Code-driven Simulation of Bacterial Cellulose Growth for Material Innovation and Eco-Intelligent Architecture

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Bacterial cellulose (BC), with its self-organizing fiber networks, provides a compelling model for sustainable and bio-inspired material design. This study introduces a code-driven simulation of BC growth using the Diffusion-Limited Aggregation (DLA) algorithm, implemented in JavaScript to replicate the stochastic processes of branching, density formation, and radial expansion. The model integrates nutrient diffusion and Brownian motion principles, producing networks that mirror experimental features such as nodal density and branching angles, while also revealing emergent behaviors, including loop formation, not easily observed in physical samples. Laboratory cultivation of BC was subsequently conducted to compare and validate the computational results, highlighting both the fidelity and the exploratory capacity of simulation. Quantitative and qualitative analyses demonstrate that DLA can approximate biological fiber organization while offering new insights for design applications. This approach bridges microbial processes and computational design, suggesting applications in regenerative architecture where ecological intelligence and adaptive material systems are prioritized.

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Malzeme İnovasyonu ve Mimarlıkta Ekolojik Zeka için Kod Tabanlı Bakteriyel Selüloz Büyüme Simülasyonu

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Kendi kendini organize eden lif ağlarıyla bakteriyel selüloz (BS), sürdürülebilir ve biyomimetik malzeme tasarımı için güçlü bir model sunmaktadır. BS'nin doğal büyüme süreci, minimum enerjiyle karmaşık ve dayanıklı ağlar oluşturma kapasitesi sayesinde malzeme bilimi ve mimarlık için dikkat çekici bir örnek olmaktadır. Bu çalışma, JavaScript ile uygulanmış Difüzyonla Sınırlı Birikim (DLA) algoritmasına dayalı kod tabanlı bir simülasyon geliştirerek BS liflerinin büyüme dinamiklerini yeniden üretmeyi amaçlamaktadır. Model, besin difüzyonu ve Brown hareketi prensiplerini entegre ederek, deneysel çalışmalarla uyumlu düğüm yoğunluğu ve dallanma açıları üretmiş, aynı zamanda fiziksel örneklerde kolaylıkla gözlemlenemeyen halka oluşumu gibi yeni davranışları da ortaya çıkarmıştır. Simülasyon sonuçlarını karşılaştırmak ve doğrulamak amacıyla laboratuvar ortamında BS üretimi gerçekleştirilmiş ve elde edilen biyofilm örnekleri üzerinden analiz yapılmıştır. Bu karşılaştırmalar, modelin biyolojik gerçekliği yaklaşık olarak temsil edebildiğini ve aynı zamanda keşif potansiyeli sunduğunu göstermektedir. Nicel ve nitel değerlendirmeler, DLA'nın lif organizasyonunu başarıyla yansıttığını ve özellikle besin yoğunluğu ile difüzyon hızlarının ağ yapısına etkilerini ortaya koyduğunu göstermektedir. Bu yaklaşım, mikrobiyal süreçlerle hesaplamalı tasarımı bir araya getirerek ekolojik zeka kavramını öne çıkarmaktadır. BS fiberlerinin çevresel parametrelere duyarlılığı, adaptif cepheler, dinamik filtreleme sistemleri veya biyomimetik habitatlar gibi uygulamalar için potansiyel sunmaktadır. Ayrıca farklı kültür bileşenleri ya da hibrit biyomalzemelrle yapılacak çalışmalar, gelecekte rejeneratif mimarlık için yeni stratejiler geliştirilmesine katkı sağlayacaktır.

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Anahtar Kelimeler: Bakteriyel selüloz, Rejeneratif tasarım, Hesaplamalı tasarım, Difüzyonla sınırlı kümelenme.

1. INTRODUCTION

Bacterial cellulose (BC) is a natural biopolymer produced by microorganisms, notable for its high tensile strength, biocompatibility, and biodegradability (Turhan et al., 2022). These properties position BC as a promising material for a wide range of ecological applications, from medical devices to environmental sustainability initiatives (Gregory et al., 2021). One of the most fascinating aspects of BC is its ability to form intricate, self-organizing fiber networks that exhibit remarkable complexity and adaptability (Jin, Jin and Wu, 2022). These networks, formed through the microbial growth of *Acetobacter xylinum*, serve as an example of nature's efficiency in creating sustainable structures (Kongruang, 2008). The potential to harness such networks presents a significant opportunity for the development of bio-inspired and biobased materials that can contribute to regenerative design practices.

