to describe chemotaxis is associated with the fact that the decision to tumble or not to tumble is not simply preprogrammed but involves assignment of individual meaning. What I mean is that the decision is performed according to the additional environmental conditions (the food concentration and other factors such as temperature, humidity, hardness

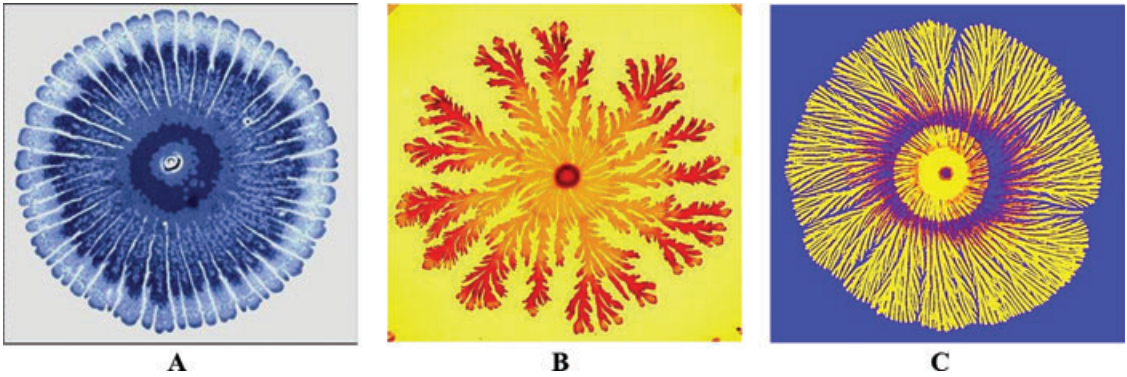


Figure 2. Engineering skills of bacteria. **(A)** Typical pattern developed at higher food levels when attractive chemotactic signaling is activated (as is concluded by comparison with model simulations). **(B)** Typical pattern when food chemotaxis dominates the growth at intermediate levels of food. **(C)** Colonial pattern at low level of food when repulsive chemotactic signaling is assumed to be intensified. The colors are added to indicate the bacterial density.

of the substrate, and existence of toxic materials), the internal state of the cell (starvation), according to the internally stored information of the specific cell (previous starvation and other stress) and signals received from other cells (quorum factor stress pheromones etc.).^{8,12,13}

Chemotactic Signaling—Rudimentary Social Intelligence

The most familiar case of chemotaxis is attraction to an external chemical, such as a nutrient. There is evidence that such chemotaxis occurs in these colonies and is responsible for an increased expansion rate and colony "bushiness" at intermediate values of the nutrient concentration (Fig. 2B). At relatively higher nutrient levels, additional bacterial density variations are visible within the branches, as seen in Figure 2A. Model simulations can be used to test the idea that the patterns result from bacterial utilizing attractive chemotactic signaling. Very different patterns form at low nutrient levels (Fig. 2C). To explain the mechanism, I recall that part of the branch-making dynamics relies on the cells going into a nonmotile state further back from the colony front, where the nutrient levels are extremely low. Based on model simulation it was proposed that cells emit a re-

pellent chemical as they are entering this state leading to the observed colony pattern in this case.²

The picture that emerges is that the basic branching pattern is sculpted by the combined action of a variety of chemotactic strategies. As these different influences sort themselves out, changing conditions and changing bacterial strains always lead to new structures. Exactly how information from the outside is utilized to help decide which, if any, of these processes need to be turned on is still an open question. Yet there are increasing hints that these decisions are made cooperatively, much like what is known to be true regarding the collective decision making of bacteria to sporulate or the decision to share genetic information. It is known for example that the same regulatory pathways that participate in sporulation/competence are also involved in the regulation of chemotaxis.

