Article

Not peer-reviewed version

From Fibonacci Anyons to B-DNA and Microtubules via Elliptic Curves

Michel Planat *

Posted Date: 8 August 2025

doi: 10.20944/preprints202508.0633.v1

Keywords: Fibonacci anyons; elliptic curves; character varieties; BSD conjecture; DNA structure; microtubules; quantum biology

Article

From Fibonacci Anyons to B-DNA and Microtubules via Elliptic Curves

Michel Planat

Institut FEMTO-ST CNRS UMR 6174, Université Marie et Louis Pasteur, 15 B Avenue des Montboucons, F-25044 Besançon, France; michel.planat@femto-st.fr

Abstract

By imposing finite order constraints on Fibonacci anyon braid relations, we construct the finite quotient $G = \mathbb{Z}_5 \rtimes 2I$, where $2I$ is the binary icosahedral group. The Gröbner basis decomposition of its $SL(2,\mathbb{C})$ character variety yields elliptic curves whose L-function derivatives $L'(E,1)$ remarkably match fundamental biological structural ratios. Specifically, we demonstrate that the Birch-Swinnerton-Dyer conjecture's central quantity: the derivative $L'(E,1)$ of the L-function at 1, encodes critical cellular geometries: crystalline B-DNA pitch-to-diameter ratios ($L'(E,1) = 1.730$ matching $34\,\text{Å}/20\,\text{Å} = 1.70$), microtubule structural parameters ($L'(E,1) = 1.579$ for GDP-tubulin ring ratios), and remarkably, the fundamental cytoskeletal scaling relationship where $L'(E,1) = 3.570 \approx 25/7$, precisely matching the microtubule-to-actin diameter ratio. This pattern extends across the hierarchy $\mathbb{Z}_5 \rtimes 2P$ with $2P \in \{2O, 2T, 2I\}$ (binary octahedral, tetrahedral, icosahedral groups), where character tables of $2O$ explain genetic code degeneracies while $2T$ yields additional microtubule ratios. The convergence of multiple independent mathematical pathways on identical biological values suggests that evolutionary optimization operates under deep arithmetic-geometric constraints encoded in elliptic curve L-functions. Our results position the BSD conjecture not merely as abstract number theory, but as encoding fundamental organizational principles governing cellular architecture. The correspondence reveals arithmetic geometry as the mathematical blueprint underlying major biological structural systems, with Gross-Zagier theory providing the theoretical framework connecting quantum topology to the helical geometries essential for life.

Keywords: Fibonacci anyons; elliptic curves; character varieties; BSD conjecture; DNA structure; microtubules; quantum biology

---

1. Introduction

For more than a century scientists have searched for a rigorous mathematical framework capable of unifying the geometry of living matter with the discrete laws that govern physical reality. Early pioneers such as D'Arcy Thompson, Nicolas Rashevsky and Alan Turing demonstrated that differential geometry, mathematical biophysics and reaction-diffusion theory could reproduce many morphogenetic motifs[1–3]. The subsequent decades witnessed the introduction of fractal geometry into genomics [4,5], knot and link theoretic analyses of DNA and DNA supercoiling [6–8], and continuum mechanical models of cytoskeletal patterning [9]. Yet most of these approaches remained largely phenomenological, lacking a unifying algebraic structure that could *predict* quantitative biomolecular dimensions. Two parallel mathematical revolutions now supply that missing structure. *Quantum topology*, through anyons, modular tensor categories and topological quantum computation, has clarified how braided quasiparticles generate robust, finite-dimensional state spaces [10,11]. Conversely, *arithmetic geometry* has revealed deep links between prime statistics and the geometry of elliptic curves, epitomised by the Modularity Theorem and by the Birch-Swinnerton-Dyer and Gross-Zagier results [12–15]. In the present work we show that these two domains intersect at precisely the scale relevant to cellular architecture: imposing finite order constraints on the Fibonacci anyon braid group produces

Preprints.org (www.preprints.org) | NOT PEER-REVIEWED | Posted: 8 August 2025 doi:10.20944/preprints202508.0633.v1

finite quotients whose $\mathrm{SL}(2,\mathbb{C})$ character varieties factor through rank one elliptic curves, and the derivatives $L'(E,1)$ of the associated L–functions reproduce, to experimental accuracy, the pitch to diameter ratio of B-DNA, key microtubule metrics, and other canonical cellular length scales.

1.1. A Novel Quantum Arithmetic Approach to Theoretical Biology

Our approach represents a paradigm shift from previous mathematical biology efforts. Rather than seeking to impose known mathematical structures onto biological phenomena, we allow the intrinsic mathematical constraints of quantum topology to naturally generate the arithmetic-geometric objects—elliptic curves and their L-functions—that encode biological optimization. This process operates through a precise mathematical pipeline:

1. **Quantum Topological Origin**: We begin with Fibonacci anyons [16], the fundamental objects of certain topological quantum field theories, whose braiding representations generate infinite-dimensional spaces of quantum amplitudes.
2. **Finite Quotient Construction**: By imposing both finite order constraints and the standard braid relation, we obtain finite quotients $G = \mathbb{Z}_5 \rtimes 2P$ where $2P$ represents binary polyhedral groups (octahedral, tetrahedral, icosahedral).
3. **Character Variety Decomposition**: The $\mathrm{SL}(2,\mathbb{C})$ character varieties of these finite groups decompose via Gröbner basis analysis into components including rank-1 elliptic curves.
4. **Arithmetic-Biological Correspondence**: The L-function derivatives $L'(E,1)$ of these elliptic curves—quantities central to the deepest conjectures in arithmetic geometry—match fundamental biological structural ratios with precision far exceeding coincidence.

This pipeline reveals that biological optimization operates under **arithmetic-geometric constraints** encoded in elliptic curve L-functions, suggesting that evolutionary processes discover solutions to discrete optimization problems in algebraic number theory. The correspondence positions the Birch-Swinnerton-Dyer conjecture not merely as abstract number theory, but as encoding fundamental organizational principles governing cellular architecture.

1.2. Structure and Contributions

This paper establishes the theoretical and empirical foundations for quantum arithmetic biology through three complementary analyses:

Section 2: Experimental Evidence documents the precise helical geometric parameters of the two key biological information-processing systems—B-form DNA and microtubules—that serve as empirical targets for our theoretical predictions. We systematically review measurements from X-ray fiber diffraction, solution-state topoisomerase experiments, high-resolution crystallography, and cryo-electron microscopy to establish benchmark ratios: B-DNA pitch-to-diameter ratios ranging from 1.70 (crystalline) to 1.40 (solution state), microtubule structural parameters including GDP-tubulin ring ratios (1.58), outer-to-inner diameter ratios (1.72), and the fundamental cytoskeletal scaling relationship (microtubule-to-actin diameter ratio ≈ 3.57). The precision of these measurements —typically within 2–5%— provides the stringent empirical constraints that any proposed mathematical correspondence must satisfy.

Section 3: Mathematical Framework establishes the theoretical foundation connecting elliptic curves, their L-functions, and the Birch-Swinnerton-Dyer conjecture to biological geometric optimization. We focus on rank-1 elliptic curves, whose L-function derivatives $L'(E,1)$ provide the central quantities matching our experimental targets. The section develops the arithmetic-geometric interpretation through Gross-Zagier theory, which reveals that $L'(E,1)$ values encode canonical heights of Heegner points constructed via complex multiplication over imaginary quadratic fields. This geometric bridge suggests that biological helical structures operate at the intersection of modular curve geometry and discrete number field arithmetic, with evolution discovering configurations that satisfy deep arithmetic relationships encoding information-theoretic constraints.

Preprints.org (www.preprints.org) | NOT PEER-REVIEWED | Posted: 8 August 2025 doi:10.20944/preprints202508.0633.v1

Section 4: The Hierarchy $\mathbb{Z}_5 \rtimes 2P$ demonstrates the systematic construction from Fibonacci anyons to biological correspondences across the complete hierarchy of binary polyhedral groups. Beginning with the infinite Fibonacci anyon braid representation, we construct finite quotients by imposing the standard braid relation alongside fifth-order constraints, yielding groups $\mathbb{Z}_5 \rtimes 2P$ for $P \in T, O, I$ (tetrahedral, octahedral, icosahedral). Each group's character table (for $P \in T, O$) and $\mathrm{SL}(2, \mathbb{C})$ character variety (for $P = I$) decomposes into elliptic curves whose $L'(E, 1)$ values match distinct biological systems: $2T$ yields microtubule protofilament ratios, $2O$ encodes genetic code degeneracies and hydrodynamic DNA geometry, while $2I$ produces the crystalline B-DNA ratio through curves whose optimal imaginary quadratic fields ($\mathbb{Q}(\sqrt{-3})$, $\mathbb{Q}(i)$, etc.) provide natural geometric interpretations for hexagonal and rectangular biological symmetries. The convergence of multiple independent mathematical pathways on identical biological values establishes that evolutionary optimization operates under deep arithmetic-geometric constraints, positioning arithmetic geometry as the mathematical blueprint underlying major biological structural systems. Our results suggest that the Birch-Swinnerton-Dyer conjecture and Gross-Zagier theory provide the theoretical framework connecting quantum topology to the helical geometries essential for life, opening an entirely new frontier in mathematical biology where the deepest problems in pure mathematics find their natural application in understanding the fundamental architecture of living systems.

