Attractor Landscape: A Bridge between Robotics and Synthetic Biology

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Genetic regulatory networks (GRNs) model the dynamics and interactions among genes. From a robotics perspective, GRNs are extremely interesting because they are capable of producing complex behaviors. Notably, cell differentiation can be modeled using GRNs, and the dynamics of this process can be studied by means of dynamical systems methods. In a nutshell, the state of a cell is represented by an attractor in the state space of a dynamical system, and the transitions between cell states correspond to transitions between attractors. This view suggests a visionary approach: apply the metaphor of landscape attractor to design specific cell dynamics that can match the attractor landscape required for attaining a target behavior in a robotic system. The constraints prescribed by the robotic application are just the correspondence between behavioral attractors in the robot and cell attractors in the cell, along with specific transitions between attractors. This perspective may lead to applications in biorobotics, and it may also help synthetic biology systems design, which may benefit from methods developed for complex dynamical systems. We believe that this level of abstraction can provide a common vocabulary and a shared set of categories between researchers in robotics and synthetic biology. In this paper, we elaborate on previous results on GRNs-controlled robots and propose some guidelines for making this approach viable, illustrating these concepts with examples and case studies in biorobotics.

Keywords: genetic regulatory networks; embodied robotics; dynamical systems; attractors; cell differentiation; Boolean network robotics

1. Introduction

Genetic regulatory networks (GRNs) are commonly used to model the dynamics and interactions among genes. GRNs are, in general, capable of producing complex behaviors: this property is of particular interest to researchers in the field of robotics, as GRNs are a computational model of a system that interacts with its environment and is capable of performing nontrivial information processing and computa-

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tions. Let us consider the example of cell differentiation: different gene activation patterns enable stem cells to undergo differentiation from a pluripotent to a mature state by following a path along the *lineage tree*; the branch taken at each choice point in the tree may be influenced by external chemical and physical inputs. The path can be reverted and, if provided with specific input signals, the cell can also move upward to a multipotent state.

Cellular systems are both robust and adaptive; that is, they can maintain their basic functions in spite of damages and noise, and they are able to adapt to new environmental conditions. Notably, cell differentiation can be modeled by means of GRN models, and the dynamics of this system can be studied by using dynamical systems methods [1]. Recently, a dynamical systems view of cell differentiation has been proposed [2, 3]. In a nutshell, the state of a cell is represented by an attractor in the state space of a dynamical system, and the transitions between cell states correspond to transitions between attractors. Transitions may be both stochastic and deterministic. This model makes it possible to capture some fundamental phenomena in cell differentiation [4, 5].

The complex behavior exhibited by cell dynamics can be interpreted from a robotics viewpoint, suggesting the possibility of achieving robust and adaptive behaviors in robots—and a group of robots—by exploiting the dynamical properties of GRN models. These models can be effectively used as *robot programs*. According to [6], we call *robot program* the computational model of the system that maps the percepts of the robot to the actions it takes, possibly according to a utility function and a goal. The key motivation of this idea lies in the possibility of applying dynamical system theory to robotics [7–9], exploiting the tight link between artificial intelligence and dynamical systems, which consists primarily in the fact that information processing can be seen as the evolution in time of a dynamical system [10, 11]. The archetypal case of this approach consists in associating the initial conditions of the dynamical system to the input of the problem and letting the system evolve in time until it reaches a steady state, which is then interpreted as the output, that is, the answer to the problem. An example in theoretical computer science is the solution of the satisfiability problem through Boolean networks (BNs) [12], while a typical example in robotics is represented by the different gait patterns in a quadruped robot, each corresponding to one specific attractor in the sensory-motor system of the robot (see [8, Chapter 4]).

Preliminary results in this direction have been achieved in controlling robots by means of BNs (GRN models introduced by Kauffman [13] and subsequently used to model important phenomena in biol-

ogy [14, 15]). The effectiveness of this approach was demonstrated through experiments on both simulated and real robots [16–19]. These experiments showed that BNs can be successfully used to control robots, and therefore that a nontrivial behavior can be attained by a system sharing some similarities with biological cells. The imagination would then run to the synthesis of specific cells controlling micro-robots, produced by synthetic biology (SB) approaches: given the GRN designed *in silico* by means of an automatic procedure, a synthetic cell is produced by composing elementary cellular bricks. Preliminary results on automatic design of GRNs for cell differentiation have been recently achieved [20]. Results on automatic design of Boolean networks have also been presented in [21]. The most natural way to achieve this goal would be either to reproduce a given GRN by means of biological material, that is, a circuit composed of wet logical gates, or to synthesize a cell characterized by a given low-level dynamic, corresponding to the target GRN. Unfortunately, this low-level approach might introduce too many constraints on the design process and turn out to be extremely complicated, if not impossible. Anyway, should this be possible in the future, the approach proposed in this contribution would still be useful. We believe that a different strategy can be successfully applied, which consists in raising the abstraction level of the analogy from the details of the dynamics to that of *attractor landscape*. Indeed, an in-depth analysis of the GRN-controlled robot dynamics showed that a robot's behavior can be decomposed into elementary behaviors, represented by attractors in the network state space and connected by trajectories that can be controlled by specific inputs.