We proposed,^{8–13} that chemotactic signaling represents rudimentary social intelligence that involves cooperative distributed information processing of the entire colony. The reasoning is that chemotactic signaling involves exchange of meaning-bearing messages so that the colony as a whole self-organizes its pattern according to the overall present and past environmental conditions. This colony self-organization involves a semantic and

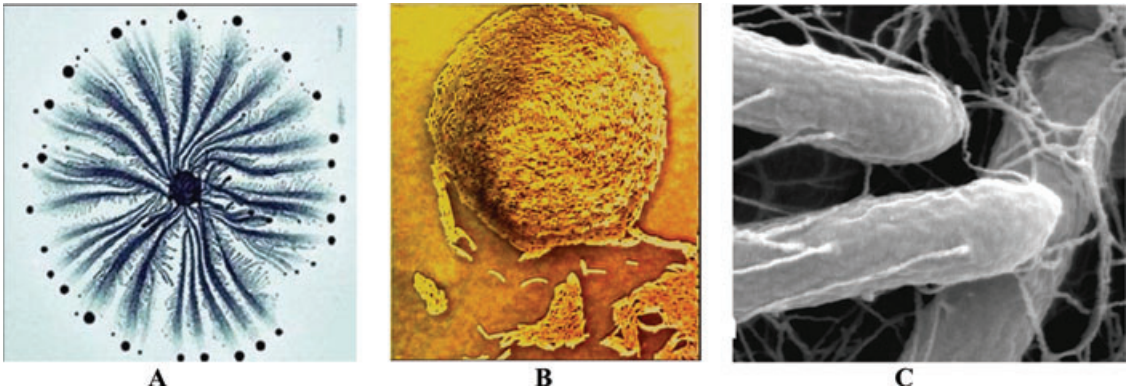


Figure 3. Modular colonial organization of the *Paenibacillus vortex* bacteria. In **(A)** we see the colony organization. The diameter of the shown colony is about 5 cm. Each dot is a module or cluster of bacteria that move (hence the term vortex). In **(B)** we see that each vortex (the 500 \times magnified picture is taken from a video clip) is composed of many cells that swarm collectively around their common center at about 10 micron/s. The vortices vary in size from tens to millions of bacteria, according to their location in the colony. The cells in the vortex replicate, and the vortex expands in size and moves outward as a unit, leaving behind a trail of motile but usually nonreplicating cells—the vortex branch. The dynamics of the vortices is quite complicated and includes attraction, repulsion, merging and splitting of vortices. Yet, from this complex, seemingly chaotic dynamics, a colony with complex but nonarbitrary organization emerges [*]. In **(C)** I show an electron microscope view of the individual bacteria showing flagella and pili (courtesy of I. Colin, Ref. 16).

pragmatic communication distribution of tasks which goes hand in hand with epigenetic cell differentiation (inheritable changes in cells identity at different locations of the colony (see figure 8 in Ref. 10).

Modular Colony Organization of the *Paenibacillus* vortex Bacteria

Some bacterial strains organize their colonies by generating modules, each consisting of many bacteria, which are used as building blocks for the colony as a whole. This behavior is observed, for example, in the lubricating bacteria *Paenibacillus vortex* shown in Figure 3.^{5,8–11} The modules of this lubricating strain are groups of bacteria that move around a common center. Model simulation suggests that the vortices are generated by the action of attractive chemotaxis and possibly physical links between bacteria.¹⁶ It is also suggested that the vortices are “pushed out” in response to repulsive chemotactic agent secreted by bac-

teria at the center of the colony. The bacteria in each vortex have high length variability with some of the cells being tens of microns long with several chromosomes. Genome sequencing results indicate that this strain (and the *P. dendritiformis*) has genes for both flagella and pili motility.¹⁴

The Complexity Challenge of Modular Organization

Maintaining the integrity of the individual vortices while they serve as higher-order building blocks of the colony requires advanced communication: each cell has to follow far more complex dynamics, being part of both a specific vortex and the whole colony, so that it can adjust its activities accordingly. A greater challenge is posed by the formation of new vortices that emerge in the trail behind a vortex. Following initiation signals the nonmotile cells in the trail start to secrete lubricating fluid and begin to move quite rapidly as a turbulent “biofluid” until an eddy forms and turns into a new vortex as the cells in the eddy generate strong