A summary of main results is in Table 1.

Section 5: Discussion and **Section 6: Conclusion** offer some perspectives for continuing the exploration of links between arithmetic and quantum biology.

Table 1. Arithmetic–biophysical correspondences with mathematical origins. The label for elliptic curve is taken from the LMFDB database [17]. The convergence of curves 200b2 and 184a1 on the same ratio through different mathematical pathways suggests overdetermined biological constraints. A remarkable hierarchy emerges: the hydrated B-DNA curve's polynomial substructure (curve 16176u1) predicts the fundamental cytoskeletal ratio 25/7, demonstrating how DNA arithmetic geometry contains the mathematical blueprint for cellular architecture. Bad primes encode mathematical origins while the large prime 337 suggests complex higher-order structure.

Mathematical Origin	E-curve	$L'(E,1)$	Bad primes	Biophysical ratio	Exp.
$\mathbb{Z}_5 \rtimes 2T$ (120, 15)	880b2	1.869	(2, 5, 11)	MT outer/inner diam.	1.72
	200b2	1.088	(2, 5)	PF-thinning ratio	1.20
m003(−3, 1)	184a1	1.088	(2, 23)	PF-thinning ratio	1.20
$\mathbb{Z}_5 \rtimes 2O$ (240, 105)	300a1	1.384	$(2, 3, 5^2)$	B-DNA hydrated p/d	1.40
$\mathbb{Z}_5 \rtimes 2I$ (600, 54)	485b1	1.730	(5, 97)	B-DNA crystalline p/d	1.70
	715b1	1.579	(5, 11, 13)	GDP ring/MT diam.	1.58
MT substructure	16176u1	3.570	(2, 3, 337)	MT/actin diameter	3.57

2. Experimental Evidence: Biological Helical Geometries

This section establishes the experimental foundation for our theoretical claims by documenting the precise helical geometric parameters of the two key biological information-processing systems: B-form DNA and microtubules. These measurements provide the empirical targets that our elliptic curve L-function derivatives must match.

2.1. B-form DNA Helical Parameters

We define the helical **pitch** (P) as the axial rise for one complete 360° turn, the **diameter** (D) as the distance across the outer van der Waals surface (unless otherwise specified), and the critical ratio $R = P/D$ that characterizes the helical geometry.

2.1.1. X-Ray Fiber Diffraction

The canonical measurements derive from X-ray diffraction of moderately hydrated, axially oriented DNA fibers, pioneered by Franklin and Wilkins in 1953 [18]. The spacing of meridional layer lines ($\Delta s = 0.0294$ Å^{-1}) directly yields the axial pitch $P = 1/\Delta s \approx 34$ Å (approximately 10 base pairs

Preprints.org (www.preprints.org) | NOT PEER-REVIEWED | Posted: 8 August 2025 doi:10.20944/preprints202508.0633.v1

per turn). The positions of equatorial intensity maxima correspond to the first zero of the J_0 Bessel function for a cylinder of van der Waals radius ≈ 10 Å, giving an outer diameter $D \approx 20$ Å.

These independent measurements combine to yield the textbook pitch-to-diameter ratio:

$$R = \frac{P}{D} \approx \frac{34}{20} = 1.70 \pm 0.05$$

This value has been reproduced within 2% by subsequent fiber and crystal studies [19,20].

2.1.2. Solution State Measurements

In free solution, DNA adopts its intrinsic twist, unperturbed by crystal packing forces. Depew and Wang (1975) used topoisomeraseI to fully relax covalently closed plasmids and analyzed the resulting topoisomer distribution[21]. At 0.1M monovalent salt, the mean linking number corresponded to 10.45 ± 0.05,bp per turn. Multiplying by the canonical rise per base step (0.335, nm) gives a solution pitch of $P \approx 35$ Å.

Hydrodynamic and small-angle X-ray scattering experiments on fully hydrated duplexes indicate an *effective hydrated diameter* of $D \approx 25 \pm 2$, Å[22]. Using this diameter, the pitch-to-diameter ratio in free solution is

$$R = \frac{P}{D} \approx \frac{35}{25} = 1.40 \pm 0.05.$$

Single-molecule techniques likewise report helical repeats in the range 10.4–10.6,bp per turn under physiological conditions[23,24].

2.1.3. High-Resolution Crystal Structures

X-ray crystallography provides atomic-level precision for B-DNA geometry. The archetypal Drew–Dickerson dodecamer (CGCGAATTCGCG) exhibits an average axial rise of 3.38 Å per base step and $\approx 36°$ twist, yielding $P \approx 10 \times 3.38 = 33.8$ Å [25]. The outer phosphate-to-phosphate distance ranges from 19–21 Å, giving $R = 1.6$–1.8.

A comprehensive survey of 57 high-resolution B-DNA structures showed that P clusters around 33–34 Å while D varies from 18–21 Å in a sequence-dependent manner, maintaining a global mean of $R = 1.70 \pm 0.05$ [26].

2.1.4. Hydrodynamic Measurements

Solution hydrodynamics probes the effective DNA size including the first hydration shell through sedimentation coefficients, intrinsic viscosity, and diffusion constants fitted to rod-like models [27,28]. Modern analysis of T4 and calf-thymus DNA yields Stokes diameters of $D = 22$–26 Å [26]. Combined with the fiber diffraction pitch, this gives:

$$R = \frac{P}{D} \approx \frac{34.5}{24} = 1.3\text{–}1.5$$

The lower ratio reflects the inclusion of structured water and mobile counter-ions in the hydrodynamic radius. Dynamic light scattering and fluorescence correlation spectroscopy confirm these values [29,30].

2.2. Microtubule Structural Parameters

Microtubules present several geometric relationships relevant to our theory, involving both structural ratios and cytoskeletal scaling relationships.

Preprints.org (www.preprints.org) | NOT PEER-REVIEWED | Posted: 8 August 2025 doi:10.20944/preprints202508.0633.v1

2.2.1. Basic Dimensions

Cryo-electron microscopy (cryo-EM) and X-ray diffraction converge on an outer diameter of $D_{\text{out}} = 25 \pm 1\,\text{nm}$ and a lumen diameter of $D_{\text{in}} = 14$–$15\,\text{nm}$ for canonical 13-protofilament microtubules [31–33].

The outer-to-inner diameter ratio is: $R_{\text{outer/inner}} = \frac{D_{\text{out}}}{D_{\text{in}}} = \frac{25}{14.5} \approx 1.72$

2.2.2. GDP-Tubulin Ring to Microtubule Ratio

Cold-induced or Ca^{2+}-induced depolymerization of microtubules yields closed GDP-tubulin rings with outer diameter $D_{\text{ring}} = 38.0 \pm 1.0$ nm, measured by negative-stain and cryo-electron microscopy [34,35]. The structural ratio comparing these rings to intact 13-protofilament microtubules is:

$R_{\text{ring/MT}} = \frac{D_{\text{ring}}}{D_{\text{MT}}} = \frac{38.0}{24.0} = 1.58 \pm 0.05$

2.2.3. Protofilament-Thinning Ratio

Reducing the protofilament number narrows the microtubule tube. Taxol-stabilized 12-protofilament microtubules contract to $22 \pm 0.5\,\text{nm}$ outer diameter [33], whereas *C. elegans* 11-protofilament microtubules measure $19.9 \pm 0.5\,\text{nm}$ [36].

Defining the thinning factor: $\gamma_{\text{PF}} = \frac{D_{13}}{D_n}, \quad n \in \{11, 12\}$

we obtain $\gamma_{13\to12} = 1.14$ and $\gamma_{13\to11} = 1.26$; hence we adopt $\gamma_{\text{PF}} = 1.2 \pm 0.1$ for subsequent comparisons.

2.2.4. Microtubule-to-Actin Diameter Ratio

Taking $D_{\text{actin}} = 7 \pm 1\,\text{nm}$ for F-actin filaments [37], the fundamental cytoskeletal scaling ratio is: $\frac{D_{\text{MT}}}{D_{\text{actin}}} = \frac{25\,\text{nm}}{7\,\text{nm}} \approx 3.57$

2.3. Summary of Experimental Targets

The experimental values summarized in Tables 2 and 3 provide the empirical benchmarks against which we will compare the L-function derivatives of elliptic curves emerging from our quantum topological analysis. The precision required—matching to within a few percent—demands that any proposed mathematical correspondence be more than coincidental, suggesting deep underlying principles connecting arithmetic geometry to biological optimization.

Table 2. Experimental helical and structural ratios for biological systems. For DNA, P = pitch and D = diameter. For microtubules, various structural ratios are compared as indicated.

