GROWMORPH: BACTERIA GROWTH ALGORITHM AND DESIGN

SALEH KALANTARI\(^1\) and MOHAMMAD HASSAN SALEH TABARI\(^2\)
\(^1\)Washington State University, United State of America
\(^1\)saleh.kalantari@wsu.edu
\(^2\)Pars University, Iran
\(^2\)mohammadhassan_salehtabari@yahoo.com

Abstract. GrowMorph is an ongoing research project that addresses the logic of bacterial cellular growth and its potential uses in architecture and design. While natural forms have always been an inspiration for human creativity, contemporary technology and scientific knowledge can allow us to advance the principle of biomimesis in striking new directions. By examining various patterns of bacterial growth, including their parametric logic, their use of responsive membranes and scaffolding structures, and their environmental fitness, this research creates new algorithmic design and construction models that can be applied through digital fabrication. Based on data from confocal microscopy, simulations were created using programming language Processing to model the environmental responses and morphology of the bacteria’s growth. To demonstrate the utility of the results, the simulations created in this research were used to design an organically shaped pavilion and to suggest a new digital knitting process for material construction. The results from the study can inspire designers to make use of bacterial growth logic in their work, and provide them with practical tools for this purpose. Potential applications include novel designs for responsive surfaces, new fabrication processes, and unique spatial structures in future architectural work.

Keywords. Synthetic Biology; Architecture; Bio-fabrication; Bio-constructs; Design Computation.

1. Introduction

Architects have always looked to the natural world for inspiration, and today’s algorithmic technology opens exciting new horizons for incorporating biological growth patterns into the realm of design and fabrication. Recent work in this area has only begun to explore the possibilities of using biological systems either as a
model for design algorithms (Duro-Royo et al. 2015) or as an actual component in fabrication processes (Araya, Zolotovsky, & Gidekel 2012). Organic processes are an ideal model for sustainable architecture, as evolution has produced brilliant arrangements that often produce little or no waste while remaining strong, durable, adaptable, and flexible (Discher, Janmey, & Wang 2005; Philp & Stoddart 1996; Vincent 2012). Our ability to model organic processes in architecture and construction is still in its infancy, as we have not yet even begun to approach the level of sophistication that is seen in the natural world (Benyus 1997; Oxman et al. 2012; Vincent 2012).

GrowMorph is a research project that advanced our knowledge in the area of bio-mimetic architectural design by analyzing the logic of bacterial cellular growth. By examining various patterns of bacterial growth, including their parametric logic, their use of responsive membranes and scaffolding structures, and their environmental fitness, this research creates new algorithmic design and construction models that can be applied through digital fabrication. This investigation stands at an interface between biological systems and architectural design, using computational techniques to simulate and model biological processes.

2. Nature-Inspired Morphogenesis

In the natural sciences, the term “morphogenesis” is used to describe how structures develop in geological formations and biological organisms. Recent decades have seen a growing interest among architectural designers in studying these natural processes as a way to inform human-created structures. Evolution has in many cases produced designs that are remarkably efficient in terms resource-use while remaining durable and resilient in variable environmental conditions (Reap, Baumeister, & Bras 2005; Vincent 2012; Vogel 1998). Contemporary design and construction technology offers exciting new opportunities to take advantage of strategies derived from the natural world. For example, Kreig and colleagues (2012) drew from biomechanical studies of the sea urchin’s form to develop a new type of jointed structural system. Ortega and colleagues (2000) used the model of organic tissues to develop new materials that are “self-healing” and tolerant of structural faults.

One of the most exciting areas of development in nature-inspired morphogenesis includes projects that analyze natural growth and configuration/adaptation over time. Moving beyond static configurations for final design solutions, and enabled by advances in “soft” robotics and nano-engineering, these approaches seek to model the natural processes through which effective designs are achieved within a local environment. For example, Tibbits (2012) has made strides toward developing self-assembling, adaptive, and programmable materials for use in industrial construction applications. Raviv and colleagues (2014) have developed a similar approach to designing complex, self-evolving structures that vary over time in response to environmental interaction.

