Evolutionary design of soft-bodied animats with decentralized control

**Michał Joachimczak · Taras Kowaliw ·
René Doursat · Borys Wróbel**

Abstract We show how a biologically inspired model of multicellular development combined with a simulated evolutionary process can be used to design the morphologies and controllers of soft-bodied virtual animats. An animat's morphology is the result of a developmental process that starts from a single cell and goes through many cell divisions, during which cells interact via simple physical rules. Every cell contains the same genome, which encodes a gene regulatory network (GRN) controlling its behavior. After the developmental stage, locomotion emerges from the coordinated activity of the GRNs across the virtual robot body. Since cells act autonomously, the behavior of the animat is generated in a truly decentralized fashion. The movement of the animat is produced by the contraction and expansion of parts of the body, caused by the cells, and is simulated using a physics engine. Our system makes possible the evolution and development of animats that can run, swim, and actively navigate toward a target in a virtual environment.

M. Joachimczak (✉)
Graduate School of Information Science, Nagoya University,
Nagoya, Japan
e-mail: mjoach@gmail.com

M. Joachimczak · B. Wróbel
Systems Modeling Laboratory, Institute of Oceanology, Polish
Academy of Sciences, Sopot, Poland

T. Kowaliw · R. Doursat
Institut des Systèmes Complexes, Paris Île-de-France (ISC-PIF),
CNRS, Paris, France

R. Doursat
School of Biomedical Engineering, Drexel University,
Philadelphia, USA

R. Doursat
Erasmus Mundus Masters in Complex Systems Science, École
Polytechnique, Paris, France

B. Wróbel
Evolutionary Systems Laboratory, Adam Mickiewicz
University, Poznań, Poland

1 Introduction

When the global behavior of a system is an emergent, unpredictable phenomenon resulting from complex interactions among a large number of simple components, evolutionary computation offers a potential means of discovering solutions that would otherwise be difficult to conceive by a human designer. Evolved solutions, even the purely simulated ones facing the "reality gap" [18], can provide new ideas and insights into how a given problem can be solved. The evolutionary approach applied to robotics, evolutionary robotics, is particularly relevant in new, biologically inspired disciplines such as modular or swarm robotics, for which proven engineering paradigms have not yet been established. An especially recent and active research field in this category is soft robotics, where robot elements can bend and reshape themselves to generate various gaits or to navigate a limited space. New ideas for elastic locomotion are currently explored, whether in simulation [3, 7, 21, 23, 24, 28, 32] or physical implementations [2, 10, 27, 30, 31], and the search for improved materials with desired properties is under way.

In this paper, we consider the problem of automatically co-designing the morphology and control of virtual soft-bodied robots. To explore the space of possible solutions,

we apply a genetic algorithm to a simulated developmental process that guides the construction of the robot body from a single cell. Inspired by the self-generation capabilities of complex multicellular organisms, our approach couples artificial development with artificial evolution, and thus can be termed "artificial evo-devo". In that sense, it belongs to a family of works called artificial embryogeny, which feature the bio-inspired growth of body plans at various levels of complexity, based on elements such as rods [17], primitives and joints [22, 29], or artificial "cells" [1, 4, 5, 6, 8, 19, 20, 25], as is the case here.

In designing our system, we assumed that robots could be made of a uniform elastic material able to modify its volume locally. The artificial cells from which a robot body develops contain the same genome, characteristic of a particular individual. A genome is linear and consists of interrelated "regulatory units" (groups of regulatory and product-coding elements), which map to the nodes of a gene regulatory network (GRN) controlling the cell's behavior. Development fundamentally depends on cell division by which the body can grow in size and shape. During growth, "chemical products" are released by the cells, diffuse across the body, and can be detected by other cells, thus supporting signal-based differentiation. Cells also interact via the simulated physical world—they have a mass, and neighbor cells are connected by springs. The lattice of physical connections delineates internal chambers that can act as a hydrostatic skeleton. Altogether, the combination of virtual spring-mass mechanics and fluid dynamics creates an emergent effect of locomoting animat without central control. Particular gaits arise from the independent, yet coordinated actions of the cells.