This result suggests the visionary approach we propose for the first time in this paper: apply the metaphor of landscape attractor to design specific cell dynamics that can match the attractor landscape required for attaining a target behavior for a robot. Indeed, the constraint prescribed by the robotic application is just the correspondence between behavioral attractors in the robot and cell attractors in the cell, along with some specific transitions between attractors. Let us suppose we have to design a micro-robot controlled by a (synthetic) cell—or a population of cells—whose dynamics in terms of attractors and transitions among them is sufficiently known. A correspondence between cell attractors and robot elementary behaviors can be defined, and the chemical signals that force the transitions between cell states can be used as inputs to the robot for changing its elementary behavior.

In Section 2, we first outline the notion of attractor landscape in cell dynamics, mainly referring to cell differentiation. Subsequently, in Section 3, we summarize the results attained in the context of robotics

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controllers based on GRNs. In Section 4, we provide concrete examples of the use of cell differentiation models to control robots. Finally, we discuss the implications of our vision and conclude in Section 5.

2. Attractors in Cell Dynamics

Although some specific and recurrent biological interactions—network motifs [22]—present in GRNs can be well explained and understood by means of relatively simple mathematical equations, we are far from a satisfactory understanding of the whole long-term dynamics generated by these complex networks. One possible explanation of this fact is that the cell phenotype is not the direct consequence of the superposition of an isolated genetic pathway [23].

Albeit abstract, a conceptual mathematical framework in which a cell is viewed as a dynamical system and its attractor states—stable equilibrium states of the GRN dynamics—underlie its observable phenotypes [24] has been proposed since the pioneering works of Kauffman [13, 25]. This framework, relying on complex systems science, aims to enrich the current understanding of cell dynamics and to overcome the classical linear causation scheme (one gene → one trait) deriving from the central dogma of biology.

We can therefore define a network state at a given time by means of a vector state $\boldsymbol{S}(t) = [x_1(t), x_2(t), \ldots x_N(t)]$ where each $x_i(t)$ represents the expression level of the i^{th} gene, which depends on the regulatory interactions between genes. So if we represent a gene expression pattern by means of this vector state, all the possible gene expression patterns constitute the state space of the GRN and, among them, those in a **stable** equilibrium condition are attractor states, and their gene expression profiles determine the observable cell types. For any initial state $\boldsymbol{S}(t = 0) = \boldsymbol{S}_0$, its *trajectory* will eventually converge to an attractor state, where the interaction forces are null. Of course, as far as GRNs are concerned, not all the states might be a biologically plausible initial condition. We call the *basin of attraction* the set of states that lead toward an attractor.

Waddington, through his "epigenetic landscape" metaphor [23], has already captured with the valley abstraction the idea of basins of attraction and discrete cell fates; the marble (network state) rolls down in the landscape topology until it reaches a local minimum (the attractor state). We can attribute to his metaphor a formal basis and in this way explain how a network of interactions, in particular its dynamics, can give rise to a particular landscape topography. Considering that at equilibrium not all network states $\boldsymbol{S}$ are equally likely, due to the interaction forces that shape the landscape, we can assign

to each state a potential $V(S) = -\ln p(S)$ where $p(S)$ is the probability that the network is at state S when the system is at equilibrium (see supplementary material of [24]). The function $V(S)$ determines the depth of the various network states in the landscape topography, and the attractor states are the local minima of this function.

The model based on the attractor abstraction, of which Waddington's landscape provides an intuitive visual representation, proved able to explain, unify and integrate various theories concerning cell dynamics in a consistent framework, free of *ad hoc* explanations.

Based on previous theoretical and in silico results of Kauffman, Huang and colleagues in [2] tried to verify, with empirical evidence, if cell types could be represented by attractor states of the GRN. For this purpose, they stimulated *in vitro* HL60 cells by two biochemically distinct stimuli, provoking in this way initially divergent trajectories and observing both sets of cells converge to a macroscopically indistinguishable neutrophil stable state. Although this is only a necessary condition for the presence of an attractor state, it is particularly important because the two sets of cells follow very different gene expression trajectories before converging to the same stable state, and we have to exclude the unique and common differentiation pathway hypothesis.