Bacterial cellulose structures are a fascinating model for this cutting-edge biomimetic design research. Industrial, scientific, and medical applications for artificially grown cellulose have already begun to emerge, and although this field
is still in its infancy engineers see a great potential due to the material’s structural integrity, hydrophilic nature, and biodegradability (Fernandez et al. 2013; Mohite et al. 2014). The use of bacterial cellulose in industry has advanced our knowledge of its properties and encouraged forward-looking designers to examine the material both as a model for architectural strategies and as a potential fabrication component.

Araya, Zolotovsky, and Gidekel (2012) explored novel modes of design and fabrication by combining digital tools and technologies with living biological systems in a controlled environment to induce specific biological functions and material production processes. Derme, Mitterberger, and Di Tanna (2016) similarly developed bio-fabrication and scaffolding techniques to control the 3D membranes and morphologies of bacterial cellulose, envisioning an application in the field of bio-materials science, digital fabrication, and material-informed computational modeling.

While the aforementioned research is compelling, there is still much work to do in the analysis of bacterial growth algorithms if we are to fully understand the morphogenesis of these materials. By learning about the morphogenesis of bacterial structures, we can learn to better engineer these materials and eventually to produce fully synthetic analogues that follow similar patterns of adaptation and development. The current research analyzes the growth patterns of bacterial cellulose both as a basis for new manufacturing/fabrication technologies and as a model for synthetic self-forming adaptive systems.

3. Method

The GrowMorph project is focused on two particular types of bacteria, Acetobacters xylinus and Synechococcus elongatus. These bacteria were selected for study based on the extent of the already-existing empirical knowledge about their growth patterns and the relevance of that knowledge to potential design applications. Early modeling investigations for both types of bacteria in this project include the analysis of image Z-stacks (multiple cross-sections stacked vertically) produced through confocal microscopy, as well as a review of relevant biological literature about cellulose structure and growth. Based on this data, simulations were created using programming language Processing to model the parametric environment and morphology of the bacteria’s growth. These models then were applied to design and fabrication processes. In more advanced modeling stages, the bacterial growth structures were reconstructed in 3D digital space, and physical models were designed and fabricated to illustrate the potential of this bacteria-based architectural logic.

3.1. ACETOBACTERS XYLINUS

The most abundant bacteria on earth, Acetobacter xylinus, are prolific producers of cellulose when grown in a sugar-rich medium. A single A. xylinus cell has multiple pores along its body through which chains of large sugar molecules are extracted. The use of cellulose produced by A. xylinus has received a great deal of attention as a more environmentally sound alternative to plant-derived cellulose
(for the production of paper, etc.), as well as for use in sophisticated biomedical applications (Helenius et al. 2006). In recent years researchers have begun to take an interest in the morphogenesis of A. xylinus under the view that controlling the bacteria’s structural development will be crucial to its uses in tissue engineering (Sano et al. 2010).

3.2. SYNECHOCOCCUS ELONGATUS

Synechococcus elongatus is a photosynthetic, single-celled bacterium that is widespread in freshwater environments. It is rod-shaped and tends to lump together in small clusters (Perkins et al. 1981; Scanlan & West 2002; Waterbury et al. 1986). Results presented by (Koblížek et al. 2000) demonstrated that the speed and extent of the bacteria’s aggregation is light-dependent. Under the right illumination, crystals of the Protein Structure Initiative (PSI) from Synechococcus elongatus form a hexagonal pattern.

4. Growth Analysis

The growth models developed in this study are based on observed bacterial behavior in the presence of light stimulation. The presence of light has been shown to activate genetic switching that, for the bacteria under study here, lead to specific patterns of cellulose production and therefore result in specific structural formations. The outcome of the process is structures that tend to open toward the light. Studying this process can help us to understand how biological assemblies adapt to environmental stimulation (Sano et al. 2010; Schubert et al. 1997; Zolotovsky 2012).

The model was constructed using programming language Processing. In the base form of this model a structural point (i.e. a cell) is programmed to select eight neighboring points in a random fashion. Four of the neighboring points are then eliminated based on distance (with the nearer points being retained). Two additional points are eliminated based on light intensity (with the darker points being eliminated). The remaining two structural points are linked by a mesh pattern based on the process of bacterial cellulose extrusion (figure 1).