We review here the ability of our system to generate functional soft animats in three tasks: walking, swimming, and chemotactic behavior. We report on previous experiments showing swimming animats in a fluid environment (more details in [12, 13, 15]), and extend them with new, preliminary results on walking creatures. The following sections provide a brief description of the genetic and developmental model used in our system, then explain and demonstrate the mechanisms of evo-devo animat design.

2 Developmental model

The evolutionary development of soft robot bodies that we present here is a modified version of Joachimczak and Wróbel's original model of 3D multicellular evolution [14], called GReaNs for "Genetic Regulatory evolving artificial Networks". In this section, we provide an overview of the essential aspects of GReaNs, referring the reader to previous papers [12, 13] for a more detailed description.
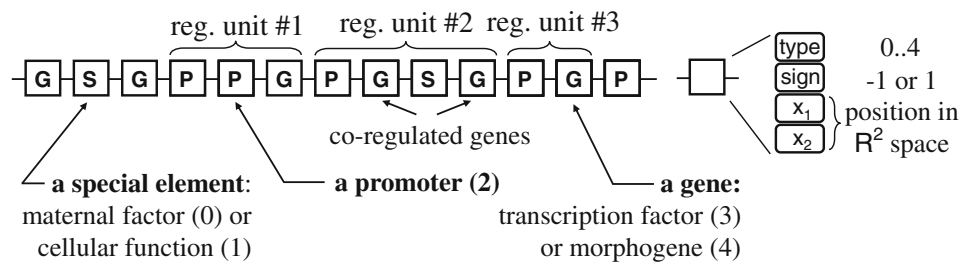
This model is an abstraction of biological processes that occur on three separate levels and time scales: (i) gene regulation through gene products binding to regulatory regions, (ii) cell interactions via diffusion of morphogens and simulated physics, and (iii) evolution of linear genomes by mutations: point mutations (which modify affinities between gene products and regulatory regions), gene duplications, and gene deletions.

2.1 Genome model

A genome in GReaNs is represented by a list of genetic elements without limitation in size. It encodes the topology of a GRN acting as a controller of cell behavior. The genetic elements belong to three classes: (i) genes, coding for products, which play the role of trans-regulators, (ii) regulatory elements, which act as cis-regulators, and (iii) special elements, which encode factors and signals. Trans-regulators can be transcription factors, which are products acting only in the cell in which they are produced, or morphogens, which are products diffusing between cells. Factors are products representing the outputs of the GRN, and signals are trans-regulators representing inputs of the GRN.

The GRN is composed of nodes, which correspond to regulatory units in the genome. Each unit is a series of cis-regulators followed by a series of elements coding for products (Fig. 1). The products encoded in the same regulatory unit are synthesized at the same rate, which is a function of the concentrations and affinities of the trans-regulators binding to the cis-regulators of the unit. Connectivity in the GRN is based on the affinity between trans- and cis-regulators, and this affinity is determined by the proximity between two abstract 2D points representing these elements in $\mathbb{R}^2$ space. Proximity between two such points means that the trans-regulator "binds" to the cis element, hence influences the synthesis rate of the products encoded by the unit. The position of the points is encoded by two fields in the genetic elements representing "coordinates". Another field, the "sign", controls whether the cis/trans interaction is excitatory (same signs) or inhibitory (opposite signs). Morphogens produced by one cell can bind to regulatory elements of other cells and influence their behavior remotely. During the lifetime of a cell, each product is represented by its real-valued concentration in [0, 1]. Concentrations change gradually in discrete time steps and degrade exponentially.

The special elements give cells the possibility to interact with the environment by sensing external inputs and performing actions. External inputs create signals that, in the same way as cell products, can bind to the

reg. unit #1   reg. unit #2   reg. unit #3

co-regulated genes

a special element:
maternal factor (0) or
cellular function (1)

a promoter (2)

a gene:
transcription factor (3)
or morphogene (4)

type   0..4
sign   -1 or 1
x_1 } position in
x_2 } $\mathbb{R}^2$ space

Fig. 1 Genome (*left*) and structure of a genetic element (*right*). Each element consists of a type field, which specifies its class (*G* gene, *P* regulatory, *S* special), a sign field, and *N* abstract coordinates (here, $N = 2$), which determine its affinity to other elements based on a distance in $\mathbb{R}^N$

regulatory elements of a cell's GRN, except that their concentration is determined outside of the organism. Signals include "maternal signals" (morphogens deposited in the egg), whose perceived concentration depends on a cell's position in space, and other chemical signals such as the ones used in chemotaxis experiments. Outputs of the GRN (factors) comprise a "division factor" (whose concentration triggers cell division above a certain threshold), an "axis factor" (which causes cells to rotate their axis of division, i.e., their cleavage plane), and "expansion and contraction factors" (which make cells expand or contract regions of the body around them during locomotion).