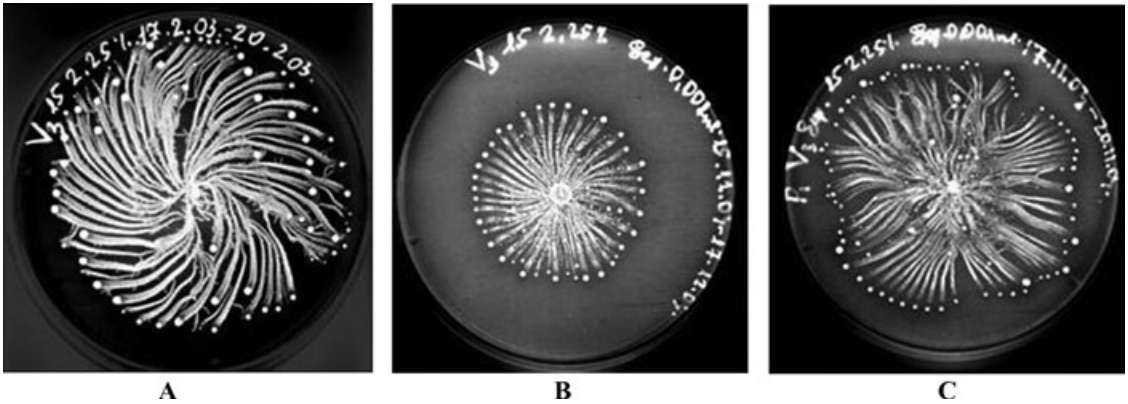


Figure 4. Learning from experience. The observations show the response of the *P. vortex* bacteria to nonlethal levels of Septrin. In **(A)** we show the normal growth pattern in the absence of antibiotic. The effect of first exposure of the bacteria to the antibiotic is shown in **(B)** and the response in a second encounter is shown in **(C)**. Learning from experience **(C)** is manifested by the fact that upon second encounter with the antibiotic the colony expands faster and the pattern has higher complexity.⁹

coupling. The entire process appears to be under advanced communication-based information-processing and cooperative control that goes hand in hand with genome-wide changes in the individual cells. For the integrity of the vortices to be maintained (because the cells replicate) the changes at the gene network level have to be inheritable. The results support the idea of “more is different on all levels”⁸ (that cells change their identity during colony organization), and that it is afforded by epigenetic memory.

Functional Complexity and Learning from Experience

Natural habituate bacteria are regularly exposed to nonlethal (subinhibitory) levels of antibiotic material. Previously,⁸ I proposed the idea of “functional complexity”—the complexity of the colony organization has an important functional role as it affords the bacteria with higher adaptability to cope with environmental stresses. For example, upon encountering antibiotic stress the bacteria reshape the colony pattern^{8,9,16} as is shown in Figure 4. Recently it has been suggested that bacteria also possess (epigenetic) memory of the past,^{9,13} which en-

ables them to keep track of how they handled previous encounters with antibiotics as is illustrated in Figure 1C. Bacteria learn from past experience and can cope better upon a second encounter with the same antibiotic as is reflected by the fact that the colony expands faster and has more complex pattern. This effect can be erased by growth in neutral conditions. One possibility is that this effect is connected with genetic shift in the population. Another possibility involves heritable (epigenetic) at the genome level.