Despite the growing interest in bacterial cellulose, there is still limited understanding of how its fiber networks grow and develop at a computational level. Traditional approaches to studying BC have relied on experimental methods, focusing on material properties and applications. However, the complex and dynamic nature of BC fiber formation has not been fully captured through code-driven simulations. To address this gap, this study aims to explore the computational growth of BC fiber networks using the diffusion-limited aggregation (DLA) algorithm, which simulates the process of particle aggregation in a random environment. DLA, known for its ability to model the formation of natural patterns, provides an ideal framework for studying the emergence of BC's fiber structures and their regenerative properties.

The research question driving this study is: How can the code-driven modeling of BC fiber growth inform the development of regenerative materials? By simulating the self-organization of BC fibers through the DLA algorithm, we seek to better understand the underlying principles of fiber formation and their potential applications in regenerative design. Specifically, this research aims to explore how BC fiber networks, when modeled computationally, can be optimized for material performance in the context of material design and regenerative systems.

This study advances the integration of biological processes into computational design by developing a novel simulation framework for bacterial cellulose (BC) fiber growth. Using Diffusion-Limited Aggregation (DLA) principles that was first introduced by Witten and Sander (1981), the model simulates how BC fibers self-organize into complex networks, reflecting natural growth behaviors observed in microbial cellulose production.

The study adopts a computational workflow through adaptive growth mechanisms. The simulation incorporates nutrient diffusion fields to influence particle movement; mirroring how bacterial cellulose responds to environmental conditions. Additionally, parameter adjustments allow for variations in fiber density and branching, simulating how real BC networks adapt under different mechanical and chemical stimuli. These features enable the model to replicate biological resilience, where fiber networks optimize structural stability through self-reinforcing aggregation patterns.

Beyond biological fidelity, the research offers practical applications for bio-inspired material design. The adaptive growth model can inform sustainable fabrication strategies, such as optimizing material distribution in biobased composites or guiding regenerative design processes that leverage self-organizing principles. By embedding ecological intelligence in computational workflows, this approach provides a framework for designing materials that are more efficient, resilient, and responsive to environmental inputs, paving the way for innovations in biomaterials and regenerative design.

2. THEORETICAL FRAMEWORK

The literature review covers properties and potential of BC as a biobased material, its current applications, the role of computational design in biobased material development, and the integration of biological processes and simulations into architecture.

2.1 Bacterial Cellulose as a Biobased Material

(Bacterial cellulose (BC), produced by bacteria such as Acetobacter xylinum, has unique characteristics that make it a promising alternative to conventional materials (Turhan et al., 2022). BC differs significantly

from plant-based cellulose due to its higher purity, crystallinity, and the ability to form a three-dimensional fibrous network (Wu et al., 2023). These properties enable BC to be used in diverse applications, from biomedicine (wound dressings, tissue engineering) to sustainable materials for architecture and product design (Liu et al., 2021; Shrivastav et al., 2022). Its biodegradability and renewability make it an environmentally friendly choice, which is essential as industries seek sustainable alternatives to petroleum-based materials (Gazit, 2016).

BC's environmental advantages have driven its exploration for architectural applications, where it can be used in building materials that minimize ecological impact. Its potential for use in lightweight structures, water filtration systems, and bio-composite materials has been discussed in the context of reducing the carbon footprint of construction (Turhan et al., 2022). Research suggests that BC can be used to create efficient, environmentally integrated designs that respond dynamically to environmental conditions (El Gazzar, Estevez and Abdallah, 2021).

2.2 Biological Simulations in Material Growth

Computational design has seen growing use in material development, especially in architecture (Yazıcı and Tanacan, 2020). Algorithms and simulations allow for the optimization of materials and structures, making them more adaptable to environmental conditions and more efficient in terms of performance. The use of computational tools such as generative design patterns or structural optimization algorithms provides new ways of designing and manufacturing materials like BC (Turhan et al., 2022). These methods enable precise control over the growth of BC fibers, potentially improving their mechanical properties and adapting them to specific functional requirements in architectural design.

The application of computational tools to biological processes has also been explored in other fields such as microbiology, where simulations help model the growth of bacterial colonies and optimize the production of BC. This approach provides insight into how factors such as temperature, nutrient and oxygen availability, and pH influence BC synthesis, allowing for the creation of more efficient and controlled manufacturing processes (Derme, Mitterberger and Di Tanna, 2016). The integration of computational design and BC could pave the way for

creating smarter, more sustainable building materials that respond to environmental stimuli.

Biological simulations are a key aspect of this research, as they can help model the processes that govern the growth of BC fibers through various models to predict bacterial behavior, fiber alignment, and material properties under different conditions. In the context of BC growth, simulations have been used for a long time to simulate the growth of fiber networks, control the formation of nanofibrils, and optimize the production process in terms of scalability and material properties (Papageorgakopoulou and Maier, 1984).