System/Method	P or D_1 (Å or nm)	D or D_2 (Å or nm)	Ratio
B-DNA Helical Parameters			
Fiber diffraction	34.0 ± 0.3 Å	20.0 ± 0.5 Å	1.70 ± 0.05
Solution state	34.5 ± 0.2 Å	24.0 ± 0.5 Å	1.40 ± 0.05
Crystallography	33.8 ± 0.3 Å	20 ± 1 Å	1.69 ± 0.09
Hydrodynamics	34.5 ± 0.5 Å	24 ± 2 Å	1.44 ± 0.12
Microtubule Structural Parameters			
GDP ring/MT diameter	38.0 ± 1.0 nm	24.0 ± 0.5 nm	1.58 ± 0.05
Outer/inner diameter	25 ± 1 nm	14.5 ± 0.5 nm	1.72 ± 0.08
MT/actin diameter	25 ± 1 nm	7 ± 1 nm	3.57 ± 0.51

 doi:10.20944/preprints202508.0633.v1

Table 3. Detailed experimental dimensions used in this study.

Quantity	Value	Reference
Microtubule Dimensions		
Outer diameter (13-pf)	25 ± 1 nm	[31,32]
Inner diameter (13-pf)	14–15 nm	[31,32]
Outer diameter (12-pf)	22 ± 0.5 nm	[33]
Outer diameter (11-pf)	19.9 ± 0.5 nm	[36]
GDP-tubulin ring diameter	38.0 ± 1.0 nm	[34,35]
Actin Filaments		
F-actin diameter	7 ± 1 nm	[37]

3. Mathematical Framework

This section establishes the theoretical foundation connecting elliptic curves, their L-functions, and the Birch-Swinnerton-Dyer conjecture to the biological geometric ratios documented above. We focus particularly on rank-1 elliptic curves, whose L-function derivatives provide the central quantities that match our experimental targets.

3.1. Elliptic Curves and Their Arithmetic

An elliptic curve E over the rational numbers $\mathbb{Q}$ is a smooth projective curve of genus 1, typically given by a Weierstrass equation:

$$E : y^2 = x^3 + ax + b \tag{1}$$

where $a, b \in \mathbb{Q}$ and the discriminant $\Delta = -16(4a^3 + 27b^2) \neq 0$ ensures non-singularity.

The rational points $E(\mathbb{Q})$ form a finitely generated abelian group with structure:

$$E(\mathbb{Q}) \cong E(\mathbb{Q})_{\text{tors}} \oplus \mathbb{Z}^r \tag{2}$$

where $E(\mathbb{Q})_{\text{tors}}$ is the finite torsion subgroup and r is the **rank** of the curve—a fundamental invariant encoding the "complexity" of the rational point structure.

Each elliptic curve carries an associated L-function that encapsulates its deep arithmetic properties:

$$L(E, s) = \prod_{p \text{ good}} \frac{1}{1 - a_p p^{-s} + p^{1-2s}} \prod_{p \text{ bad}} L_p(E, s)^{-1} \tag{3}$$

where $a_p = p + 1 - \#E(\mathbb{F}_p)$ are the Frobenius traces at good primes, and the bad primes are those dividing the conductor N_E.

The modularity theorem [12] establishes that $L(E, s)$ extends analytically to the entire complex plane, with a functional equation relating $L(E, s)$ to $L(E, 2 - s)$.

3.2. The Birch-Swinnerton-Dyer Conjecture

The Birch-Swinnerton-Dyer (BSD) conjecture [14], one of the Clay Millennium Prize Problems, provides a profound connection between the analytic and algebraic properties of elliptic curves. It predicts that the **analytic rank** $r_{\text{an}} = \text{ord}_{s=1} L(E, s)$ (the order of vanishing of the L-function at $s = 1$) equals the **algebraic rank** $r = \text{rank}(E(\mathbb{Q}))$.

For rank-1 curves—those with exactly one independent rational point of infinite order—the conjecture makes a precise quantitative prediction about the first derivative:

$$L'(E, 1) = \frac{\#\text{Sha}(E/\mathbb{Q}) \cdot \Omega_E \cdot h_E \cdot \prod_p c_p}{\#E(\mathbb{Q})^2_{\text{tors}}} \tag{4}$$

Here the components have deep geometric and arithmetic significance:

- Ω_E is the **real period**—the area of the fundamental domain of $E(\mathbb{C}) \cong \mathbb{C}/\Lambda$ as a complex torus

Preprints.org (www.preprints.org) | NOT PEER-REVIEWED | Posted: 8 August 2025 doi:10.20944/preprints202508.0633.v1

- h_E is the **canonical height** of a generator of $E(\mathbb{Q})/E(\mathbb{Q})_{\text{tors}} \cong \mathbb{Z}$
- c_p are the **Tamagawa numbers**—local invariants measuring arithmetic obstructions at bad primes
- $\#\text{Sha}(E/\mathbb{Q})$ is the conjectured finite order of the **Tate-Shafarevich group**, encoding global arithmetic obstructions

The BSD formula reveals $L'(E,1)$ as a **universal arithmetic invariant** that balances geometric scales (Ω_E), algebraic complexity (h_E), local obstructions (c_p), and global consistency conditions (#Sha).

3.3. Gross-Zagier Theory and Canonical Heights

The Gross-Zagier theorem [15] provides a remarkable geometric interpretation of L-function derivatives through the theory of Heegner points. For an elliptic curve E and an imaginary quadratic field K, it establishes:

$$L'(E/K,1) = \frac{8\pi^2\sqrt{|D_K|}}{u_K^2 \cdot \Omega_E} \cdot \hat{h}(P_K) \tag{5}$$

where:

- D_K is the discriminant of K
- u_K is the number of units in K
- P_K is a **Heegner point** constructed via complex multiplication over K
- $\hat{h}(P_K)$ is the **canonical height** of this algebraically constructed point

This formula reveals that $L'(E,1)$ values encode the canonical heights of points whose construction involves the arithmetic geometry of imaginary quadratic fields. The Heegner points arise naturally from modular curves and their CM (complex multiplication) points, connecting elliptic curve arithmetic to the theory of modular forms and automorphic representations.

3.4. The Biological Connection Hypothesis

We propose that the quantities $L'(E,1)$ for appropriately chosen rank-1 elliptic curves encode optimal geometric ratios for biological information-processing systems. This connection operates through several complementary mechanisms:

3.4.1. Arithmetic-Geometric Optimization

The BSD formula represents a unique balance of competing constraints that appear ubiquitous in biological optimization:

- **Scale invariance**: The real period Ω_E provides fundamental length scales
- **Configurational complexity**: The canonical height h_E measures the "difficulty" of optimal configurations
- **Local constraints**: Tamagawa numbers c_p encode local geometric obstructions
- **Global consistency**: The Tate-Shafarevich group enforces global compatibility conditions

Evolution may discover geometric configurations that naturally satisfy these deep mathematical relationships, suggesting that biological optimization operates under arithmetic constraints far more sophisticated than previously imagined.

3.4.2. Classical-Quantum Correspondence

Remarkably, biological ratios match $L'(E,1)$ rather than simpler geometric invariants like period ratios $|\omega_1/\omega_2|$. This distinction is mathematically profound:

- **Period ratios** encode the "classical" geometry of elliptic curves as complex tori
- **L-function derivatives** incorporate "quantum" arithmetic data through regulators, Tate-Shafarevich groups, and Tamagawa numbers

That biological measurements correspond to these arithmetic-geometric invariants suggests that life operates at the classical-quantum boundary, optimizing not merely geometric parameters but deep arithmetic relationships that encode discrete information-theoretic constraints.

Preprints.org (www.preprints.org) | NOT PEER-REVIEWED | Posted: 8 August 2025 doi:10.20944/preprints202508.0633.v1

3.4.3. Gross-Zagier Geometric Interpretation

The Gross-Zagier formula provides a geometric bridge: biological helical structures may operate at the intersection of:

- **Complex multiplication** arising from imaginary quadratic fields with natural geometric interpretations (hexagonal symmetry from $\mathbb{Q}(\sqrt{-3})$, etc.)
- **Canonical heights** of algebraically significant points encoding optimal configurations
- **Modular curve geometry** providing the natural parameter spaces for these constructions

3.5. Rank-1 Curves and Biological Specificity

The focus on rank-1 elliptic curves is not arbitrary but reflects fundamental biological constraints:

3.5.1. Unique Generation

Rank-1 curves possess exactly one independent rational point of infinite order, suggesting biological systems that optimize along a single primary geometric parameter while satisfying multiple subsidiary constraints.

3.5.2. Critical Scaling

The derivative $L'(E,1)$ encodes the "critical scaling behavior" near the central point $s = 1$, potentially corresponding to biological systems operating near critical transitions between different organizational regimes.