Distributed Information Processing on all Levels

As was pointed out,^{8–13} bacteria sense the environment and perform internal information processing (according to the internally stored information) to extract latent information embedded in the complexity of their environment. The latent information is then converted into usable or “active” information that affects the bacterium activity as well as intracellular changes.^{12,13,18}

As I mention in the introduction, while an individual bacterium can sense only a limited area between replications, in a colony that

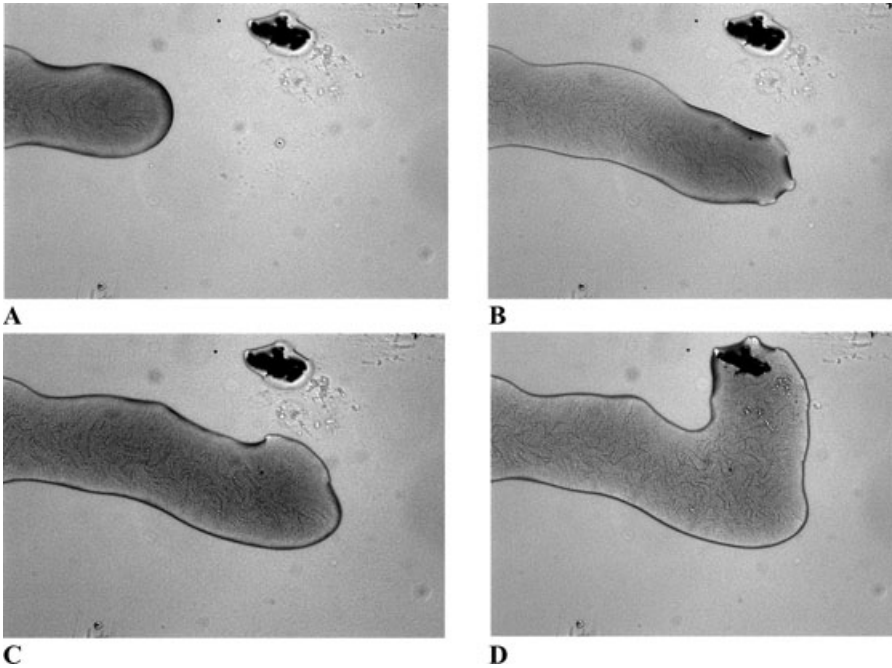


Figure 5. Swarming intelligence of the *P. vortex* bacteria. The pictures (50× magnification) show snapshots from a video clip of a branch of a colony of *P. vortex* bacteria moving on 0.3% w/v Mueller–Hinton agar (M–H agar). As the branch is extending, we added some more food (extracellular material derived from washes of swarming cells was delivered by toothpick and allowed to soak into the agar). The time lapse between the first and last picture is about 50 s.

is composed of billions of cells the bacteria can sense a large area and over long time periods and collectively glean relevant latent information embedded in the complex environment. To coordinate such cooperative ventures, bacteria have developed various methods of biochemical communication (e.g., quorum sensing) by using a variety of mediators ranging from simple molecules to polymers, peptides, complex proteins, genetic material, and even “cassettes of genetic information” (e.g., plasmids, viruses).^{8,9,12,13,19} The intercellular communication is afforded by the evolution of highly complex and intricate intracellular signaling mechanisms involving signal transduction networks²⁰ and genetic language to turn genes off and on.²¹ These mechanisms exhibit functional complexity, which generates intrinsic meaning for contextual interpretations of

chemical messages and for formulating appropriate complex responses.

One of the cardinal differences between the bacterial information processing and the Universal Turing Machine is that while in the latter the software is separate from the hardware, while in the case of the bacteria the hardware is changing according to the input, the stored information, the processing of information, and the desirable output. The expected output affects the well being of the cell, hence the computations are not “objective” and there is no separation between input and output. Different inputs will be given different weight/priority and will be processed in a different way. I emphasize that this can also be done by a Turing Machine, but then it is an external user assigning priorities for his benefit, not the computer for “its benefit.” I also note that different cells