The traditional approach to explain and understand cell regulation is based on the identification of functional signaling pathways activated by the high-specificity ligand-cell surface receptor binding; this generates a cascade of signals, which in turn activate specific genes for one cell fate, or more generally, a cell behavior. In [26], the authors highlight various experimental aspects not coherent with this old paradigm because: (*i*) a growth factor can induce—conversely to what is believed to be true—the activation of a very large set of genes; (*ii*) a biochemical signal can lead to different results depending on the cell state or the cell type itself; and (*iii*) "nonspecific" mechanical stimuli can induce the same cell fates of growth factors that with high specificity bind to their receptors. These mechanisms and dynamics suggest that the cell fates are organized as attractors. In order to provide a mathematical support to this intuition and to take into account the cell fate switch produced by mechanical stimuli, they make use of a simple mathematical network model. They made a simple model of the signaling system within capillary endothelial cells, including the growth factors and cell shape modulation as inputs of the model. They noticed that shape modulation in living endothelial cells produces changes within cells, related to both gene expression and signal transduction, very similar to those induced by growth factors and by computer simulation of their model. These results suggested that specific molecular signals and also mechanical forces are translated into

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patterns of gene expression that represent attractors of the network model dynamics. The attractors are the stable and robust operating ways of functioning of a cell—such as cell types or cell behavioral modes like growth, quiescence, differentiation and apoptosis—that arise from the constraints of the regulatory networks. The resulting attractor—and in the last instance the observable phenotype—is determined by the initial condition of the cell and by the subsequent stimuli or perturbations that regardless of their nature—chemical, mechanical, thermal fluctuations or other—place the dynamics in its basin of attraction.

In [24], Huang et al. present the idea of "cancer attractors," resuming previous ideas of Kauffman. In that paper, the authors try to contextualize tumorigenesis within developmental biology, avoiding the traditional vision of cancer as an aberrant product of the evolutionary process. Explanations of cancer manifestations by means of "plausible mutations" reveal their paradoxical nature if we consider that no mutations are required to produce the various cell phenotypes generated during the development of a multicellular organism. Recalling Waddington's metaphor, the authors propose to consider tumor types as *latent* cell types. Thus, nongenetic perturbations can facilitate cells to visit them, by placing the cell state into their basins of attractions. Remarkably, this framework does not exclude genetic mutations as possible causes of tumorigenesis, but relegates them to one of the possible causations of tumorigenesis; since they change the network architecture, they can significantly modify the attractor landscape and facilitate the visit of cancer attractors.

Recently, a powerful mathematical model able to reproduce the main abstract properties of cell differentiation as different degrees of differentiation, stochastic and deterministic differentiation, limited reversibility, induced pluripotency and induced change of cell type has been proposed by Serra and Villani [4, 27]. This model considers a cell subject to intrinsic noise, and as such, its dynamics may not remain trapped in an attractor, and jumps between attractors can occur. This model can be seen as a generalization of the attractors model; indeed the threshold ergodic set (TES) is the main abstraction of this formalization, and it is defined as the set of attractors in which the dynamics remains trapped, under the hypothesis that attractor transitions with probability less than a certain threshold are not feasible. The threshold concept is strictly related to the noise level present in the cell, and by varying it, the network dynamics can generate different TES landscapes, which represent the various steps of a cell differentiation process.

3. Attractors in Robotics Behavior

The concept of attractors in robotics was introduced in the context of a dynamical systems approach to designing robotic systems in the early 1990s (see [7, Chapter 9]). Here the rationale is the one already proposed in cybernetics and cognitive complex systems, which states that the steady states of the system (i.e., its attractors) represent its typical behaviors. A prototypical example is that of different kinds of gait shown by a robot: despite the fact that the controller is always the same, different environmental conditions coupled with the controller itself give rise to and at the same time establish the final attractors of the system (e.g., walking or trotting). See [8], page 98.