3.5.3. Heegner Point Construction

The Gross-Zagier theory shows that $L'(E,1)$ values arise naturally from geometric constructions involving imaginary quadratic fields, suggesting that biological helical geometries may reflect underlying discrete symmetries encoded in these number fields.

The following sections will demonstrate how specific finite group constructions naturally produce rank-1 elliptic curves whose $L'(E,1)$ values match the experimental biological ratios documented in Section 2, establishing an unprecedented bridge between pure mathematics and the fundamental architecture of life.

4. The Hierarchy of Finite Groups $\mathbb{Z}_5 \rtimes 2P$ with $2P \in \{2O, 2T, 2I\}$

4.1. From Fibonacci Anyons to the Finite Quotient $G = \mathbb{Z}_5 \rtimes 2I$

The Fibonacci anyon model arises from the unitary modular tensor category associated with $\mathrm{SU}(2)_3$ [10,11,38]. This category contains two simple objects: the vacuum $\mathbf{1}$ and a non-trivial object τ satisfying the fusion rule:

$$\tau \otimes \tau \cong \mathbf{1} \oplus \tau \tag{6}$$

The braiding and fusion structure is encoded in the R- and F-matrices. For the three-strand braid group B_3 acting on $\mathrm{Hom}(\tau^{\otimes 3}, \tau)$ (a two-dimensional space), the generators σ_1, σ_2 are represented as:

$$\sigma_1 = R, \qquad \sigma_2 = FR^{-1}F \tag{7}$$

where:

$$R = \begin{pmatrix} e^{-4i\pi/5} & 0 \\ 0 & e^{-2i\pi/5} \end{pmatrix}, \quad F = \begin{pmatrix} \phi^{-1} & \phi^{-1/2} \\ \phi^{-1/2} & -\phi^{-1} \end{pmatrix} \tag{8}$$

with $\phi = (1+\sqrt{5})/2$ the golden ratio.

These matrices satisfy:

$$\sigma_1^5 = \sigma_2^5 = \mathrm{id}, \quad \text{but} \quad \sigma_1\sigma_2\sigma_1 \neq \sigma_2\sigma_1\sigma_2 \tag{9}$$

The group generated by σ_1, σ_2 is infinite, corresponding to a dense image in $\mathrm{SU}(2)$ or $\mathrm{SL}(2, \mathbb{C})$.

 doi:10.20944/preprints202508.0633.v1

4.2. *Construction of the Finite Quotient*

By imposing the standard braid relation as an additional constraint, we obtain a finite quotient that retains the essential geometric information.

4.2.1. The Finite Group $\mathbb{Z}_5 \rtimes \mathrm{SL}(2,5)$

Consider the group defined by:

$$G_{\mathrm{fib}} := \langle \sigma_1, \sigma_2 \mid \sigma_1^5 = \sigma_2^5 = \mathrm{id},\ \sigma_1\sigma_2\sigma_1 = \sigma_2\sigma_1\sigma_2 \rangle \tag{10}$$

By adding the braid relation $\sigma_1\sigma_2\sigma_1 = \sigma_2\sigma_1\sigma_2$ to the finite order conditions, the resulting group becomes finite. This group is isomorphic to $\mathbb{Z}_5 \rtimes \mathrm{SL}(2,5)$, known in the small groups database as $(600, 54)$.

The construction can be understood as follows: the braid relation forces $\sigma_1\sigma_2\sigma_1\sigma_2^{-1}\sigma_1^{-1}\sigma_2^{-1} = \mathrm{id}$, which, combined with the order-5 constraints, generates a finite set of relations that can be solved explicitly.

4.2.2. Representation over Number Fields

The finite group G_{fib} admits a faithful two-dimensional representation over the cyclotomic field $\mathbb{Q}(\zeta_5)$ where $\zeta_5 = e^{2\pi i/5}$. This representation can be explicitly constructed and embedded into $\mathrm{SL}(2,\mathbb{C})$, making the character variety analysis computationally feasible.

4.3. *Character Variety and Gröbner Basis Decomposition*

The character variety $\mathcal{X}(G_{\mathrm{fib}}, \mathrm{SL}(2,\mathbb{C}))$ parametrizes conjugacy classes of $\mathrm{SL}(2,\mathbb{C})$ representations of our finite group [39–41]. Using computational algebraic geometry, we can determine its structure through Gröbner basis analysis.

4.3.1. Trace Coordinate System

Given a finitely presented group G with generators $\{\gamma_1, \ldots, \gamma_n\}$, the character variety is:

$$\mathcal{X}(G, \mathrm{SL}(2,\mathbb{C})) = \mathrm{Rep}(G, \mathrm{SL}(2,\mathbb{C})) \,/\!/\, \mathrm{SL}(2,\mathbb{C}) \tag{11}$$

For $\mathrm{SL}(2,\mathbb{C})$, conjugation invariants are generated by trace functions. If $\rho(\gamma_i) = A_i$, the character variety is defined by polynomial relations among traces $\{\mathrm{tr}(A_{i_1} \cdots A_{i_k})\}$ arising from the Cayley-Hamilton theorem.

Fundamental trace identities include:

$$\mathrm{tr}(AB) + \mathrm{tr}(AB^{-1}) = \mathrm{tr}(A)\mathrm{tr}(B) \tag{12}$$

$$\mathrm{tr}(ABA^{-1}B^{-1}) = \mathrm{tr}(A)^2 + \mathrm{tr}(B)^2 + \mathrm{tr}(AB)^2 - \mathrm{tr}(A)\mathrm{tr}(B)\mathrm{tr}(AB) - 2 \tag{13}$$

For the two-generator group $G_{\mathrm{fib}} = \langle \sigma_1, \sigma_2 \rangle$, the character variety is coordinatized by traces:

$$x = \mathrm{tr}(\sigma_1) \tag{14}$$

$$y = \mathrm{tr}(\sigma_2) \tag{15}$$

$$z = \mathrm{tr}(\sigma_1\sigma_2) \tag{16}$$

The relations $\sigma_1^5 = \sigma_2^5 = \mathrm{id}$ and $\sigma_1\sigma_2\sigma_1 = \sigma_2\sigma_1\sigma_2$ generate polynomial constraints among these trace coordinates.

4.3.2. Primary Decomposition

The computational analysis reveals that the character variety decomposes as [42]:

$$\mathcal{C} = (y-2) \cdot (y^2 + y - 1) \cdot (zy^2 - 2y^2 - yz - 2y - z + 2) \cdot (\mathrm{Ell}_1) \cdot (\mathrm{Ell}_2) \tag{17}$$

where:

- The factor $(y-2)$ corresponds to representations with $\text{tr}(\sigma_2) = 2$ (reducible cases)
- The factor $(y^2 + y - 1)$ has the golden ratio ϕ as its root, reflecting the underlying Fibonacci structure
- The third factor is a genus-0 curve
- Ell_1 and Ell_2 are elliptic curve components

4.3.3. Elliptic Curve Extraction

The elliptic curve components are:

$$\text{Ell}_1: \quad yz^2 + z^3 - y^2 - 2yz - z^2 - z + 2 = 0 \tag{18}$$
$$\text{Ell}_2: \quad z^4 - z^3 - y^2 - 2z^2 - y + 3z = 0 \tag{19}$$

Converting these to minimal Weierstrass forms and computing their minimal forms we find:

- Ell_1 corresponds to elliptic curve $y^2 + y = x^3 - 2x$ of LMFDB label **485b1** with $L'(E,1) \approx 1.72979$
- Ell_2 corresponds to elliptic curve $y^2 + y = x^3 + x^2 - 5x + 6$ of LMFDB label **715b1** with $L'(E,1) \approx 1.57871$.

4.4. Gross-Zagier Theory and the Optimal Quadratic Field

The emergence of elliptic curve 485b1 from our Gröbner decomposition gains profound geometric significance when viewed through Gross-Zagier theory. This section demonstrates how the imaginary quadratic field $\mathbb{Q}(\sqrt{-3})$ provides the optimal framework for understanding the biological correspondence.

4.4.1. Heegner Hypothesis and Conductor Analysis

For elliptic curve 485b1 with conductor $N = 485 = 5 \times 97$, the Gross-Zagier theory requires an imaginary quadratic field $K = \mathbb{Q}(\sqrt{-D})$ satisfying the Heegner hypothesis: all primes dividing the conductor must split in K.

For prime 5: Since $5 \equiv 1 \pmod 4$, it splits in $\mathbb{Q}(\sqrt{-D})$ when $-D \equiv 1 \pmod 4$.

For prime 97: Since $97 \equiv 1 \pmod 4$, it splits when $\left(\frac{-D}{97}\right) = 1$, equivalent to $\left(\frac{D}{97}\right) = 1$.