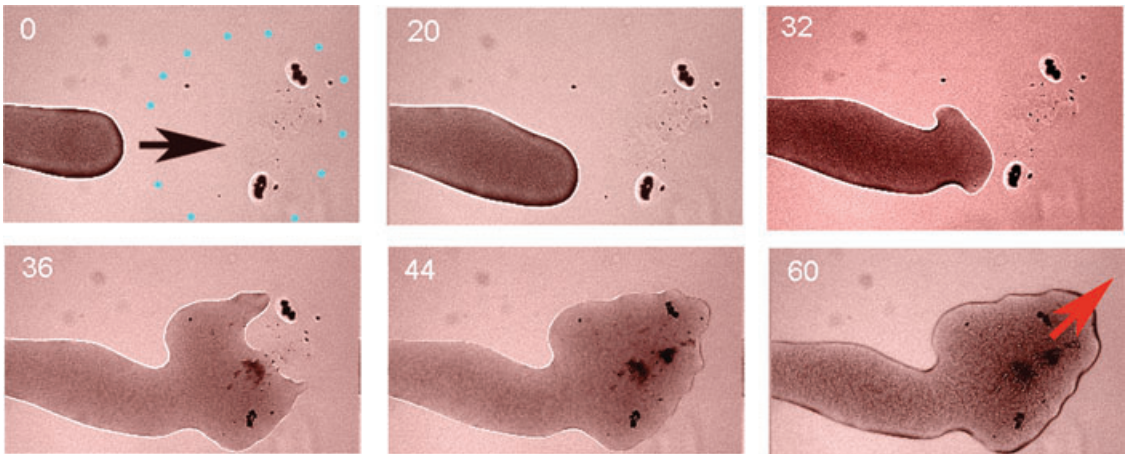


Figure 6. Swarming intelligence of the *P. vortex* bacteria. Similar to Figure 5, the pictures (50 \times magnification) show snapshots from a video clip of a branch of a colony of *P. vortex* bacteria moving on 0.3% w/v Mueller–Hinton agar (M–H agar). The branch is extending into an area where extracellular material derived from washes of swarming cells was delivered by toothpick and allowed to soak into the agar. Time of frame capture is noted in seconds. Starting ($t = 0$): Area of extract outlined in blue dots with direction of cell mass elongation shown by the black arrow. Dark marks inside the area of the extract are disturbances due to the toothpick contacting the agar. Stage $t = 32$: cell mass starts to disperse as it contacts the area of the extract. Stage $t = 44$: Cell mass has dispersed into area of extract. Stage $t = 60$: Additional cells are moving into this area from further back in the colony; the cell mass is growing in volume at the tip and extends in the direction of the red arrow. The video is courtesy of I. Colin, Ref. 16.

can exchange information in the form of hardware (genetic material). It can be done through different mechanisms, such as absorption of plasmids from the environment, injection of genetic material by viruses, or direct transfer of genetic material by conjugation that is used for transfer of the genetic information.²² Such exchange of genetic material between bacteria would correspond to two computers exchanging hardware and rebuilding their hardware according to the computations to be executed. The picture at the colony level is that of interacting (communicating) different units that are assigned specific tasks so as to optimize their task for the benefit of the network as a whole.

Collective Decision Making

Observations suggest that bacteria exchange information extracted from the environment, process the information, and act accordingly. The *P. vortex* bacteria, while moving

on Mueller–Hinton (M–H) agar, form snake-like swarms hundreds of bacteria wide.¹⁶ The swarm can expand very efficiently and collectively change its swarming when a new signaling source is added, as shown in Figure 5. To coordinate such search strategy, the individual bacteria must respond not only to local gradients in food concentration but also to the food concentration and gradients measured by other cells at remote locations. The results shown in Figure 5 illustrate the level of advanced distributed information processing that is ongoing as the bacteria swarm propagates on the surface. As explained in detail in Ref. 16, what we added (the dark location in the figure) was extracellular material derived from washes of swarming cells. This extract has additional food but also signaling molecules that the cells secrete. Hence the results in this figure illustrate not only the collective change in propagation of the swarm but also that the bacteria secrete and respond collectively to communication signals.