Along this line are the experiments in *Boolean network robotics* [16–19]. A BN is a discrete-time, discrete-state dynamical system whose state is an N-tuple in $\{0, 1\}^N$, $(x_1, \ldots, x_N)$. The state is updated according to the composition of N Boolean functions $f_i\left(x_{i_1}, \ldots, x_{i_{K_i}}\right)$, where K_i is the number of inputs of node i, which is associated to Boolean variable x_i. Each function f_i governs the update of variable x_i and depends upon the values of variables $x_{i_1}, \ldots, x_{i_{K_i}}$. BNs were introduced by Kauffman [13] as GRN models and proved able to capture important phenomena in biology [14, 15]. In BN robotics, the robot is controlled by means of a BN: the value of some nodes of the BN are imposed from the robot sensor readings, and the actuators of the robot take the value of some BN nodes. The BN is trained by means of a learning algorithm that manipulates the Boolean functions (and possibly also node connections). The algorithm employs as learning feedback a measure of the performance of the BN-controlled robot (in the following, BN-robot) on the task to perform, such as in evolutionary robotics [28]. For example, it was shown that a BN-robot can learn a composite mission, in which the first task is to perform phototaxis; then, after a sharp sound is perceived, the robot performs anti-phototaxis [16–19]. A dynamical systems' analysis shows that the behavior of the robot is mainly composed of three attractors: in the first the robot steadily rotates and in the second the robot goes straight. When the frontal light sensor switches on, the BN trajectory exits from a "rotate" attractor and jumps into a "go straight" attractor. Subsequently, when the sound is perceived, the trajectory exits from this attractor and moves to a third attractor, the one corresponding to the action "escape from light." This dynamic emerges from the learning (evolutionary) process that shaped the BN. The results achieved in BN robotics are still preliminary, yet quite promising, as they show that a GRN model can be effectively used to control a robot that has to attain a nontrivial goal.

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Further results on GRN models used in robotics are summarized in a survey by one of the authors of this paper [29]. Related to BN robotics are works in evolutionary robotics, where robots are controlled by artificial neural networks, which are designed by means of evolutionary computation techniques [28]. An important research line in evolutionary robotics that is quite relevant for BN robotics and the perspective presented in this work is the one that emphasizes the role of *embodiment* in evolved robots [9, 30]. Indeed, the behavior of a BN-robot emerges from the interaction among its sensors and actuators (and the body of the robot itself), the BN dynamics and the environment. In a sense, the experiments in BN robotics are an instance of the evolution of minimally cognitive behaviors [31, 32]. The problem of programming and reprogramming evolved GRNs has been recently addressed from the perspective of algorithmic complexity and causality [33]. This study proposes a *causal interventional calculus* that makes it possible to steer complex evolved systems. Such an approach may be extremely useful in the context of GRN-controlled robots. For the sake of completeness, we also mention the fact that the automatic design of control software for robots is currently a prominent topic in robotics research, especially when swarms of robots are involved [34].

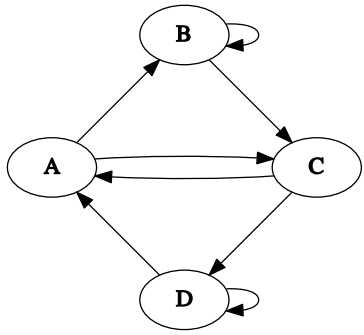
Following these recent advancements and mainly the achievements in BN robotics, in the next section we will illustrate the use of an attractor landscape to bridge robotics and SB.

4. Robotics Meets Synthetic Biology

The abstraction of attractor landscape is the space where robotics meets SB. In this section, we illustrate this vision by discussing two paradigmatic examples in which a genetic network is used as control software for robots.

4.1 Boolean Network Model of a Simple Genetic Network

An illustrative example of a BN modeling the basic cellular states of a cell is provided by Huang in [26]. This BN is a minimalistic example of a biologically plausible GRN, as the genes regulating functions consist of Boolean encoding of relations that can be typically found among genes in real cells. Here we introduce the model and discuss the properties that are relevant for the purpose of this contribution. The network is composed of four genes, named A, B, C and D. In Figure 1, the relations among genes and their functions are illustrated. The state of the network is given by a binary vector of four components, representing the activation state of the genes. For example, state 0001 represents a situation in which genes A, B and C are inactive, while gene D is active. The network is supposed to update its



C	D	A
0	0	0
0	1	1
1	0	1
1	1	1

A	B	B
0	0	0
0	1	1
1	0	1
1	1	1

A	B	C
0	0	0
0	1	0
1	0	0
1	1	1

C	D	D
0	0	0
0	1	1
1	0	0
1	1	0

Figure 1. Boolean network representing a simple genetic network. Left: graph representing the relations among genes. Right: Boolean functions computed by the nodes.

node synchronously, therefore—in the absence of external perturbations—each state has a unique successor. Under this updating scheme, the dynamics of the network starting from any initial state (i.e., gene activation profile) is a *trajectory* composed of a transient—if any—and a cyclic attractor, which may be a degenerate cycle involving only one state, that is, a *fixed point*. The graph representing all the possible transitions between network states is depicted in Figure 2. We observe that the dynamics are characterized by four attractors: three fixed points 0000, 0100 and 1110 and a cycle of period 2, (1100,0110). The attractors represent the main cell states, as they constitute the steady states in the dynamics of the cell. For this reason, they assume a particular importance, as also shown in the original example by Huang, who associates one specific cell behavior to each attractor. The state space (i.e., the space of all possible gene configurations) can be partitioned into basins of attraction, each containing all the states that, if assumed as initial condition, lead to one specific attractor. For example, the basin of attraction of the cyclic attractor (1100,0110) is composed of the states {1010,1011,0111,1100,0110}.