2.2 Multicellular development

The developmental process starts from a single cell and proceeds through multiple divisions. Each cell of the body contains the same GRN, but the concentrations of products, factors, and perceived signals vary depending on this cell's spatial position and neighborhood. A cell can divide and produce a daughter cell, whose own axis of division can differ from its mother's. Cell divisions push the existing cells away, causing movements based on elastic collisions, adhesion, and fluid drag, which all contribute to shaping the final morphology.

Before evaluating the performance of a fully developed animat on a given task, we compute the connectivity between cells using a Gabriel graph [9]. This creates a nonconvex shape, in which two cells are connected if no third cell is located in the smallest circle passing through them. In the original version of our model [12, 15], graph computation took place only once, after development was finished. In a more recent version [13], the graph was computed continually as the embryo was growing (Fig. 2). Concerning the physical interactions between cells, the choice of graph also influences how mutual adhesion and repulsion are calculated. Here, instead of defining the neighbors within a certain radius (metric neighborhood), they are given by the Gabriel connectivity (topological

(a) t=0   **(b)** t=98   **(c)** t=142   **(d)** t=218

(e) t=267   **(f)** t=285   **(g)** t=400, final shape
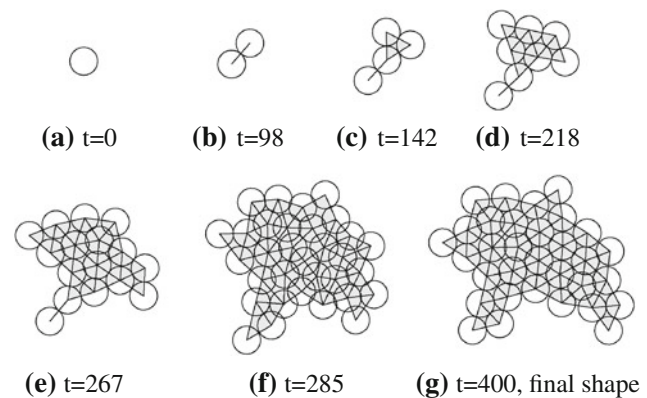
Fig. 2 Example of developmental mechanics (individual shown in Fig. 4, *left*). Cells are represented by *circles* of radius *r* and connected by springs of resting length 2*r*

neighborhood). The two versions of the model differ in the way that morphogens diffuse. In the continual graph computation, a morphogen produced by a cell reaches only its graph neighbors, and its total amount is conserved (divided) over the neighborhood. When the graph was computed only at the end of development, all cells were considered potential sources, thus the concentration of a morphogen in one cell was the sum of all these contributions, each of them calculated as a decreasing function of distance (and also delayed in time proportionally to the distance).

Development is simulated during a fixed number of time steps, typically 400. After development halts, the connectivity between the cells is "frozen" and does not change during the locomotion stage of the animat's life. For computational reasons, we also use a hard limit on the total number of cells, for example 32. This limit was almost always reached by the fittest individuals, since neither the number of cells nor the quantity of actuators (the springs between cells) was penalized. Thus, a larger animat increased its ratio of available power (proportional to its volume, i.e., surface area in 2D) over drag forces (proportional to its cross section).