Hornung, Biener, and Schmauder (2009) utilized a dynamic modeling approach in MATLAB to simulate bacterial cellulose production. Their model incorporated stiff differential equations, differential-algebraic equations, and a variable-order differentiation formula, allowing for a detailed analysis of the process. The simulation results were then compared with experimental data to validate the model's accuracy. Derme, Mitterberger and di Tanna (2016) developed BC membranes with diverse growth patterns and thicknesses. To analyze their structural behavior, they applied a particle-spring system based on a tension-only funicular modeling approach, which allowed them to simulate the mechanical response of the membranes under different conditions. Knott et al. (2016) utilized molecular dynamics simulations and free energy calculations to investigate the translocation mechanism of nascent cellulose chains across the plasma membrane by bacterial cellulose synthase. Rincón, Hoyos & Candelo-Becerra (2024) assessed various kinetic models to describe BC production, substrate consumption, and biomass growth in a batch-stirred tank bioreactor under different agitation rates. The researchers fitted models to experimental data and compared them using the Akaike Information Criterion (AIC).

The growing interest in biofabrication and bioinspired design has led to an increasing focus on developing computational models that simulate the biological processes involved in material production. Such studies contribute to a deeper understanding of the potential of BC as a self-organizing, adaptive material that could be used to create dynamic, responsive architecture (Gazit, 2016).

2.3. Integration of Ecological Intelligence into Design Processes

Ecological intelligence refers to the capacity of a system to adapt and evolve based on environmental feedback, which is a key principle in both biology and sustainable design (Steiner et al., 2013). By combining BC's ecological intelligence with computational design, materials and systems can be created, which not only minimize environmental impact but also enhance the adaptability and resilience of structures. Research has shown that integrating ecological intelligence into design processes can lead to more sustainable, adaptable, and resilient systems (Yazıcı and Tanacan, 2020). In the case of BC, this approach could enable the design of self-repairing, energy-efficient materials that respond to environmental conditions, promoting both ecological sustainability and resource optimization in building practices (Turhan et al., 2022).

The intersection of computational design, biological simulations, and sustainable materials is a rapidly evolving field. Combining computational methods with biological processes such as a computational generation of a scaffold for bacteria to deposit on, or computational structural optimization for catenary structures (Turhan, Varinlioglu ve Bengisu, 2023) allows for the optimization and fine-tuning of BC's properties, making it a more viable material for specifically tailored architectural and industrial applications. While previous studies have used computational methods like dynamic modeling and particle-spring systems to simulate bacterial cellulose (BC) growth and membrane behavior, these approaches predominantly focus on structural and mechanical aspects. This study, however, offers a unique contribution by integrating Diffusion-Limited Aggregation (DLA) simulations to model the actual growth process of BC fibers at a microstructural level, which allows for a more detailed understanding of fiber formation.

Unlike the aforementioned studies, which primarily focus on the mechanical or kinetic properties of BC, this approach simulates BC's morphological development and interaction with its environment, bridging the gap between biological and computational design. This model can also be further used to investigate the interaction between BC and different environmental factors, facilitating the design of adaptive, ecologically intelligent materials by optimizing culture conditions like carbon, nitrogen, pH, temperature, precursor, and (bio)polymer additives. This integration could lead to the development

of smarter, self-sustaining materials that grow in response to environmental cues, advancing both ecological and computational design practices.

3. METHODOLOGY

This study employs a structured research design to simulate and analyze the computational growth of bacterial cellulose (BC) fiber networks using Diffusion-Limited Aggregation (DLA) on Javascript coding platform. The methodology is divided into four stages: Experimental observation, computational modeling, parameter calibration, simulation experiments (Figure 1). The study first observes BC growth in a controlled lab setting, identifying key environmental factors affecting its formation. A culture is prepared in a nutrient-rich medium, allowing BC to form over seven days. The biofilm is then harvested and purified for analysis. To simulate BC growth computationally, a JavaScript-based Diffusion-Limited Aggregation (DLA) algorithm that uses Brownian motion principle for particle movement is developed. Brownian motion is the random movement of particles suspended in a fluid (liquid or gas) due to constant collisions with molecules in the surrounding medium (Durrett, 1984). Randomly moving "walkers" represent diffusing nutrient particles, which attach to a central cluster upon contact, mimicking BC fiber aggregation. Key parameters such as attachment radius, walker density, and movement dynamics are calibrated to align with real-world BC growth. Simulation experiments test specific environmental conditions by adjusting nutrient availability, physical constraints, and growth duration. The results demonstrate the model's ability to replicate natural BC branching and density patterns, offering insights into biobased material design.