In the absence of perturbations, after a (possibly empty) transient, a cell rests in one attractor. However, when the network in an attractor is perturbed, it might exit from the basin of attraction of the current steady state and move to another one. Usually, in these models a perturbation affects just one node at a time [27], therefore it is possible to draw the *attractor graph*, which represents the possible transitions between steady states. The attractor graph of the example we are discussing is depicted in Figure 3. The graph is obtained by

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perturbing each node of each attractor and connecting attractor α to attractor β with an arrow from α to β if the perturbation in α produces a trajectory ending in β—or, equivalently, if the perturbation on α produces a state in the basin of attraction of β. In the case of the cyclic attractor of period two, we numbered the states and denoted by a subscript the perturbed genes as a function of the state. We can observe that it is possible that the same gene, if perturbed, leads the trajectory to different steady states, depending on the attractor state in which the gene is perturbed. For example, gene A leads to attractor 1110 if perturbed in state 0110 and to attractor 0100 if flipped in state 1100.

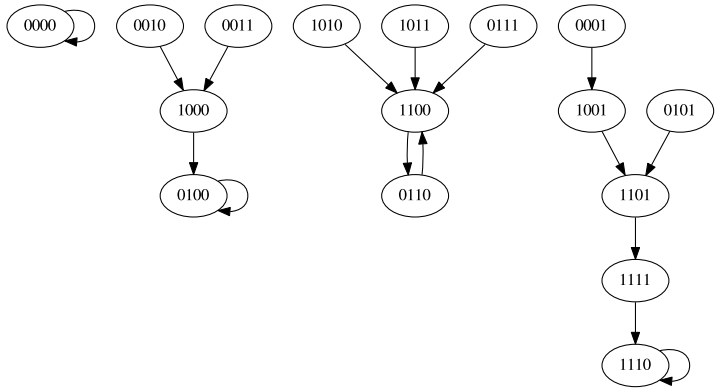

Figure 2. State graph of the network defined in Figure 1. Note the four attractors: three fixed points 0000, 0100 and 1110 and a cycle of period 2 (1100,0110).

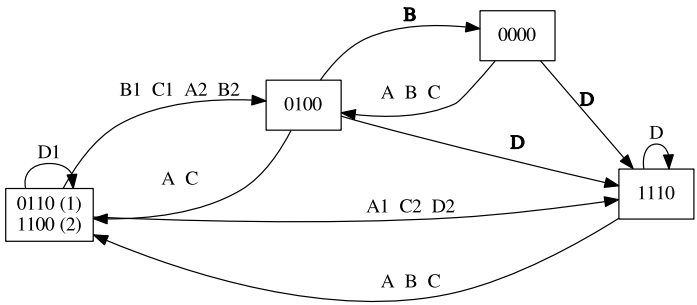

Figure 3. Attractor graph of the network defined in Figure 1. For clarity, the transients are omitted and only macro transitions between attractors are depicted. A transition occurs after the transitory flip of the value of a gene. The labels on the edges denote the genes that, if flipped, cause the transition.

The network described models a typical case of cell dynamics, and it was used in [26] to illustrate the notion of attractors in cell dynamics. In the following subsections, we show how this network can be used to control a robot performing a minimal yet not trivial cognitive task. The key idea is that attractors are associated to robot behaviors, in the same way as they represent cell behaviors in the biological interpretation.

4.2 Example 1: Controlled Phototaxis

In this first example, we exploit the properties of the attractor landscape to control the speed of a robot performing phototaxis, that is, moving toward a light source. Here and in the following case studies, we have directly introduced a mapping between attractors and robot behaviors. However, this mapping can be the result of an adaptive process, as indeed is done in nature, where the interactions between a system (e.g., a cell or even an organism) and the environment emerge as an adaptive process that exploits some regularities in the environment. This process is analogous to the emergence of sensors in nature, where regularities, correlations and sufficiently robust patterns are captured by organisms' parts that assume the role of sensor devices—see [35–38] for a discussion on the evolution of sensors, both in nature and in robotics. Intermediate situations are possible between these two extreme possibilities, such as in the case studies in BN robotics that we have previously mentioned (see Section 3). In those BN-robots, some nodes of the network are directly connected to a sensor (e.g., a light or a proximity sensor), their value is imposed by sensor readings, and actuators are directly controlled by the values of some predefined node. Despite this *a priori* setting, nothing is imposed on the way the network will use the information set on its inputs nor the way it will control the robot actuators, as the connections among nodes and node functions are the result of an evolutionary process. In a sense, we may say that this evolutionary process defines the semantics of the information received and elaborated by the robot.