2.3 Animat movement

Each developed animat is treated as a spring-mass system, in which cells correspond to point masses and neighboring cells are connected by elastic springs. The natural resting length of a spring, L_{ij}^0, is equal to the distance between the cells i and j that it connects at the end of the developmental stage. Cells also produce factors that can temporarily reduce or increase the resting length of all the springs attached to them as follows:

$$L_{ij} = \left(1 + 0.2(e_i + e_j - c_i - c_j)\right)L_{ij}^0 \tag{1}$$

where e_i, e_j, c_i, and c_j represent, respectively, the concentrations of "expansion factors" and "contraction factors" produced by cells i and j. These variations result in the expansion or contraction of the areas surrounding the cells. Furthermore, to prevent excessive deformations, such as overlaps between springs, we introduce a reaction mechanism in the form of a *hydrostatic skeleton*. It means that each polygonal region of the body delimited by springs also acts as a pressure chamber that can resist changes in volume (i.e., surface area here). Pressure forces F_p act outward, perpendicularly to every edge of the region and proportionally to its current length L:

$$F_p = c_p \cdot L \cdot \left(1 - \frac{S}{S_0}\right) \tag{2}$$

where S and S_0 represent the current and equilibrium surface areas of the region, and c_p is a global coefficient controlling the body's resistance to compression.

3 Genetic algorithm and evolution

In all the scenarios discussed in this paper, we used a genetic algorithm to evolve 3D morphologies (as in [16]). The population size was constant at 100 individuals, and selection was based on elitism, tournament selection, and multipoint crossover during sexual reproduction of 20% of the population. Genetic operators could modify either a genetic element (e.g., by changing its coordinates) or the whole genome, by deleting a sequence of elements or duplicating and inserting them at random locations. Evolutionary runs were initialized with a population of randomized individuals. A run was terminated when 500 generations passed without improvement. The experiments described in this paper lasted a few thousand generations.

For each individual, the developmental stage covered 400 GRN time steps, while the locomotion stage was of the order of 2,000 time steps. The fitness function and exact protocol used for the locomotion phase depended on the problem and are described in the sections below.
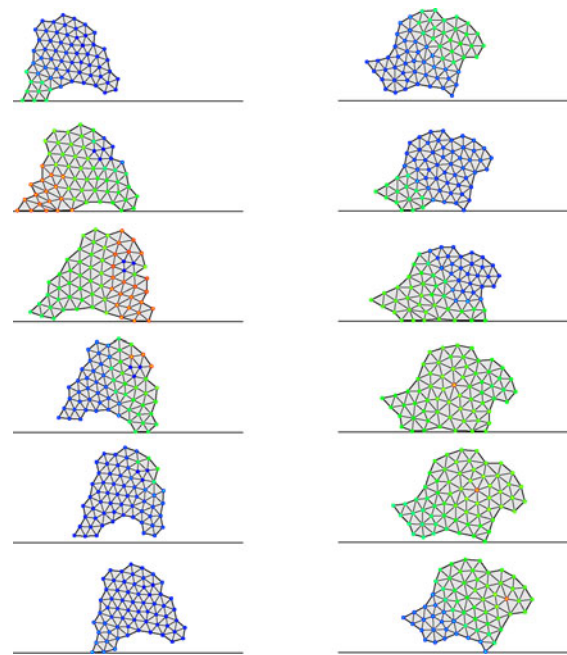
Fig. 3 Examples of gaits where animats lifted themselves off the ground. *Left* one individual "ran" by swinging from one appendage to another and floating above ground in-between. *Right* another individual used its internal elasticity to jump forward. *Colors* indicate whether the cell was contracting (*blue*), expanding (*red*) or at equilibrium (*green*). Both individuals were evolved under a hard limit of 64 cells. Videos available at: http://youtu.be/uVD47xGwdbU and http://youtu.be/2ijecKYe5u4

4 Results

We have successfully applied our evo-devo system to three tasks: ground locomotion, swimming in a fluid-like environment, and chemotactic navigation toward a target (also in a virtual fluid). In all cases, neither the morphology nor the type of motion control was prespecified or in any way explicitly favored. All obtained solutions demonstrated the creative potential of the evolutionary process under the specified fitness.

4.1 Evolution of walking behaviors

To allow for the evolution of walking gaits, we introduced a flat rigid ground in the environment (here, a straight line) and enabled gravitation. Nodes on the outline of an animat in contact with the ground were also subject to friction forces. Since the world was 2D, the animat could move to the left or to the right. The developmental stage occurred in weightlessness to avoid skewing morphologies toward flattened individuals. This is not very different from animal morphogenesis, where the embryo is insulated from the effects of the environment that it encounters after birth (gravitational pull is negligible compared to density in an egg or a womb).