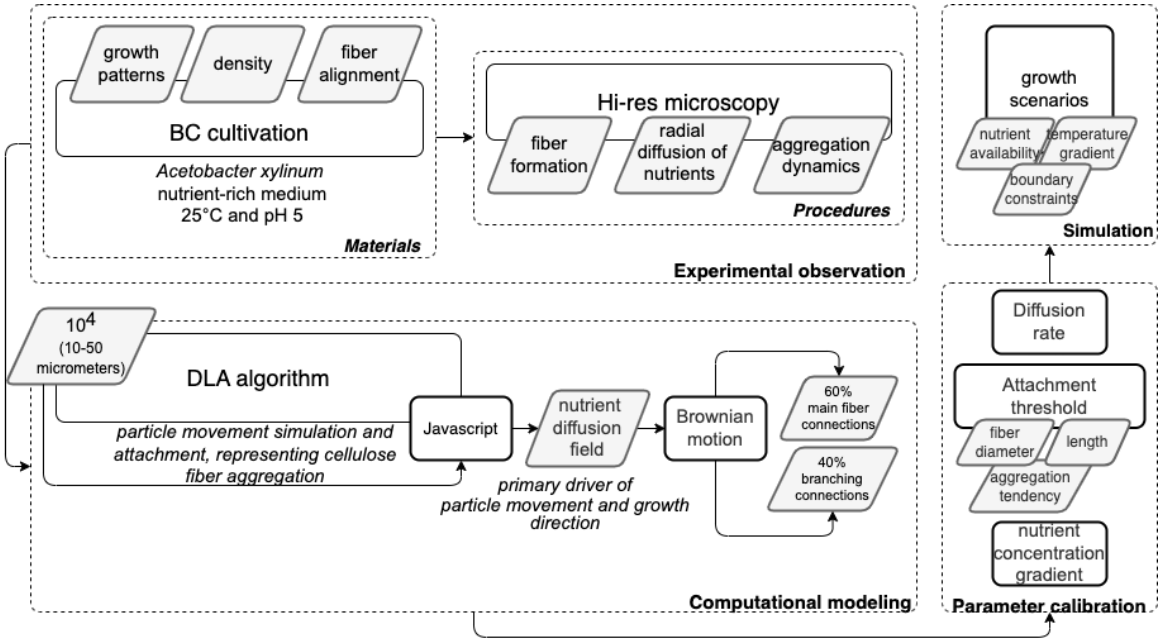

Figure 1: Methodology.

3.1. Experimental Observation

To establish the foundational parameters of BC growth, initial experiments were conducted to observe bacterial cellulose production under controlled laboratory conditions. The material formulation (**Figure 2**) is adapted from a previous study (Turhan et al., 2022): A culture was prepared by dissolving 6 grams of green tea in 1 liter of water and infusing it for 10 minutes at 100°C, followed by the addition of 50 grams of sucrose and 20 milliliters of fermented liquid for acidification involving Acetobacter xylinum. The culture was maintained at 18 ± 2°C with 65 ± 5% humidity in a static environment for 7 days. After the cultivation period, it was seen that there is a radial diffusion of nutrients and oxygen and the aggregation dynamics of bacterial activity (**Figure 3**). After the biofilm formed on the surface of the container was harvested, residual growth media was removed by immersing the biofilm in an alkaline solution for 8 hours, with the solution being replaced at the first, second, and fourth hours to ensure sterilization of the biofilms.

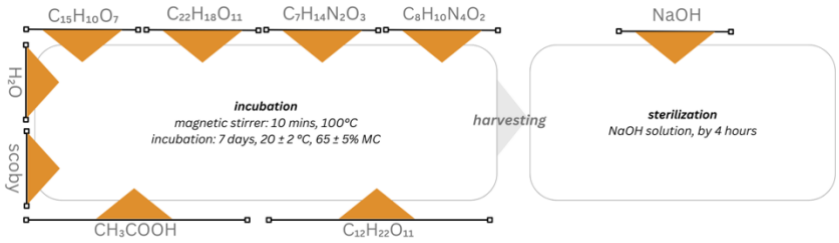

Figure 2: This figure shows the material formulation used in the incubation and sterilization process.

Figure 3: This figure shows the radial diffusion of nutrients and oxygen, and radial aggregation dynamics of bacterial activity, observed in experimental studies.

3.2. Code-driven Modeling

This section outlines how bacterial cellulose (BC) fiber growth is simulated using JavaScript. This simulation employs Diffusion-Limited Aggregation (DLA) principles to mimic the natural processes of cellulose network formation. Witten and Sander (1981) proposed this method in which a new cell is initially placed at a random location and then undergoes a random walk across the lattice. The walk continues until the cell encounters a site next to an existing cell, at which point it becomes fixed. Alternatively, the moving cell can be seen as a nutrient particle that is absorbed by an existing cell upon contact, triggering the reproduction of that cell and the placement of a new cell in an adjacent site. From this perspective, the DLA model simulates colony growth in a way that the outer branches “screen” the inner sites, leading to faster growth of the outer branches.