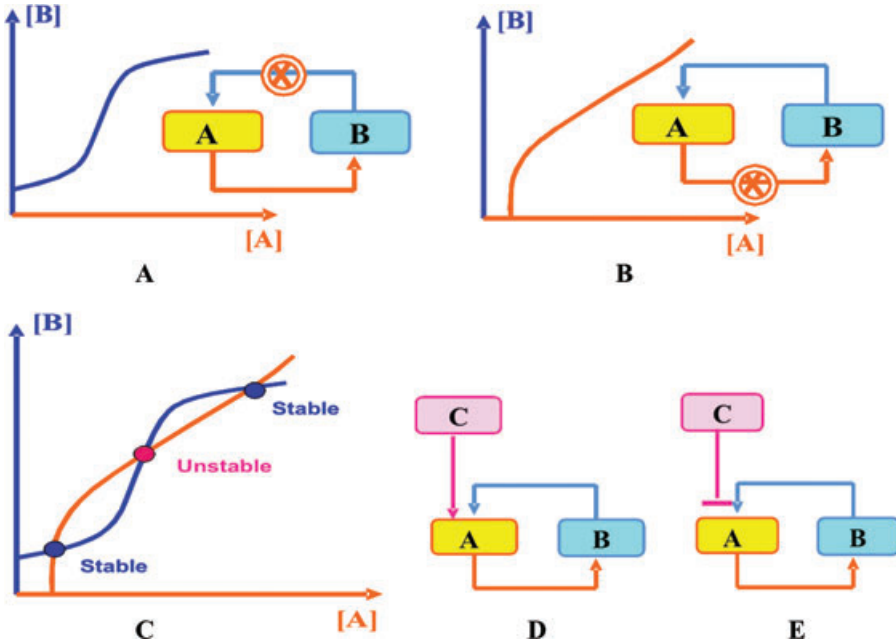


Figure 7. A hypothetical flip-flop or bistable genetic circuit. Two genes, [A] and [B], are mutually excitatory (they upregulate each other). **(A)** shows the dependence of the level of [B] on [A] and **(B)** shows the dependence of [A] on [B]. When both are active, there are three possible states as shown in **(C)**. The two stable states correspond to a situation that [A] and [B] are both in high concentration (this state can be denoted (1,1)) and a (0,0) state in which the concentrations of both [A] and [B] are low. **(D)** shows how a third gene [C] can cause a (0,0) \rightarrow (1,1) transition and **(E)** shows what is needed for the reverse (1,1) \rightarrow (0,0) transition.

Solving the Dilemma of Choice (Buridan’s Donkey)

To further assess the extent of bacteria’s social intelligence we pose to the swarm a Dilemma of Choice (the medieval Buridan’s Donkey logic dilemma) by placing two extracts in front of the propagating swarm.¹⁶ The results shown in Figure 6 are quite astonishing and hint that the bacteria developed a very sophisticated optimization strategy.

Intracellular Computation

In this section I present some examples of intracellular gene computation circuits or gene logical elements.²¹ The circuits can either represent gene circuits or regulatory pathways. A simple bistable circuit or flip-flop logical mem-

ory element is represented in Figure 7. The element has two stable logic states: I. a (0,0) state which corresponds to low concentrations of two proteins (A) and (B), and a (1,1) state which corresponds to high concentrations of the two proteins. In computer science language, these two states can be described as $|A,B\rangle$ using the quantum mechanics (quantum computing) notations of cat and bra to indicate that these two states are subset of two stable states out of the four states $\{|0,0\rangle; |1,0\rangle; |0,1\rangle; |1,1\rangle\}$. Regulation of either gene (A) or (B) by a third gene (C) may be viewed as operations that transfer between the states. For example, upregulation of (A) causes a transition $|0,0\rangle \rightarrow |1,1\rangle$, and down-regulation of (A) causes the reverse transition.