Turning on gravity at the end of development introduced a discontinuity into the system. Since there was no sense of up or down during development, the animat could not be expected to stand still once it was dropped. Rather, it tumbled and fell on one of its sides (a portion of the 1D contour of the shape). To prevent the evolutionary process from exploiting the energy of this sudden, artefactual movement, we initialized each animat as follows. First, given a random global orientation, the lowest node at the periphery was put in contact with the ground. Then, we allowed the physics simulation (gravity vs. ground forces) to proceed for a transitional period until the structure stabilized. Only then was the dynamics of the GRN resumed, and the subsequent locomotion taken into account by the evolutionary process. The fitness function was designed to reward the total distance traveled during the allowed lifetime of an animat, starting from the stable position.

Under these conditions, we were able to identify three main classes of organisms that were able to solve the walking challenge and emerged repeatedly across evolutionary runs. The first class relied on the elasticity of the structure to make forward "jumps" iteratively. One example individual (Fig. 3, right) was driven by a wave of cellular contractions that propagated from its back to its front, first lifting the rear protrusion off the ground, then the front one.

The second class of solutions employed a motion pattern akin to "running". The morphology of the animats in this class was supported by two protrusions, or "legs" (Fig. 3, left). Here, the agent's elasticity was also exploited by a wave of contractions propagating from the back to the front of the animat. This caused the center of mass to oscillate between the front and rear protrusions, which lifted themselves off the ground between waves. This type of strategy was the fastest we observed.

The third class of solutions (Fig. 4) was characterized by the presence of a larger mass of cells on either the front or the rear of the body. Here, organisms exploited shape changes to cyclically shift their center of gravity and drive the motion. One individual (Fig. 4, left) expanded a cell mass on its back, causing one protrusion to bounce off the ground and push the whole mass toward the front. Only the rear cells of this animat were actuating. The second example organism (Fig. 4, right) kept bending a cell mass forward, which resulted in temporarily increased friction on the front appendage and pulled the back part of the body forward.

4.2 Evolution of swimming

For the evolution of swimming gaits, we introduced a simulated fluid to create drag forces by acting on the edges that belonged to the outline of an animat. We modeled this
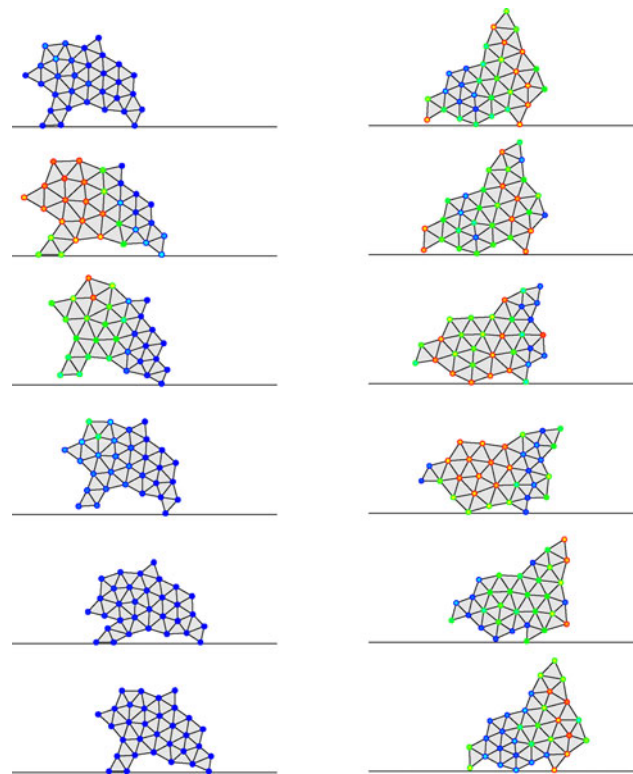