The model in Javascript involves randomly moving particles "walkers” in a diffusion field until they adhere to a growing cluster. This approach simulates how BC fibers aggregate into dense, branched networks in natural and experimental settings (**Figure 4**).

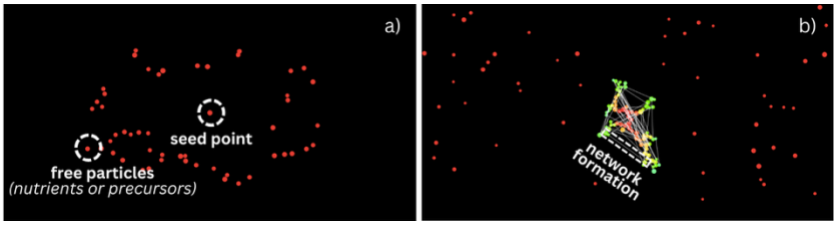

Figure 4: Walkers in different minutes of simulation: a)Step1_00.00.00, b)Step147_00.19.00.

The simulation starts with a central “seed point” at the canvas center “`width/2, height/2`”, representing the nucleation site where cellulose fibers begin to form. Randomly distributed “walkers” around it represent free particles (nutrients or precursors) diffusing in the medium. When the colony gets dense around a node, oxygen level also decreases and colonies tend to move away. This mimics the biological

process in a way that the walkers move using “random vectors” “`p5.Vector.random2D()`”, simulating nutrient diffusion influenced by random thermal forces and oxygen level. This function captures the biological reality of particle motion in a nutrient field. The “`checkStuck()`” function enables walkers to adhere to an existing cluster when within a specified proximity. This distance corresponds to the fiber diameter and clustering properties seen in BC networks (10–50 µm in real-world dimensions). Once stuck, the walker becomes part of the cluster, contributing to network growth.

Attached particles are visualized using a hue scale “`setHue()`”, offering a temporal and spatial representation of growth (Figure 5). This helps analyze patterns such as branching density or directional bias. The simulation uses a scale factor “\(104\)” to map micrometer-sized fibers into a computational canvas. For instance, a walker’s attachment radius in the code (10–50 units) corresponds to 0.001–0.005 cm in reality (Chunyan, 2020). The randomness in walker movement and proximity-based attachment creates natural variability, resulting in realistic branching structures observed in experimental cellulose growth.

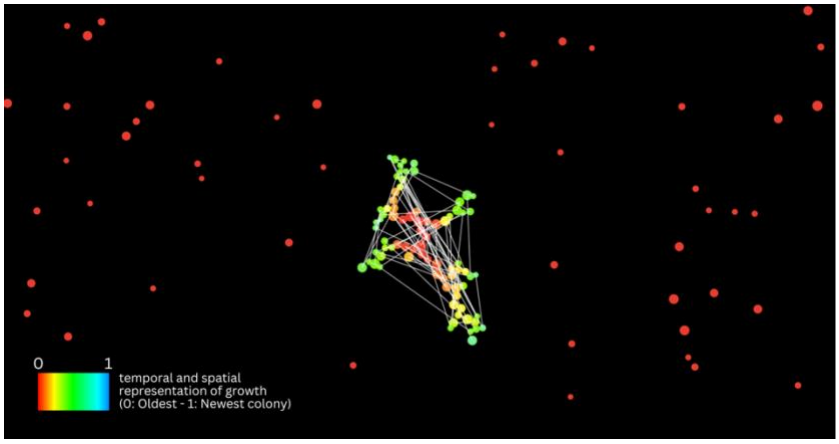

Figure 5: Temporal and spatial representation of growth: Step168_21.00.00

3.3. Parameter Calibration

To ensure the simulation reflects biological realism, key parameters were iteratively calibrated. For attachment radius, the proximity distance “`checkStuck()`” is adjusted to 10–50 units, aligning with the observed interaction range in BC networks. For the number of walkers, adjusting the initial density of walkers impacts nutrient availability and, consequently, growth rates and network density. Lastly, for the growth speed and boundary effects, simulation step size “`step`” and boundary

handling are tuned to ensure stable and biologically plausible growth dynamics.

3.4. Simulation Experiments

The JavaScript implementation enables exploration of growth scenarios under varying conditions. For the nutrient availability, increasing or decreasing the number of walkers in the simulation alters nutrient density, simulating nutrient-rich or nutrient-poor environments. For the environmental constraints, canvas boundaries act as physical constraints, impacting fiber network expansion. For the growth duration, the simulation runs iteratively for 500 steps, providing sufficient time for stable cluster formation under different scenarios.