Figure 8 shows examples of gene circuits that are used for: 1. delay operation—the coherent feed-forward loop (C-FFL) shown

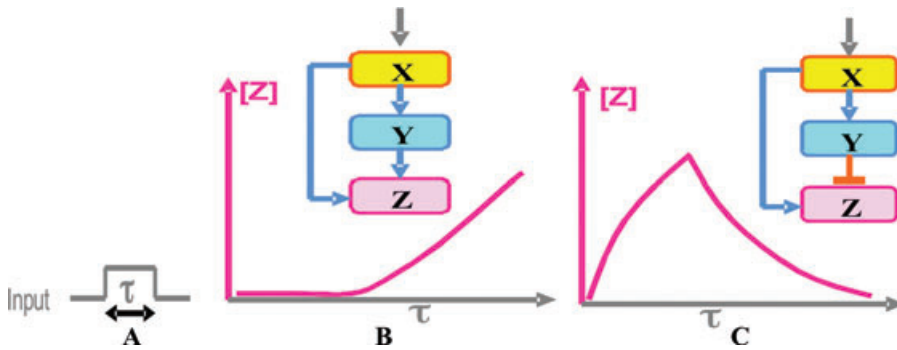


Figure 8. Illustrations of the coherent (B) and incoherent (C) gene circuit motifs [23,24] and the way an input signal with width τ is processed by these circuits.

in Figure 8A.^{23,24} 2. filtering—the incoherent feed forward loop (ICFFL) shown in Figure 8B.^{23,24}

Let's assume that an input signal drives a flip-flop element via an IC-FFL, in this case, only an input signal with a well defined time width τ can cause $|0,0\rangle \rightarrow |1,1\rangle$ transition of the logic memory (the flip-flop element). If, instead, the flip-flop element is driven via a C-FFL, the time width of the input signal must be larger than some minimal width that is determined by the magnitude of the signal (wider for lower magnitude) to induce transitions between the stable states of the flip-flop element. Once the principles are clear, more complicated circuits can be envisioned, such as two coupled flip-flop elements and so on.

Concluding Remarks and Looking Ahead

I demonstrated how complex colonial forms (patterns) emerge through the communication-based singular interplay between individual bacteria (the micro-level) and the colony (the macro-level). Each bacterium is, by itself, a biotic autonomous system with its own internal cellular gel that possesses informatics capabilities (storage, processing, and interpretation of information). These afford the cell certain freedom to select its response to biochemical messages it receives as part of the distributed information processing of the colony as a whole,

including self-alteration and broadcasting messages to initiate alterations in other bacteria. Such self-plasticity and decision-making capabilities elevate the level of bacterial cooperation during colonial self-organization.

As the individuals in a growing colony begin to respond to the colony itself (i.e., information flow from the colony to the individual), these individuals respond by regulating their movements, growth rates, various tasks they perform, the chemical signals they send to other bacteria, and even their gene-network state (phenotypic state) according to the received signals.

According to this picture, new features collectively emerge during biotic self-organization which involves natural information processing on every level, from the individual cells via cell modules to the whole colony. The cells thus co-generate new information that is used to collectively assume newly engineered cell traits and abilities that are not explicitly stored in the genetic information of the individuals. For example, bacteria can not genetically store all the information required for creating the colonial patterns. In the new picture they do not need to because the required information is cooperatively generated as self-organization proceeds by bacterial communication, informatics, and self-plasticity capabilities. Thus, the bacteria need only have genetically stored the guidelines for producing these capabilities and using them to generate new information as required.

It seems that bacteria have some sort of collective memory by which they keep track of how they handled their previous encounters with antibiotics. They know how to collectively glean information from the environment, “talk” with each other, distribute tasks, generate collective memory, and turn their colony into a “cybernetic system”—a massive “brain” that can perform natural distributed information processing, learn from past experience, and possibly alter the genome organization or even create new genes to better cope with novel challenges.^{8–13,17,18}

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Conflicts of Interest

The author declares no conflicts of interest.

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