The attractors of the network are characterized by a different number of active genes, from 0 to 3. This property can be easily exploited as a control factor for the speed of the robot: the larger the number of active genes in the state, the higher the speed of the robot. The control genes are D, which is temporarily switched on when the robot sees the light, and B, which is temporarily deactivated whenever the luminescence gradient perceived by the light sensors exceeds a given threshold. As an aside, we observe that while we are using the terminology typical of robotics, we are just describing a dynamical system interacting with the environment, like a cell. The network starts in

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attractor 0000, which represents the quiescent state where the robot's wheels do not move. When the robot perceives the light, gene D is switched on—as if it were activated by an external molecule. At each control step of the robot, the network updates its state; therefore, after the perturbation occurring on gene D, the network enters the basin of attraction of fixed point 1110, which is reached in a few steps. Then the robot moves toward the light and progressively slows down, as an effect exerted by gene B, which is temporarily suppressed (i.e., set to 0) as soon as the light intensity detected exceeds a fixed value. Eventually, the robot stops when it is close to the light source. Note that the stop state corresponds to fixed point 0000, which is reached from attractor 0100 just by setting B to 0. The video of a representative run is available in the supplementary material [39] as video-01. The same network can be used to control a group of robots performing the same task. We performed this and the following experiments in a simulated environment by the means of ARGoS [40], which is one of the most widespread robotics simulators. The main steps of this dynamics are depicted in Figure 4, and a video of the simulation is available as video-02.

In case this network is used to control the behavior of a swarm of robots, one may want to attain a final situation in which robots are evenly distributed across the light sources, similarly to clustering phenomena in cell biology. To attain this goal, the very same network can be used, and gene D is activated as long as the robot density perceived by a robot (through its proximity sensors) exceeds a given threshold. In this way, the temporary activation of gene D moves the network to the attractor corresponding to the maximal speed, so that the robot has the chance to move and find another less crowded light source. The main phases of these dynamics are depicted in Figure 5, while the video of a typical simulation is available as video-03.