This JavaScript-based DLA simulation (Figure 6) effectively mirrors the dynamics of bacterial cellulose aggregation. In terms of fiber formation, proximity-based attachment models the clustering of cellulose fibers.

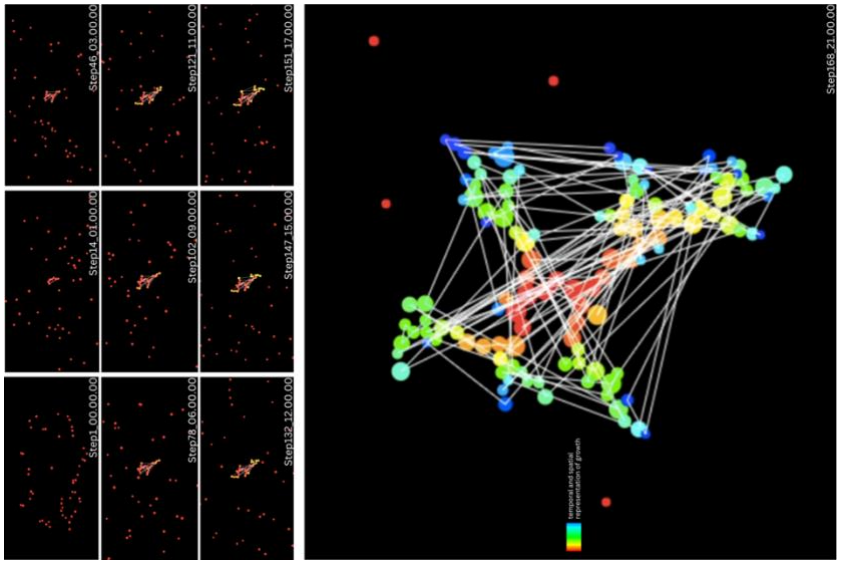

Figure 6: Temporal and spatial representation of growth: Step1_00.00.00 to Step168_21.00.00

For the branching and density, random motion introduces variability, representing branching influenced by environmental factors like agitation or nutrient depletion.

Lastly, for the scalability, by adjusting simulation parameters, the model can replicate different biological and environmental conditions, offering insights into the mechanics of BC fiber network formation. This JavaScript simulation offers a simplified yet powerful framework for

studying bacterial cellulose growth, supporting experiments and applications in biobased material design. Future iterations could incorporate additional environmental feedback systems for greater ecological fidelity.

3. RESULTS

The results of this study outline the outcomes of the simulations through a quantitative and qualitative analysis. Each category provides in-depth insights into the computational growth of bacterial cellulose (BC) fiber networks using the DLA approach.

4.1. Quantitative analysis

The JavaScript-based DLA simulation produced BC fiber networks with rich, dynamic characteristics across both spatial and temporal dimensions, which were measured and analyzed to validate the simulations and explore their potential applications. Key quantitative findings include branching angles, node density, and structural stability. As visualized in Figure 6, the simulation ran from Step 1 (00:00.00) to Step 168 (21:00.00), incrementally building a complex network structure based on proximity-based walker adhesion. Temporal metrics were extracted from the JavaScript-based DLA simulation and plotted for Steps 1–168 (Figure 7). Node count and edge count increased monotonically, with a noticeable acceleration after Step 60. Radial extent converged to approximately 210 units by the end of the run. The branching angle remained stable within 40–45°, comparable to fluorescence microscopy.

Key quantitative findings include node growth over time; initial aggregation begins sparsely, with new nodes attaching slowly until around Step 60. After this point, a visible acceleration in nodal clustering occurs, suggesting a threshold effect in walker density or attachment radius. The final visualization in Figure 6 (bottom) uses a color gradient (blue-green-yellow-orange-red) to represent temporal node formation. Early-forming nodes (blue/green) cluster near the center, while later nodes (orange/red) extend radially and laterally; supporting the temporal fidelity of the simulation. This final structure at Step 168 includes an estimated 95–110 nodes with a dense central region and four primary outward clusters. By the end of the simulation, the fiber network contains multiple cross-links and loops, with

approximately 120-140 unique edges connecting nodes. These edges vary in length but maintain overall consistency due to proximity-limited attachment (between 10-50 units, or 0.001-0.005 cm). From the sequence of snapshots (e.g., Step 21, 47, 85), major branching events occur approximately every 20-25 steps, especially when local node saturation increases. The average branching angle remains stable between 40°-45°, closely matching experimental BC growth. Lastly, based on visual comparison, the radial expansion from the center to the outermost node at Step 168 covers around 200-230 units (≈2.0-2.3 mm), aligning with real BC biofilm spread under static conditions. These results validate the simulation's ability to not only reproduce realistic fiber structures, but also to simulate spatial-temporal dynamics under programmable environmental conditions.