Fig. 4 Examples of "walking" individuals that could never entirely lift themselves off the ground during motion. *Left* one individual relied on a pulsating mass of cells on its back to bounce its rear appendage off the ground. *Right* another individual repeatedly bended a mass of cells on the front to pull the rest of its body forward. Colors indicate whether the cell was contracting (*blue*), expanding (*red*) or at equilibrium (*green*). Both individuals were evolved under a hard limit of 32 cells. Videos available at: http://youtu.be/8uhxZEiREQo and http://youtu.be/C1z0eUR4vbY

virtual fluid after an original simulation of undulatory robotic locomotion by Sfakiotakis and Tsakiris [26]. It assumes a stationary fluid where only the spring-edges on the outline of the animat are subjected to drag. The total force F exerted on an edge of length L is the sum of a tangential component $F_T = -d_T L v_T^2 \text{sign}(v_T)$ and a normal component $F_N = -d_N L v_N^2 \text{sign}(v_N)$, both proportional to the squares of the respective velocity components v_T and v_N via drag coefficients d_N and d_T (where $d_N = 200 \, d_T$).

We have analyzed the detailed motion patterns obtained by this approach in two recent publications [12, 15]. To summarize, we observed a number of recurring strategies, among which three commonly encountered patterns: (a) use of protrusions, (b) undulatory locomotion, and (c) "jellyfish-like" movements, which are shown in Fig. 5.

The swimming patterns were found to rely on cyclically contracting cells, with a phase gradient that depended on the type of gait. (a) For individuals employing symmetric protrusions to propel themselves forward, the oscillations of cell actuation exhibited a phase shift along the anterio-

Fig. 5 Example individuals evolved for their swimming abilities. The plots under each individual show the actuation patterns of two particular cells overtime. *Vertical axis* value 1 corresponds to the maximum expansion signal, and −1 to the maximum contraction signal for the resting length of the springs. Reproduced from [12]. Corresponding videos available at: http://youtu.be/vYBJS7V0s-g, http://youtu.be/I2GHEFCt738 and http://youtu.be/BiE_SVVjFm0
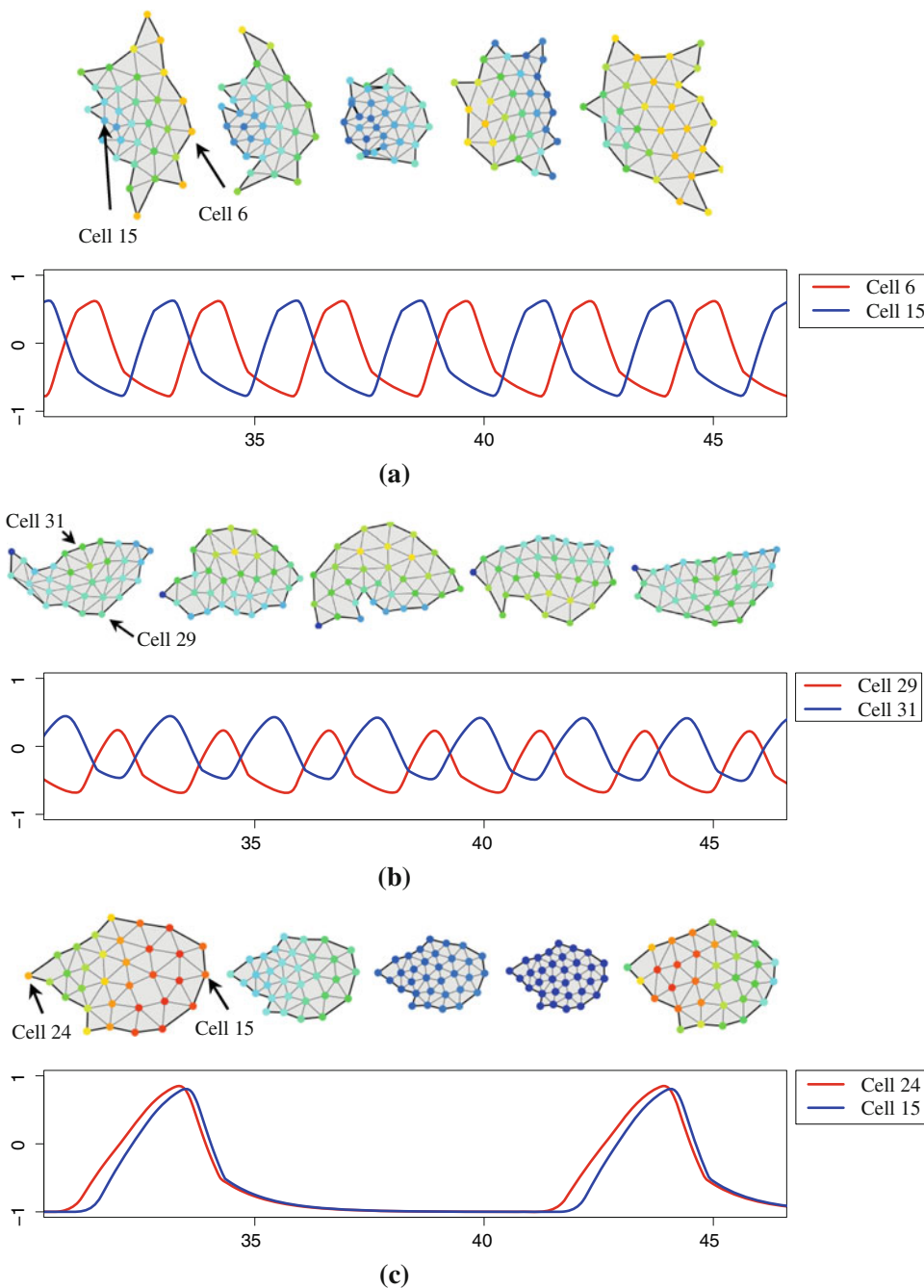
posterior axis. This resulted in a wave of contractions propagating from the back to the front of the animat. (b) Individuals relying on undulatory movements (Fig. 5b) were elongated in the direction of motion and developed a half-period phase shift along the lateral body axis. They were, in effect, driven by a wave of contractions propagating along this axis. (c) The jellyfish-like individuals employed an almost synchronous contraction across their whole body (Fig. 5c). This type of gait exploited the fact that fluid drag was proportional to velocity squared:

directional motion resulted from a whole body pulsation involving a difference in speed between contraction and expansion and the existence of a pointy end on the body.

Although each evolutionary run ended with a different solution, we observed that in an environment with low fluid drag, i.e., a less viscous fluid, the fastest individuals were the ones using protrusions (Fig. 5a). Under high-drag environments, however, the fastest solutions were elongated in the direction of motion and employed some form of undulatory movement.
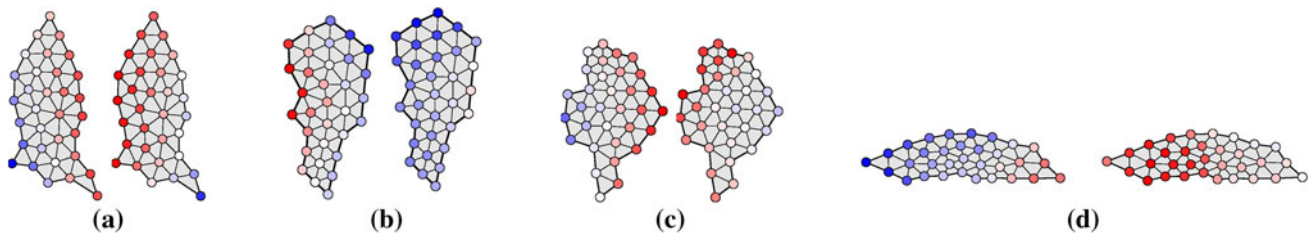
Fig. 6 Change in average cell activation (i.e., concentration of expansion minus contraction products) when moving toward a food particle from the left or right side to the front of an individual. *White* cell: no change; *blue* average activation is lower; *red* higher. The four pairs from **a** to **d** correspond respectively to individuals #1 to #4. All animats shown moving upward. Reproduced from [13]. Corresponding videos available at: http://youtu.be/zi3p164aefY, http://youtu.be/TS8Q0JfI7o0, http://youtu.be/-HoN7ZGU6W4 and http://youtu.be/rvM2T8gpDnU

4.3 Evolution of chemotaxis

In the third task, we wanted to obtain virtual swimming animats that could sense their environment and use this sensory information to approach a target placed at an arbitrary location. This was realized by letting the target emit a chemical "scent", whose concentration decreased linearly with the distance and could be detected by all the cells of the organism. To facilitate detection of this signal, we allowed the concentration of the associated factor to vary between 0 and 10. Although previously obtained motion strategies could in principle be used as starting points for the evolution of the chemotactic behavior, we preferred avoiding any bias toward a particular solution. We were interested to see if the evolutionary search could produce animats that were capable of moving and showing chemotaxis entirely de novo.