One method for simulating the complex formations of the bacteria cellulose is to process the volumetric formation as a point cloud, and to evaluate the cloud in a single step. The cellulose-based mesh pattern used in this model is derived from the “marching cubes” algorithm developed by Lorensen and Cline (1987). Taken together, the eight neighboring points initially selected for consideration can be considered a “cube” surrounding the origin cell, and the growth pattern resulting from a combination of randomness and light simulation as a possible means of segmenting the cube. When the resulting form is combined with the results of the neighboring cubes (i.e., the cellulose extrusions of other cells), an overall mesh pattern emerges and expands over time (figure 2).
4.1. PARAMETRIC CONDITION ONE

The parameters of the model were adjusted to investigate structural forms resulting from various kinds of observed bacterial behavior. The first parametric condition was the base model as described above. It simulates the behavior of A. xylinum bacteria when stimulated by a UV light source (Sano et al. 2010). As mentioned, each cell in the model is programmed to identify eight random nearby locations, eliminate six of the locations based on distance and light levels, and then extrude a mesh toward the remaining two points. One of the simulations resulting from this growth pattern is shown in figure 3.

4.2. PARAMETRIC CONDITION TWO

In this version of the model the growth pattern has been adjusted to describe the more cohesive and aggressive behavior of A. xylinum in conditions of abundant nutrients, again under the stimulation of a UV light source (Sano et al. 2010). The point selection under Parametric Condition Two is different from the previous algorithm. Each cell again selects eight random nearby locations. The algorithm then defines a polygon based on those locations, and the cell selects six new points.
on the surface of the polygon, choosing the points on the surface that are closest to the origin cell. The process is repeated, defining a new, smaller polygon based on these six points, and then choosing the three nearest points on the new polygon. Of these three, the one with the lowest light intensity is discarded, and a mesh is extruded toward the other two points. The overall result of this process is that the chosen points tend to be much closer to the origin cell in comparison with the base model. One of the simulations resulting from this growth pattern is shown in figure 4.

Figure 3. Simulation based on Parametric Condition One.

Figure 4. Simulation based on Parametric Condition Two.

4.3. PARAMETRIC CONDITION THREE
The third variation of the model is based on the symbiotic combination of Synechococcus elongatus with Acetobacter xylinum (Schubert et al. 1997). For this simulation we modified the base model by setting some random points to act as S.
elongatus. The notable feature of this addition is that the S. elongatus cells, under the influence of a UV light source, will form hexagonal space groups that interact with the surrounding A. xylinus growth patterns. One of the simulations resulting from this growth pattern is shown in figure 5.

Figure 5. Simulation based on Parametric Condition Three.

5. Conclusions and Future Work

This project studied the growth patterns of Acetobacters xylinus and Synechococcus elongatus as a potential basis for computer-mediated architectural assemblies. The resulting simulations can be used as a means to understand the structural morphogenesis of bacterial cellulose for the purpose of developing controlled-growth applications, and it can also be analyzed in itself as a model for human-created environmentally responsive structures. Three versions of the simulation were created, incorporating different parametric conditions based on observed bacterial behavior (Sano et al. 2010; Schubert et al. 1997).

The results from the study can inspire designers to make use of bacterial growth logic in their work, and provide them with practical tools for this purpose. The 3D models produced in the research provide concrete examples of how bacterial growth logic can be used in design (figure 6), and can inspire new techniques of artificial material fabrication and assembly. The ultimate goal of abstracting biological growth patterns into code-driven models and tools is to gain new insights into how nature deals with physical dynamics, environmental parameters, and feedback within cell and tissue structures. The potential applications include novel designs for responsive surfaces, new fabrication processes, and unique spatial structures in future architectural work.

While this study presents a first step toward simulating bacterial cellulose growth in computer-aided design, there remains a tremendous amount of opportunity for analyzing organic assemblages. By linking the biological sciences to the
computational design process we can open significant new horizons for organically inspired design. In future work, we plan to design a plug-in for the Grasshopper software package that will allow users to explore various biological growth parameters. Producing actual edifices based on bacterial growth logic will help to inspire and further promote this design research area. Finally, future work may seek to apply organic growth models directly to digital fabrication, leading to new techniques in material production.

Figure 6. An organically shaped pavilion that was designed using the base model created in this study.

References


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