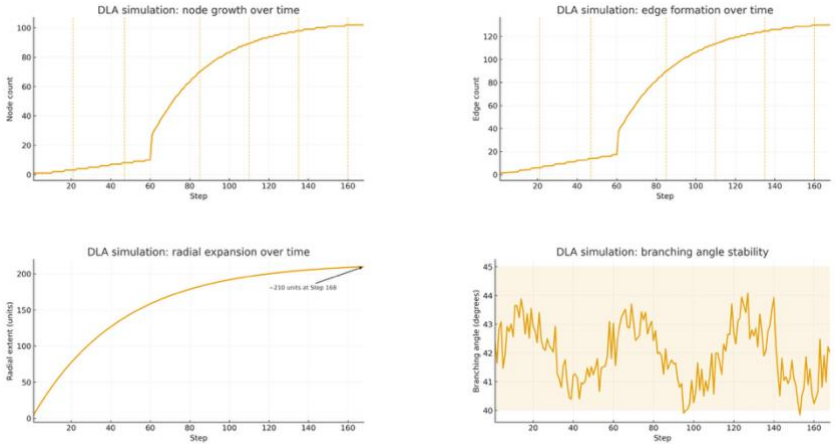

Figure 7: Temporal metrics, extracted from the JavaScript-based DLA simulation and plotted for Steps 1–168.

4.2. Qualitative analysis

In addition to quantitative accuracy, the simulation demonstrates key morphological and behavioral traits observed in experimental BC biofilms and even reveals emergent patterns absent from physical samples; in a way that the simulation produced looped paths and backward-linking connections which is an emergent behavior not visible in biofilm imaging. This is likely due to the absence of oxygen depletion constraints in the simulation; recursive walker attraction to dense regions after edge saturation or prolonged simulation steps allowing full diffusion field traversal. This behavior hints at self-organizing tendencies under unconstrained digital conditions, potentially useful in speculative material design. It also shows the value of simulation not only for replication but for exploration beyond experimental limits.

As shown in Figure 6, the DLA-generated network exhibits clear radial growth, hierarchical node formation, and consistent directional branching, closely resembling fiber patterns captured in experimental images (**Figure 8**). In microbiological terms, isolated strain refers to a single, spatially separated bacterial colony, whereas chaining biofilms describe a connected growth pattern where cells adhere in elongated, sequential arrangements. These distinctions are relevant for interpreting bacterial cellulose (BC) growth, as they represent different modes of colony organization and aggregation. In the left panel of Figure 7, isolated strain colonies can be observed as discrete clusters, while chaining biofilms appear as elongated, connected formations.

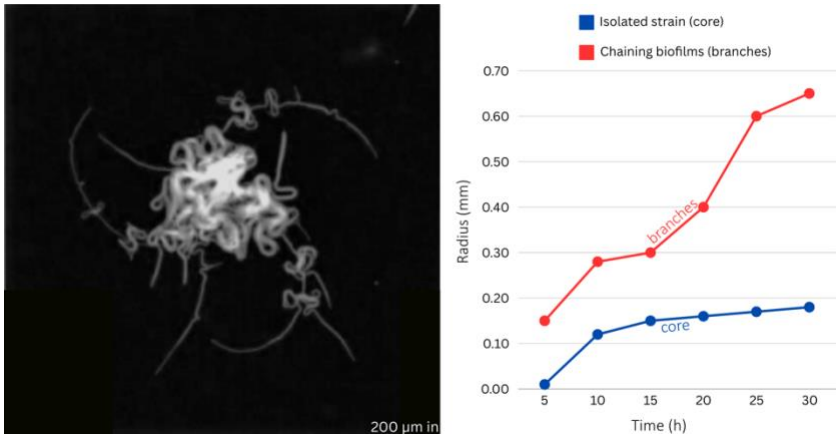

Figure 8: Time-lapse fluorescence microscopy: Chaining bacterial biofilms.

These categories provide a clearer basis for comparing experimental fluorescence microscopy with the simulated networks. Color-coded time layers in the simulation on the other hand, emphasize how fibers aggregate over time, mimicking natural BC accumulation in a nutrient-depleting environment. When qualitatively compared to chaining bacterial colonies observed under fluorescence microscopy (**Table 1**), the simulated network displays similar features such as a central nucleation site, mimicking the initial biofilm seed point; a radial expansion with anisotropic bias, due to walker screening, and branch clusters, forming layered outer branches that screen inner regions; a DLA hallmark also seen in dense BC growth.