Trying different versions of the fitness function, we found that the chances of discovering chemotaxing individuals were best if, beside rewarding the ability to approach a target, we also explicitly rewarded the ability to move forward. To this effect, we used a fitness function that consisted of a set of tests. First, it assessed the ability of the animat to move forward in the absence of a target. Then, based on a calculated direction of motion, a target would be placed either on the left or on the right of the animat's projected path. Since moving efficiently is a prerequisite to chemotaxis, rewarding forwardness helps the search algorithm find more promising domains in genomic space.

As in the simple swimming task, independent evolutionary trials under the same environmental settings produced diverse solutions in the chemotaxis task (Fig. 6). Various strategies for turning toward the target spontaneously emerged. Analyzing the set of these evolved strategies, we found that the most common type of solution relied on some form of synchronized pulsation across the whole body (Fig. 6a–c) similar to the jellyfish-like motion observed in the swimming experiments (Fig. 5c). This strategy was often combined with an additional way to generate thrust, such as wiggling a tail-like appendage

(e.g., Fig. 6b,c). A few animats employed symmetric appendages to propel themselves (Fig. 6d), which constituted one of the fastest method.

To understand how the animats accomplished turns, we analyzed them by comparing the average expansion of cells in the body between moving forward and turning either left or right in response to a target. Although the strategies for the forward motion of the animats varied, there was a clear difference in average contraction between the left and right sides of the body, depending on the direction of turn. Interestingly, the intuitive solution of contracting the side closer to the target (which reduces the drag on this side and causes a turn; Fig. 6a,c,d), was not the only option—some animats turned by contracting the opposite side more (Fig. 6b). Further analysis allowed us to investigate whether the strategies were purely "reactive", i.e., each cell was simply modulating contraction in response to concentration, or not. Although it was the case in some of the individuals (Fig. 6a), other motion patterns exhibited more complex interactions between the external chemical signal and the internal state. We refer the reader to the original paper [13] for a more in-depth analysis of the turning strategies.

5 Summary and future work

Our results show how a biologically inspired model of development can tap into the creative potential of evolution to achieve the automatic design of nonrigid robots well suited to various locomotive tasks. We demonstrated the success of an evo-devo approach in this new domain, where engineering methods are still emerging. Most importantly, in all our experiments evolution started de novo, i.e., without prior assumptions about the preferred types of morphologies or locomotion. Obtained solutions were neither bounded nor influenced in any way by existing engineering paradigms. In this sense, we share the view that the ability to discover nonintuitive yet efficient strategies is one of the most important features of evolutionary design [11].

These experiments can serve as a starting point and a source of inspiration for physically realistic 3D hardware implementations. In fact, our virtual soft bodies composed of locally expanding and contracting material are not far from current physical prototypes of elastic robots, for example crawlers with internal chambers in which pressure change actuates the body [27], or robots made of materials such as foam that differentially expand in response to external pressure change [10].

Also inherent to our approach is the lack of any central controller. The behavior of the evolved multicellular animats emerges from the collective action of cells that make independent "decisions". This already demonstrates how much of soft-bodied control can be realized owing entirely to local rules. It will be interesting to investigate further, in other scenarios, the benefits of this type of decentralized control in which cells react only to signals coming from their immediate neighborhood. In particular, we want to introduce noise in the system, or see if the shape can undergo local deformations when trying to walk over an obstacle or fit into a small opening. We are currently conducting experiments where new forms of local communication between cells can emerge, to explore the benefits this would bring in the case of damaged or failing components.

Another issue not addressed in the current system is energy efficiency. In the experiments described here, all cells were allowed to be actuators. Since energy was not limited, and since more active cells contributed to higher forces and generated greater motion, most of the successful individuals exploited all of their cells to move. Given the elastic structure of the virtual robot, however, it is likely that other energy-efficient motion patterns are also possible. These would involve only a subset of the cells while using other parts of the body as a passive medium to store and transfer potential energy between the springs. Modifying the fitness function to promote energy efficiency should help to improve the relevance of solutions to future physical instantiations.

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