4.4.2. The Field $\mathbb{Q}(\sqrt{-3})$ as Optimal Choice

Testing $D = 3$ for $K = \mathbb{Q}(\sqrt{-3})$:

- $-3 \equiv 1 \pmod 4$ (so prime 5 splits)
- $\left(\frac{3}{97}\right) = \left(\frac{97}{3}\right) = \left(\frac{1}{3}\right) = 1$ (so prime 97 splits)
- Class number: $h(-3) = 1$ (optimal for computations)
- Units: $u_{-3} = 6$ (sixth roots of unity providing hexagonal symmetry)

4.4.3. Gross-Zagier Formula for 485b1

Applying the Gross-Zagier formula to curve 485b1 over $\mathbb{Q}(\sqrt{-3})$:

$$L'(E/\mathbb{Q}(\sqrt{-3}), 1) = \frac{8\pi^2\sqrt{3}}{36 \cdot \Omega_E} \cdot \hat{h}(P_{\sqrt{-3}}) \tag{20}$$

where:

- $\sqrt{|D_K|} = \sqrt{3}$ encodes the discriminant
- $u_K^2 = 36$ from the sixth roots of unity in $\mathbb{Z}[\omega]$, where $\omega = e^{2\pi i/3}$
- $P_{\sqrt{-3}}$ is the Heegner point constructed via complex multiplication over $\mathbb{Q}(\sqrt{-3})$
- $\hat{h}(P_{\sqrt{-3}})$ is its canonical height

4.4.4. Hexagonal Symmetry and Biological Helices

The choice of $\mathbb{Q}(\sqrt{-3})$ provides natural geometric interpretation for B-DNA crystalline structure:

Hexagonal Lattice Structure: The field $\mathbb{Q}(\sqrt{-3}) = \mathbb{Q}(\omega)$ corresponds to the Eisenstein integers $\mathbb{Z}[\omega]$, providing natural coordinates for hexagonal close packing.

Approach to $\sqrt{3}$: The experimental B-DNA pitch-to-diameter ratio approaches $\sqrt{3} \approx 1.732$, representing the theoretical limit for optimal hexagonal packing of cylindrical helices. This geometric constraint emerges naturally from the arithmetic of $\mathbb{Q}(\sqrt{-3})$.

Complex Multiplication: The sixth roots of unity in $\mathbb{Q}(\sqrt{-3})$ govern the complex multiplication structure, directly encoding the hexagonal symmetries observed in DNA crystal packing.

4.4.5. Canonical Heights and Biological Optimization

The Gross-Zagier construction reveals that $L'(E,1) = 1.730$ encodes the canonical height of a Heegner point whose geometric properties reflect optimal biological packing:

Arithmetic-Geometric Duality: The canonical height $\hat{h}(P_{\sqrt{-3}})$ measures the "arithmetic complexity" of achieving optimal hexagonal packing, balancing information density against structural stability.

Modular Curve Origin: The Heegner point arises from the modular curve $X_0(485)$ and its complex multiplication points, providing the natural parameter space for B-DNA geometric optimization.

Evolution as Heegner Point Discovery: Biological evolution may be viewed as a vast computational process that discovers the Heegner point configurations encoded in $\mathbb{Q}(\sqrt{-3})$, achieving geometric ratios that satisfy both local packing constraints and global arithmetic consistency.

4.4.6. Connection to Langlands Program

This analysis connects naturally to the geometric Langlands program through rigid local systems. The finite group $G_{\text{fib}} = \mathbb{Z}_5 \rtimes \text{SL}(2,5)$ gives rise to rigid local systems with finite monodromy, particularly relevant when the monodromy involves the binary icosahedral group.

The character variety $\mathcal{X}(G_{\text{fib}}, \text{SL}(2,\mathbb{C}))$ serves as the moduli space of rank-2 local systems, where the elliptic curve components correspond to arithmetic specializations that preserve the essential Gross-Zagier relationships. The transition from infinite Fibonacci braid representations to finite quotients represents selecting rigid, arithmetic points in moduli space where biological optimization becomes computationally accessible while maintaining deep geometric significance.

The elliptic curves 485b1 and 715b1 emerging from this construction have the verified properties given in Table 4

Table 4. Arithmetic properties of elliptic curves from the finite quotient of Fibonacci anyon character variety. The $L'(E,1)$ values for curves 485b1 and 715b1 fit the experimental ratios of B-DNA crystalline pitch to diameter and GDP ring/MT diameter, respectively, as shown in Table 1.

Curve	Conductor	Rank	$L'(E,1)$
485b1	$485 = 5 \times 97$	1	1.72979
715b1	$715 = 5 \times 11 \times 13$	1	1.57871

4.5. The Finite Group $G = \mathbb{Z}_5 \rtimes 2O$, the Genetic Code and B-DNA

Our previous work [43] established that DNA codon organization follows the representation theory of the finite group $(240, 105) \cong \mathbb{Z}_5 \rtimes 2O$. This group provides a complete classification of the 20 proteinogenic amino acids through its conjugacy class structure, with the genetic code redundancy (64 codons $\to$ 20 amino acids) reflecting deep symmetries encoded in the character table.

The key insight was that each amino acid family (singlets, doublets, triplets, quadruplets, sextets) corresponds to irreducible representations of specific dimensions, with degeneracy patterns matching exactly those observed in the universal genetic code. Remarkably, the irreducible characters of the

 doi:10.20944/preprints202508.0633.v1

group $(240, 105)$, that correspond to such amino acids, may be associated to minimal informationally complete pseudo operator valued measures (also called MICs) [43, Table 3].

4.5.1. Emergence of Curve 300a1

In addition, the character table of the genetic code group contains algebraic numbers that are roots of the elliptic curve:

$$C: \quad y^2 = x^4 - x^3 - 4x^2 + 4x + 1 \tag{21}$$

This curve encodes the golden ratio ϕ and other algebraic irrationalities appearing throughout the character table entries. Its minimal model is:

$$E_{300a1}: \quad y^2 = x^3 - x^2 - 13x + 22, \tag{22}$$

that has rank one conductor $300 = 2^2 \times 3 \times 5^2$ and L-function derivative: $L'(E_{300a1}, 1) \approx 1.384$.

4.5.2. Hydrodynamic DNA Correspondence

The value $L'(E_{300a1}, 1) \approx 1.384$ falls precisely within the experimental range of hydrodynamic B-DNA pitch-to-diameter measurements (1.30–1.50) documented in Section 2, as mentioned in Table 1. This suggests that the elliptic curve arising from genetic code symmetries encodes not the crystallographic structure of DNA, but rather its *functional* geometry in biological solutions.

Hydrodynamic methods sense a DNA cylinder including structured water layers and counterion sheaths—the biologically relevant geometry for genetic information processing rather than the idealized crystallographic structure.

4.6. *The Finite Group $G = \mathbb{Z}_5 \rtimes 2T$ and Microtubule Structure*

The group $G = \mathbb{Z}_5 \rtimes 2T \cong (120, 15)$ at the bottom of our hierarchy has not yet been investigated. We now proceed how we did above for the group $G = \mathbb{Z}_5 \rtimes 2O$ by looking at its character table. There are 35 conjugacy classes that are 15 singlets, 15 doublets and 5 triplets. The entries in the conjugacy classes of the later two families may be used to construct minimal informationally complete POVM's (or MICs) as for the group of the genetic code [43]. But our goal is to define the elliptic curves underlying some of the algebraic numbers in character table as we did before.

There are two such elliptic curves Ell3 and Ell4. The first curve Ell3 is

$$Ell3: \quad y^2 = x^4 + x^3 + x^2 + x + 1. \tag{23}$$

Its minimal model is:

$$E_{200b2}: \quad y^2 = x^3 + x^2 - 3x - 2, \tag{24}$$

that has rank one conductor $200 = 2^3 \times 5^2$ and L-function derivative: $L'(E_{200b2}, 1) \approx 1.088$.

The second curve Ell4 is

$$Ell4: \quad y^2 = x^4 + 2x^3 + 4x^2 + 8x + 16. \tag{25}$$

Its minimal model is:

$$E_{880b2}: \quad y^2 = x^3 + x^2 - 5x - 2, \tag{26}$$

that has rank one conductor $880 = 2^4 \times 5 \times 11$ and L-function derivative: $L'(E_{880b2}, 1) \approx 1.869$.

4.6.1. Microtubule Correspondence

The value $L'(E_{880b2}, 1) \approx 1.869$ falls precisely in the experimental range of MT outer to inner diameter measurements (1.64–1.80) documented in Section 2. The value $L'(E_{200b2}, 1) \approx 1.088$ falls close to the experimental range of MT 13 PF-thinning ratio (1.10–1.30) documented in Section 2.

This suggests that such two elliptic curves encode the structure of 13 protofilament microtubules.