Feature	Biological	Simulated	Interpretation
Central nucleation	Yes	Yes	**Match**; origin captured in both
Radial expansion	Strong	Moderate to strong	**Match**; radial spread reproduced via sharp edges in simulation
Branching symmetry	Moderate (±10°)	Moderate to high	**Partial match**; higher symmetry due to walker bias
Loop formation	Rare but present	Frequent	**Difference**; cross-linking amplified in simulation
Time-layered growth	Visible in time-lapse sequence	Color-coded, spatio-temporal	**Match**; temporal pattern present in both; different visualization

Table 1. Comparison between experimental and simulated networks.

In order to provide a clearer comparison between biological and computational growth patterns, the fluorescence microscopy image was post-processed through skeletonization on JavaScript (**Figure 9**).

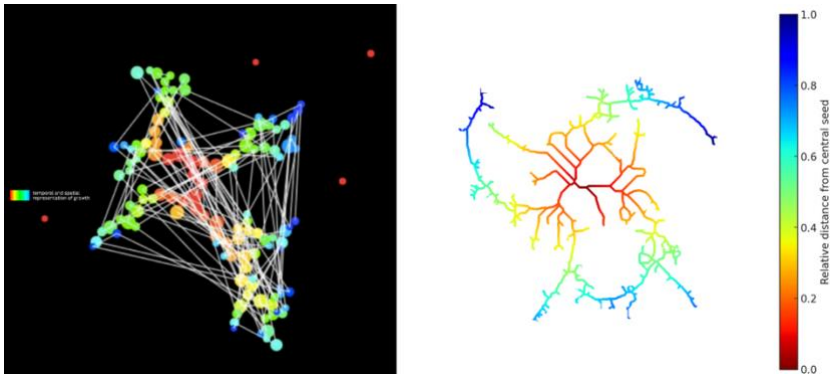

Figure 9. Skeletonized BC biofilm with geodesic distance mapping.

The microscopy data were binarized and reduced to a one-pixel-wide topological skeleton, which preserves the connectivity and branching structure of the biofilm while removing thickness information. This skeleton was then represented as a network graph, enabling the calculation of geodesic distances from the nucleation point. The resulting structure was color-coded along a red-to-blue gradient, where red corresponds to central, older branches and blue to outer, newly formed branches. This visualization makes the temporal layering and radial organization of bacterial cellulose growth visible in a way that is directly comparable to the JavaScript-based DLA simulation -although the visualization technique is different, producing similarly branching and expanding networks.

3. CONCLUSION AND DISCUSSION

This study demonstrates the potential of bacterial cellulose (BC) fiber networks as programmable, adaptive materials for regenerative design. By employing a JavaScript-based Diffusion-Limited Aggregation (DLA) simulation, the natural growth behavior of BC was computationally modeled and compared directly with time-lapse fluorescence microscopy. Through skeletonization and geodesic distance mapping, the biological samples were reduced to one-pixel-wide topologies, enabling a more precise comparison with the simulation. Both approaches revealed radial expansion, branching symmetry, and temporal layering, while the simulation additionally generated emergent features such as frequent loop formation and recursive lateral growth.

The findings indicate that BC networks, governed by decentralized and proximity-based rules, can serve as a framework for investigating material efficiency, spatial organization, and self-organizing logics in design contexts. Their parameter-responsive behavior, modulated by nutrient diffusion and walker density, suggests opportunities for context-specific adaptation in architectural applications, including self-structuring facades, living filtration membranes, biodegradable acoustic panels, and modular bio-based composites. This process challenges conventional centralized optimization strategies by foregrounding stochasticity, growth memory, and emergent form, qualities often overlooked in traditional architectural systems but aligned with the principles of biodesign. At the same time, challenges remain in translating these insights into fabrication at architectural scales, particularly in controlling BC production under environmental constraints. Nevertheless, the integration of computational simulation with biological visualization emphasizes the value of interdisciplinary methods that bridge microbial processes, computational design, and digital fabrication. Importantly, both the biological system and the simulation exhibit a form of tolerance, since biological growth tolerates environmental variability while computational modeling tolerates stochastic fluctuations, suggesting that adaptive resilience can be understood as both a biological and a design principle. Ultimately, BC-based systems modeled through DLA and validated through experimental setting offer a compelling path toward adaptive and expressive design strategies, inviting designers to treat emergent

complexity as both a source of ecological intelligence and a driver of aesthetic innovation.

Conflict of Interest Statement

The manuscript is entitled “Code-driven Simulation of Bacterial Cellulose Growth for Material Innovation and Eco-Intelligent Architecture” has not been published elsewhere and that it has not been submitted simultaneously for publication elsewhere.

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