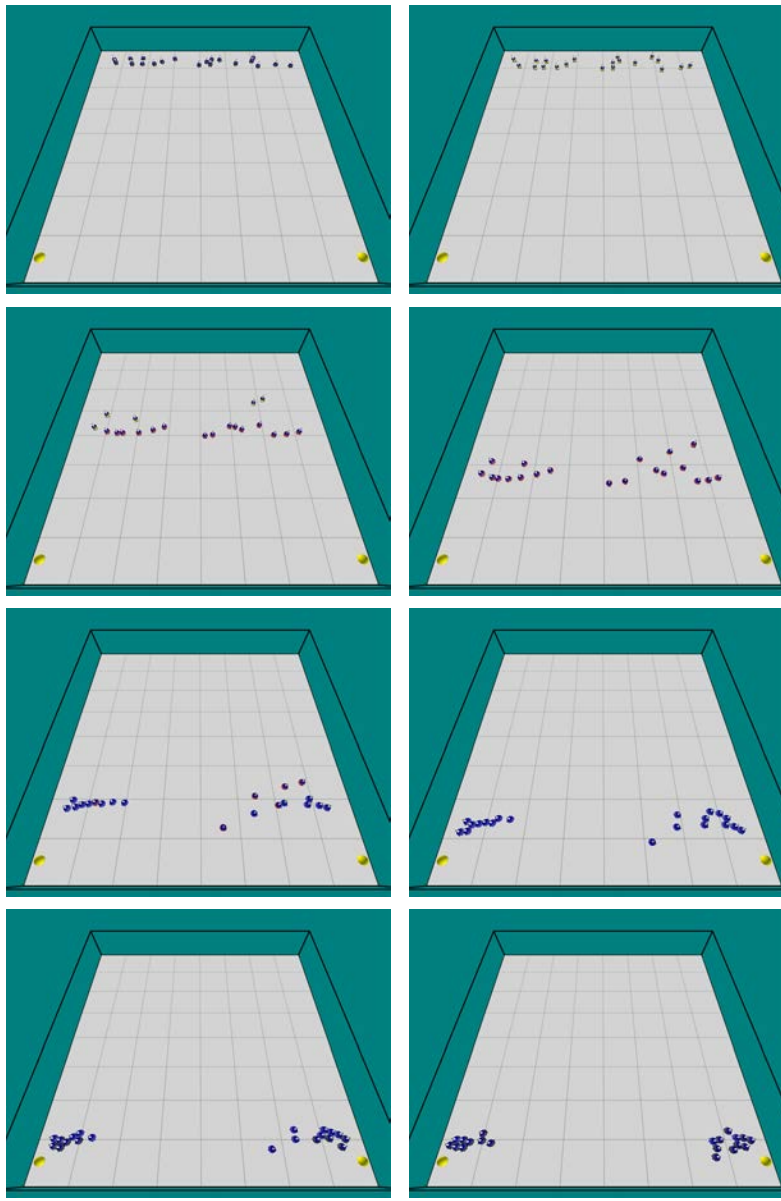

Figure 4. Main phases of the phototaxis behavior of a group of robots (from top to bottom and left to right). Robot colors denote their attractor (and consequently, their speed): black → 0000, yellow → 1110, red → (0110, 1100), blue → 0100.

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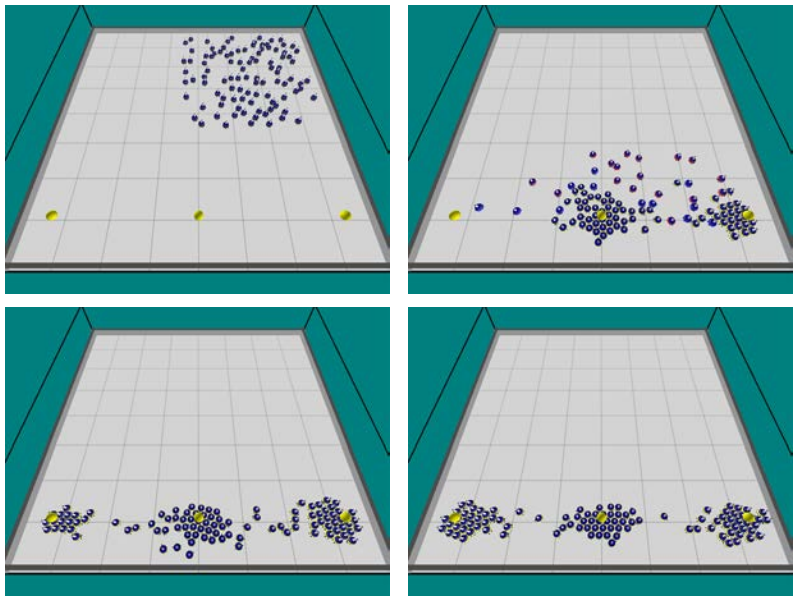

Figure 5. Main phases of the phototaxis behavior of a group of robots (from top to bottom and left to right), trying to gather around a light source so as to split into approximately equal groups. Also in this case, robot colors denote their attractor (and consequently, their speed): black → 0000, yellow → 1110, red → (0110, 1100), blue → 0100. Note that robots in a dense group are colored yellow; that is, they are moving at a high speed. Therefore, in this case, the equilibrium reached at the end of the run is dynamic, rather than static.

4.3 Example 2: Actions Triggered by an External Stimulus

As a second example of the use of the dynamical properties of a cell model, we show an alternative approach to encode inputs and outputs in the network. In the previous example, the mapping between cell model and robot was achieved by temporarily setting some gene to a specific activation state and using the entire genetic profile to decide the actions the robot should take (in the previous case, the speed of the robot). Another approach consists in directly connecting some genes of the network to external inputs—that is, treating them as receptors—and using the value of some specific genes to directly control some low-level robot actions. In the example we discuss here, we consider a simple scenario in which a robot is placed in a corridor that has to be traversed so as to reach a target. In Figure 6, the initial situation is depicted; the target is represented by a light source, but it may be any source of a signal that the robot can perceive, such as

sound or temperature. On the biological side, this source can be any chemical source, and the phenomenon would be chemotaxis. The network controlling the robot is the same as the one used in the previous example, just with a different encoding of inputs and outputs.

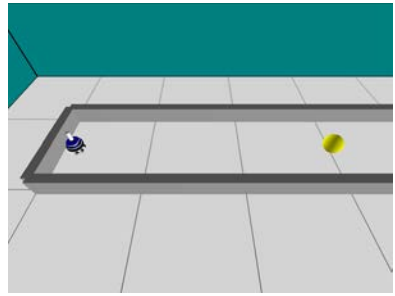

Figure 6. Corridor scenario: the robot points toward a goal and its movement is triggered by an external stimulus.

Here we suppose that an input gene is clamped to 0 or 1 as a consequence of an external signal; when a network node is forced to a constant value, the network state graph changes and some transitions (along with some states) no longer exist. To adhere to the biological framework depicted by Huang, we suppose that signals exert their effect on the network to condition the transitions from an attractor to another one. In this way, attractors still represent the main behaviors of the robot, and the transitions between them are achieved by clamping a node to a constant value so as to control the transient from an attractor to another one.