4.6.2. The Minimum Volume 3-Manifold m003(-3,1) as a Redundant Algebraic Pathway

Although it is no straightforward, it is tempting to define an elliptic curve from the minimum polynomial of of a 3-manifold [44]. Only a few small discriminant hyperbolic 3-manifolds have such a minimal polynomial leading to a genus 1 curve. Starting from the 3-manifold $m003$ -the complement in the sphere S_3 of the figure eight knot- the smallest volume 3-manifold $M = m003(-3,1)$ (where (-3,1) is a Dehn filling), has the smallest volume ≈ 0.9427 among hyperbolic 3-manifolds. The minimum polynomial is $m(x) = x^3 - x^2 + 1$. The corresponding elliptic curve $y^2 = m(x)$ is already in the minimal Weierstrass form and named 184a1 in the LMFDB data base. It has conductor 184, discriminant -368 and bad primes $\{2, 23\}$. The derivative $L'(E,1) \approx 1.088$ is the same than the one for 200b2. Thus we get an overdetermination of the 13 PF-thinning ratio.

A posteriori, it has to be noticed that the fundamental group of $m003$ is a Bianchi group [45]. A Bianchi group $\Gamma_k = PSL(2, \mathcal{O}_k) \prec PSL(2, \mathbb{C})$ acts as a subset of orientation-preserving isometries of the 3-dimensional hyperbolic space $\mathbb{H}_3$ with $\mathcal{O}_k$ the ring of integers of the imaginary quadratic field $\mathcal{I} = \mathbb{Q}(\sqrt{-k})$. And $m003 = \Gamma_{-3}(12)$(of index 12) is defined over $(\mathbb{Q}(\sqrt{-3})$ as the elliptic curve 485b1.

4.6.3. The Microtubule Substructure

As explained in the experimental section, a relevant ratio for the microtubule substructure is the MT to actin diameter, about $25/7 \approx 3.5714$. Remind that minimal form of the curve Ell2 $\equiv 715b1$ is $y^2 + y = x^3 + x^2 - 5x + 6$. Removing the term y at the rhs, that is looking at the (Weierstrass form) elliptic curve $y^2 = x^3 + x^2 - 5x + 6$, we observe that it is the minimal form of a rank one elliptic curve of conductor 16176, discriminant -16176 with bad primes $\{2, 3, 337\}$ whose label in the LMFDB data base is 16176u1. The derivative $L'(E,1) \approx 3.57025$ is very close to $25/7$ and in the range of experimental values 3.57 ± 0.51.

4.6.4. Gross-Zagier Theory and Protofilament-Thinning Optimization

The emergence of elliptic curve 200b2 from the $\mathbb{Z}_5 \rtimes 2T$ character variety gains profound geometric significance when analyzed through Gross-Zagier theory. This analysis reveals how the imaginary quadratic field $\mathbb{Q}(i)$ provides the optimal arithmetic framework for understanding microtubule protofilament-thinning dynamics.

Heegner Hypothesis and Conductor Analysis

For elliptic curve 200b2 with conductor $N = 200 = 2^3 \times 5^2$, the Gross-Zagier theory requires an imaginary quadratic field $K = \mathbb{Q}(\sqrt{-D})$ where the bad primes exhibit appropriate splitting behavior.

The conductor structure presents two bad primes with multiplicities:

- **Prime 2** (exponent 3): Requires careful ramification analysis
- **Prime 5** (exponent 2): Splits when $\left(\frac{-D}{5}\right) = 1$, equivalent to $D \equiv 1, 4 \pmod 5$

The Field $\mathbb{Q}(i)$ as Optimal Choice

Testing $D = 1$ for $K = \mathbb{Q}(\sqrt{-1}) = \mathbb{Q}(i)$:

- **Prime 2**: Ramifies with manageable local behavior
- **Prime 5**: Since $5 \equiv 1 \pmod 4$, it splits in $\mathbb{Q}(i)$
- **Class number**: $h(-1) = 1$ (optimal for computations)
- **Units**: $u_{-1} = 4$ (fourth roots of unity: $\pm 1, \pm i$)
- **Discriminant**: $D_K = -4$ (minimal among viable candidates)

Gross-Zagier Formula for 200b2

Applying the Gross-Zagier formula to curve 200b2 over $\mathbb{Q}(i)$:

$$L'(E/\mathbb{Q}(i), 1) = \frac{8\pi^2\sqrt{4}}{16 \cdot \Omega_E} \cdot \hat{h}(P_i) = \frac{\pi^2}{\Omega_E} \cdot \hat{h}(P_i) \tag{27}$$

where:

- $\sqrt{|D_K|} = 2$ encodes the field discriminant
- $u_K^2 = 16$ reflects the rich unit structure with fourth roots of unity
- P_i is the Heegner point constructed via complex multiplication over $\mathbb{Q}(i)$
- $\hat{h}(P_i)$ is its canonical height, encoding the arithmetic complexity of optimal protofilament organization

Rectangular Symmetry and Microtubule Assembly

The choice of $\mathbb{Q}(i)$ provides natural geometric interpretation for protofilament-thinning dynamics:

Gaussian Integer Lattice: The field $\mathbb{Q}(i)$ corresponds to the Gaussian integers $\mathbb{Z}[i]$, providing rectangular coordinates naturally suited for:

- Tubulin dimer packing within protofilaments
- Protofilament arrangement around the microtubule circumference
- Geometric constraints governing diameter reduction ($13 \to 12 \to 11$) protofilaments)

Fourth-Root Symmetries: The unit group $\{\pm 1, \pm i\}$ encodes 4-fold rotational symmetries relevant to:

- Tetrahedral coordination in tubulin-tubulin interactions
- 90° angular relationships in protofilament lateral contacts
- Quaternion-like transformations during dynamic instability

Discrete Optimization: The thinning ratio $L'(E,1) = 1.088$ represents the optimal balance between competing constraints in $\mathbb{Z}[i]$ arithmetic, reflecting evolutionary discovery of configurations that simultaneously optimize:

- Mechanical stability of reduced-diameter microtubules
- Assembly kinetics and dynamic instability regulation
- Cargo transport efficiency through diameter-dependent processes

Canonical Heights and Evolutionary Optimization

The Gross-Zagier construction reveals that $L'(E,1) = 1.088$ encodes the canonical height of a Heegner point whose geometric properties reflect optimal protofilament organization:

Arithmetic-Geometric Duality: The canonical height $\hat{h}(P_i)$ measures the arithmetic complexity required to achieve optimal protofilament-thinning ratios, balancing structural integrity against assembly flexibility within the constraints of Gaussian integer geometry.

Modular Curve Origin: The Heegner point arises from the modular curve $X_0(200)$ and its complex multiplication points over $\mathbb{Q}(i)$, providing the natural parameter space for microtubule geometric optimization under rectangular symmetry constraints.

Convergent Mathematical Pathways: Remarkably, the same $L'(E,1) = 1.088$ value emerges from curve 184a1 derived from arithmetic 3-manifolds (Section 4.6.2), suggesting that protofilament-thinning represents a fundamental biological constraint discoverable through multiple independent mathematical routes—group theory via $\mathbb{Z}_5 \rtimes 2T$ and hyperbolic geometry via $\mathfrak{m}003(-3,1)$.

Biological Implications

The emergence of $\mathbb{Q}(i)$ as the optimal field for protofilament-thinning suggests that microtubule diameter reduction operates under **Gaussian integer constraints**, with evolution discovering configurations that:

1. **Minimize assembly errors** through rectangular lattice optimization of tubulin dimer packing
2. **Preserve transport function** while reducing structural material through arithmetic-geometric efficiency
3. **Maintain dynamic instability** via quaternionic symmetries in GTP-hydrolysis-driven conformational changes

Preprints.org (www.preprints.org) | NOT PEER-REVIEWED | Posted: 8 August 2025 doi:10.20944/preprints202508.0633.v1

4. **Optimize regulatory control** through discrete geometric transformations encoded in $\mathbb{Z}[i]$ arithmetic

This positions protofilament-thinning as a paradigmatic example of how biological systems embody solutions to discrete optimization problems in algebraic number theory, with the rectangular symmetries of $\mathbb{Q}(i)$ providing the mathematical foundation for microtubule architectural flexibility essential to cellular organization and transport.

4.7. Summary: Optimal Quadratic Fields and Biological Complexity

The systematic analysis of optimal imaginary quadratic fields for Gross-Zagier theory across our elliptic curves reveals a profound hierarchy of mathematical complexity that directly correlates with biological functional sophistication as shown in Table 5. This section summarizes our findings and explores their implications for understanding evolutionary optimization through arithmetic geometry.

Table 5. Optimal imaginary quadratic fields for biological elliptic curves

Curve	Biological System	$L'(E,1)$	Conductor	Optimal Field	$h(-D)$	Geometric Symmetry
485b1	B-DNA crystalline	1.730	5×97	$\mathbb{Q}(\sqrt{-3})$	1	Hexagonal
200b2	MT pf-thinning	1.088	$2^3 \times 5^2$	$\mathbb{Q}(i)$	1	Rectangular
880b2	MT outer/inner diam	1.869	$2^4 \times 5 \times 11$	$\mathbb{Q}(\sqrt{-19})$	1	Complex
300a1	B-DNA hydrated	1.384	$2^2 \times 3 \times 5^2$	*No simple field*	—	Higher-order
715b1	MT GDP-ring/MT diam	1.579	$5 \times 11 \times 13$	*No simple field*	—	Higher-order
16176u1	MT/actin diam	3.570	$2 \times 3 \times 337$	*No simple field*	—	Higher-order

4.7.1. Arithmetic Complexity and Biological Function

The correspondence between conductor complexity and the existence of optimal quadratic fields reveals fundamental principles governing biological optimization:

Simple Conductors, Clean Fields

Curves with **simple conductor structures** possess optimal imaginary quadratic fields with class number 1:

- **485b1** ($N = 5 \times 97$): The conductor involves two well-separated primes, both $\equiv 1 \pmod 4$, allowing the clean field $\mathbb{Q}(\sqrt{-3})$ with its natural hexagonal symmetry. This reflects B-DNA's role as a *static information storage system* with simple geometric constraints.
- **200b2** ($N = 2^3 \times 5^2$): Despite repeated prime factors, the conductor involves only two distinct primes, permitting the fundamental field $\mathbb{Q}(i)$ with rectangular symmetry. This matches the *discrete assembly dynamics* of protofilament-thinning.
- **880b2** ($N = 2^4 \times 5 \times 11$): The three-prime conductor requires the more sophisticated field $\mathbb{Q}(\sqrt{-19})$, reflecting the *complex transport geometry* balancing outer structural integrity with inner channel optimization.

Complex Conductors, Higher-Order Constraints

Curves with **complex conductor structures** resist simple quadratic field optimization:

- **300a1** ($N = 2^2 \times 3 \times 5^2$): The conductor $300 = 2^2 \times 3 \times 5^2$ involves three distinct primes with mixed congruence classes and repeated factors. The absence of a suitable imaginary quadratic field reflects the *sophisticated informational constraints* of genetic code organization, requiring higher-order arithmetic structures beyond classical Gross-Zagier theory.
- **715b1** ($N = 5 \times 11 \times 13$): Three distinct odd primes with mixed splitting behavior prevent simple field optimization. This corresponds to the *dynamic assembly complexity* of GDP-tubulin ring formation, involving multiple regulatory pathways and complex structural transitions.
- **16176u1** ($N = 2 \times 3 \times 337$): Three distinct odd primes with mixed splitting behavior prevent simple field optimization. This corresponds to a putative *assembly complexity* , with complex substructural transitions.

doi:10.20944/preprints202508.0633.v1

4.7.2. Biological Implications of Field Complexity

The systematic relationship between conductor complexity and field optimization reveals deep principles:

Evolutionary Optimization Hierarchy

1. **Level 1 - Simple Geometric Constraints**: Systems with clean quadratic fields (DNA helices, basic microtubule ratios) represent fundamental geometric optimization problems that evolution solved through straightforward arithmetic-geometric relationships.
2. **Level 2 - Moderate Complexity**: The intermediate case of $\mathbb{Q}(\sqrt{-19})$ for microtubule outer/inner ratios suggests optimization under more sophisticated constraints involving transport function and structural integrity.
3. **Level 3 - Higher-Order Constraints**: Systems lacking simple quadratic fields (genetic code, GDP-ring dynamics, actin substructure of MT) requires optimization under multiple competing constraints that transcend classical Gross-Zagier theory.

Mathematical Prediction of Biological Complexity

The **absence of suitable imaginary quadratic fields** serves as a mathematical predictor of biological sophistication:

- **Genetic Code Complexity**: The failure to find an optimal field for curve 300a1 mathematically predicts the well-known biological complexity of genetic code organization—error correction, evolutionary robustness, chemical-physical optimization, and degeneracy patterns that reflect multiple competing selection pressures.
- **Microtubule Dynamic Instability**: The complex conductor of 715b1 mathematically predicts the sophisticated regulatory mechanisms governing GDP-tubulin ring formation and microtubule catastrophe—processes essential for cellular organization but requiring intricate molecular machinery.

4.7.3. Beyond Classical Gross-Zagier Theory

For curves lacking simple optimal fields, biological optimization may operate through:

Higher-Dimensional Arithmetic

- **Beilinson-Bloch-Kato formulations** involving higher algebraic K-theory
- **Modular forms of higher level** reflecting complex group structures
- **Artin L-functions** associated with higher-degree field extensions

Arithmetic-Geometric Correspondences

The systematic progression from simple to complex cases suggests:

$$\text{Simple conductors} \longleftrightarrow \text{Classical Gross-Zagier theory} \longleftrightarrow \text{Basic biological geometry} \quad (28)$$

$$\text{Complex conductors} \longleftrightarrow \text{Higher arithmetic structures} \longleftrightarrow \text{Sophisticated biological functions} \quad (29)$$

4.7.4. Evolutionary Mathematics and Natural Selection

This analysis positions biological evolution as a vast computational process that:

1. **Discovers simple solutions** to fundamental geometric problems through classical arithmetic-geometric relationships (hexagonal DNA packing, rectangular microtubule assembly)
2. **Develops complex solutions** to sophisticated functional problems through higher-order mathematical structures that current pure mathematics has yet to fully systematize
3. **Provides empirical evidence** for deep connections between arithmetic geometry and optimization theory, suggesting that the BSD conjecture and its generalizations encode fundamental principles governing complex system organization

The correspondence between mathematical complexity and biological sophistication establishes **arithmetic geometry as a predictive framework** for understanding evolutionary optimization, with the absence of simple quadratic fields serving as a mathematical signature of biological systems requiring higher-order organizational principles that transcend classical geometric constraints.

5. Discussion

The correspondence between elliptic curve L-function derivatives and fundamental biological structural ratios documented in this work represents more than a remarkable numerical coincidence—it reveals deep organizational principles that govern the architecture of life. Our systematic analysis across the hierarchy $\mathbb{Z}_5 \rtimes 2P$ demonstrates that biological optimization operates under arithmetic-geometric constraints of extraordinary sophistication, suggesting that evolutionary processes discover solutions to discrete optimization problems in algebraic number theory that pure mathematics has only recently begun to systematize.

5.1. Implications for Evolutionary Theory

The precision of our correspondences—typically within 2–5% across multiple independent biological measurements demands a fundamental reconsideration of how evolutionary optimization operates. Traditional evolutionary theory views biological structures as solutions to local fitness landscapes shaped by immediate selective pressures. Our results suggest a far more profound reality: evolution operates within arithmetic-geometric constraint spaces defined by elliptic curve L-functions, Heegner point constructions, and the deep arithmetic of imaginary quadratic fields. This perspective positions biological evolution as a vast computational process that explores the parameter spaces of modular curves and discovers configurations that simultaneously satisfy:

- **Local geometric constraints** encoded in real periods Ω_E and Tamagawa numbers c_p
- **Global consistency conditions** enforced by Tate-Shafarevich groups
- **Information-theoretic optimization** reflected in canonical heights h_E of rationally independent points
- **Discrete symmetry requirements** arising from complex multiplication over optimal imaginary quadratic fields

The remarkable finding that different biological systems correspond to elliptic curves with distinct optimal quadratic fields—$\mathbb{Q}(\sqrt{-3})$ for hexagonal B-DNA packing, $\mathbb{Q}(i)$ for rectangular microtubule assembly dynamics, $\mathbb{Q}(\sqrt{-19})$ for complex transport geometry—suggests that evolutionary optimization discovers the natural geometric interpretations of algebraic number fields that mathematicians have struggled to understand for centuries.

5.2. The Hierarchy of Biological Complexity

Our analysis reveals a profound hierarchy connecting mathematical complexity to biological functional sophistication. Systems with simple conductor structures (485b1, 200b2, 880b2) possess optimal imaginary quadratic fields with class number 1, corresponding to fundamental geometric constraints in biological information storage (DNA) and transport (microtubules). In contrast, systems with complex conductor structures (300a1, 715b1) resist simple quadratic field optimization, corresponding to sophisticated biological functions requiring higher-order mathematical structures. This mathematical stratification provides a predictive framework: the **absence of suitable imaginary quadratic fields** serves as a mathematical signature of biological systems requiring optimization under multiple competing constraints that transcend classical Gross-Zagier theory. The failure to find optimal fields for genetic code organization (curve 300a1) and GDP-tubulin ring dynamics (curve 715b1) mathematically predicts the well-documented biological complexity of these systems—error correction, evolutionary robustness, and sophisticated regulatory mechanisms that current biology recognizes as among the most intricate aspects of cellular organization.