In the scenario we discuss in this example, the control gene is again D and the output gene is A, which acts as a binary selector: if $A = 0$, then the robot holds; otherwise, it moves straight forward. The initial state is the quiescent one (0000) and, when an external signal is performed (e.g., a sound) and during the time interval it is perceived by the robot, gene D is clamped to 1. As shown in Figure 7, as soon as D is set to 1, the network state moves to 0001 and, while $D = 1$, the network trajectory eventually reaches 1111, which is a fixed point as long as $D = 1$. We may call this particular steady state a *conditional attractor*, that is, an attractor conditioned to an external conditioning on some genes, to distinguish this case from that of *original attractors*, which are the ones characterizing the *autonomous* dynamics of the network. In the context of dynamical systems, an autonomous system has no inputs and it is subject to an internal dynamics. Once this conditional attractor is reached, the external stimulus can be detached from D and the network freely reaches the original fixed point 1110. Along this trajectory, gene A is always 1 and so the robot moves

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straight. The possibilities opened by clamping one or more genes to a specific value until a new attractor is reached make it possible to also introduce a stopping condition to this behavior: when we want the robot to stop, both C and D have to be clamped to 0, and so after two steps a new conditional attractor is reached with $A = 0$ and the robot stops. At this point, the plasticity of the network enables us to again control the movements of the robot toward the light source by keeping C clamped to 0 and activating or inhibiting D, which then will act as a switch to make the robot move and rest. Videos of these behaviors can be watched at [39] as video-04 and video-05.

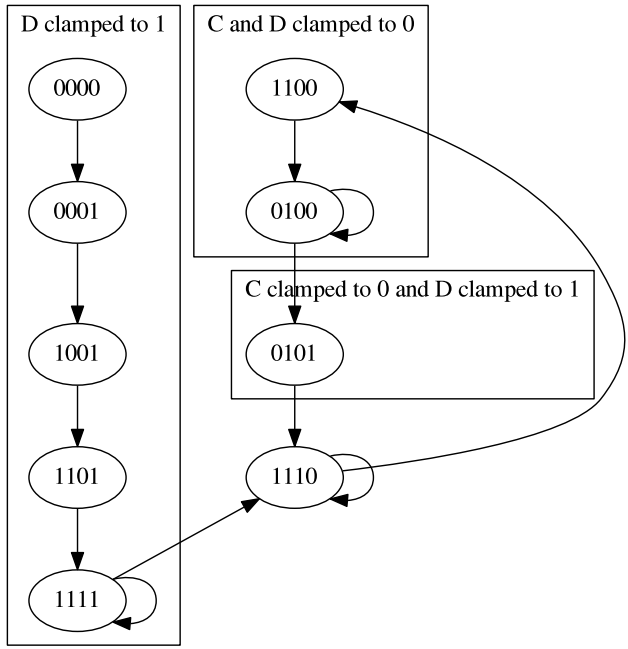

Figure 7. State graph of the network controlling the robot. While the network is the same as the one in the previous example, its state graph is different because some genes are clamped to either 0 or 1 from an attractor until a new attractor is found.

5. Conclusion: Implications for Robotics and Synthetic Biology

We believe that the notion of attractor landscape provides an effective abstraction level for cross-fertilization between robotics and synthetic biology (SB). On the one hand, robotics may exploit advances in SB so as to devise unconventional control systems. Indeed, the examples we have presented in the previous section illustrate a viable approach

to combining robotics and SB, which consists in exploiting synthetic cellular circuits to control robots. This "understanding by building" cross-discipline methodology can produce unforeseen developments in both fields. Indeed, results obtained from the evaluation—in simulation or in the real world—of robots designed to exploit these cellular synthetic bricks may provide biological insights and hypotheses to motivate new experiments, which in turn may lead to the construction of new bricks. In addition, this approach opens the possibility of designing and building hybrid robots, also made of biological components. Typical scenarios of such creatures are environments where human exploration is not possible, such as oceans, human and animal bodies and also plants, where swarms of micro-robots may collectively accomplish a mission. On the other hand, the design of synthetic cellular systems may be formalized in terms of an embedded agent perceiving the environment and acting on it—as is done in robotics—and design techniques for control software in robots may be used in SB design.

We are aware that the approach we have sketched is more a vision, rather than an actual research project. However, we strongly advocate the use of high-level concepts from dynamical systems, and in particular, attractor landscapes, not just as metaphors but as design guidelines. In addition, we believe that this level of abstraction can provide a common vocabulary and a shared set of categories between researchers in artificial intelligence and SB, and that this bridge between cell and robot dynamics is worth pursuing in the future.

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