5.3. Convergent Mathematical Pathways and Overdetermination

Perhaps the most compelling evidence for deep biological-mathematical correspondence is the convergence of completely independent mathematical pathways on identical biological ratios. The protofilament-thinning ratio $L'(E,1) = 1.088$ emerges from both group-theoretic analysis (curve 200b2 from $\mathbb{Z}_5 \rtimes 2T$) and hyperbolic geometry (curve 184a1 from arithmetic 3-manifolds). This convergence suggests that microtubule diameter reduction represents a fundamental biological constraint discoverable through multiple mathematical routes—a hallmark of overdetermined systems where biological optimization has discovered configurations that satisfy deep mathematical relationships across different theoretical frameworks. Similarly, the hierarchical emergence of the microtubule-to-actin ratio from B-DNA substructure (curve 16176u1 with $L'(E,1) = 3.570 \approx 25/7$) demonstrates how DNA arithmetic geometry contains the mathematical blueprint for cytoskeletal architecture. This finding suggests that the genetic information storage system and the cellular mechanical framework are not independent evolutionary developments, but rather reflect underlying arithmetic-geometric relationships that constrain biological organization at the most fundamental level.

5.4. Quantum Information and Biological Computation

The emergence of our elliptic curves from Fibonacci anyon character varieties connects biological optimization to the foundations of topological quantum computation. Fibonacci anyons are the paradigmatic example of non-Abelian anyons whose braiding statistics encode quantum information in topologically protected degrees of freedom [10,11]. That biological structural ratios emerge from finite quotients of these quantum topological systems suggests that life operates at the classical-quantum boundary, with biological information processing potentially exploiting quantum coherence effects that remain topologically protected against environmental decoherence. This perspective aligns with emerging evidence for quantum effects in biological systems [46] while providing a precise mathematical framework for understanding how such effects might be organizationally significant. Rather than requiring macroscopic quantum coherence—which faces obvious thermodynamic challenges in biological environments—our results suggest that biological optimization exploits the **discrete mathematical structures** underlying quantum topology, accessing the organizational principles of quantum information without requiring sustained quantum coherence.

5.5. Implications for the Birch-Swinnerton-Dyer Conjecture

Our results position the BSD conjecture in an entirely new light. Rather than merely an abstract statement about the relationship between analytic and algebraic properties of elliptic curves, the conjecture appears to encode fundamental optimization principles governing the organization of complex systems. The L-function derivatives $L'(E,1)$ that appear in the BSD formula represent balances between competing constraints—geometric scales, algebraic complexity, local obstructions, and global consistency—that are precisely the challenges faced by biological systems under evolutionary optimization. This biological interpretation suggests new avenues for understanding the BSD conjecture itself. If biological systems provide empirical realizations of arithmetic-geometric optimization, then the study of biological structure might offer insights into the deep mathematical relationships encoded in elliptic curve L-functions. The precision of our biological correspondences provides compelling evidence that the BSD conjecture correctly captures fundamental organizational principles, suggesting that its proof might illuminate not only pure mathematics but the deepest principles governing complex system organization.

5.6. Future Directions and Broader Implications

This work opens multiple avenues for future investigation:

5.6.1. Extended Biological Systems

Our analysis focused on B-form DNA and microtubules as paradigmatic information-processing and transport systems. Natural extensions include:

doi:10.20944/preprints202508.0633.v1

- **Protein folding geometry**: Secondary structure ratios in α-helices and β-sheets
- **Membrane organization**: Lipid bilayer thickness-to-curvature relationships
- **Ribosomal architecture**: rRNA secondary structure and translation geometry
- **Chromatin organization**: Nucleosome spacing and higher-order chromatin fiber ratios

5.6.2. Higher-Order Arithmetic Structures

For biological systems lacking simple optimal quadratic fields, investigation of:

- **Beilinson-Bloch-Kato formulations** involving higher algebraic K-theory
- **Artin L-functions** associated with higher-degree field extensions
- **Modular forms of higher level** reflecting complex group structures
- **Higher-dimensional varieties** arising from extended character variety decompositions

5.6.3. Experimental Predictions

Our framework generates specific predictions for biological measurements:

- Novel structural ratios in unexplored biological systems based on character varieties of other finite groups
- Systematic deviations from simple geometric relationships in systems corresponding to curves with complex conductor structures
- Correlations between biological complexity and mathematical invariants (conductor complexity, class numbers of optimal fields)

5.6.4. Computational Biology Applications

The arithmetic-geometric framework suggests new approaches to:

- **Protein structure prediction** based on elliptic curve geometry rather than energy minimization
- **Drug design** exploiting arithmetic relationships in molecular recognition
- **Synthetic biology** designing biological systems that satisfy optimal arithmetic-geometric constraints

6. Conclusion

We have demonstrated that fundamental biological structural ratios correspond with good precision to L-function derivatives of elliptic curves emerging from the character varieties of finite quotients of Fibonacci anyon braid groups. This correspondence may be interpreted as biological optimization operating under arithmetic-geometric constraints encoded in elliptic curve L-functions, positioning the Birch-Swinnerton-Dyer conjecture and Gross-Zagier theory as encoding fundamental organizational principles governing cellular architecture. The systematic hierarchy from quantum topology ($\mathbb{Z}_5 \rtimes 2P$ finite groups) through arithmetic geometry (elliptic curves and their L-functions) to biological structure (DNA and microtubule ratios) establishes a still now not discovered bridge between the deepest problems in pure mathematics and the fundamental architecture of life. The convergence of multiple independent mathematical pathways on identical biological values, the predictive relationship between conductor complexity and biological sophistication, and the natural geometric interpretations provided by optimal imaginary quadratic fields collectively demonstrate that evolutionary optimization operates within mathematical constraint spaces far more sophisticated than previously imagined. Our results suggest that biological evolution represents a vast computational process exploring the parameter spaces of arithmetic geometry, discovering configurations that satisfy deep mathematical relationships connecting discrete optimization, quantum topology, and the organizational principles encoded in elliptic curve L-functions. This positions arithmetic geometry not merely as abstract number theory, but as the mathematical blueprint underlying the helical geometries essential for life. The correspondence opens an entirely new frontier in mathematical biology where the most abstract achievements of pure mathematics—the theory of elliptic curves, the Birch-Swinnerton-Dyer conjecture, Gross-Zagier theory, and topological quantum field theory—find their natural application in understanding how

 doi:10.20944/preprints202508.0633.v1

life achieves its remarkable organizational sophistication through evolutionary optimization under arithmetic-geometric constraints. Future investigations along these lines promise to illuminate both the principles governing biological organization and the mathematical structures that evolution has discovered through billions of years of optimization within the constraint spaces of algebraic number theory.

As a very final note, let us mention that the present paper belongs to a series whose goal is to establish a connection between $SU(2)_k$ anyons and physics/geosphere (when $k = 2$)[47], biology/biosphere (when $k = 3$) and neutrinos/noosphere (when $k = 4$) [48]. The famous trilogy geosphere-biosphere-noosphere is a philosophical concept developed and popularized by the biogeochemist Vladimir Vernadsky and philosopher and Jesuit priest Pierre Teilhard de Chardin [49]. The later concept will be explored in a paper to come [50].

Funding: This research received no external funding.

Data Availability Statement: All numerical calculations and theoretical derivations presented in this work can be reproduced using standard mathematical software packages such as Magma and SageMath. Labels and values for elliptic curves are available in the LMFDB database[17].

Acknowledgments: The author would like to acknowledge the contribution of the COST Action CA21169, supported by COST (European Cooperation in Science and Technology).

Conflicts of Interest: The authors declare no conflicts of interest.

References

1. Thompson, D.W. *On Growth and Form*; Cambridge University Press: Cambridge, UK, 1917.
2. Rashevsky, N. *Mathematical Biophysics: Physico-Mathematical Foundations of Biology*; University of Chicago Press: Chicago, IL, USA, 1939.
3. Turing, A.M. The chemical basis of morphogenesis. *Philos. Trans. R. Soc. Lond. B Biol. Sci.* **1952**, *237*, 37–72.
4. Mandelbrot, B.B. *The Fractal Geometry of Nature*; W.H. Freeman: New York, NY, USA, 1983.
5. Perez, J.C. Codon populations in single-stranded whole human genome DNA are fractal and fine-tuned by the golden ratio. *Interdiscip. Sci.* **2010**, *2*, 228–240.
6. Kauffman, S.A.; Smolin, L. Combinatorial dynamics in quantum gravity. *Lect. Notes Phys.* **2000**, *541*, 101–129.
7. White, J.H. Self-linking and the Gauss integral in higher dimensions. *Am. J. Math.* **1969**, *91*, 693–728.
8. Fuller, F.B. The writhing number of a space curve. *Proc. Natl. Acad. Sci. USA* **1971**, *68*, 815–819.
9. Murray, J.D. *Mathematical Biology II: Spatial Models and Biomedical Applications*, 3rd ed.; Springer-Verlag: Berlin, Germany, 2003.
10. Freedman, M.H.; Kitaev, A.; Larsen, M.J.; Wang, Z. Topological quantum computation. *Bull. Am. Math. Soc.* **2003**, *40*, 31–38.
11. Nayak, C.; Simon, S.H.; Stern, A.; Freedman, M.; Das Sarma, S. Non-Abelian anyons and topological quantum computation. *Rev. Mod. Phys.* **2008**, *80*, 1083–1159.
12. Wiles, A. Modular elliptic curves and Fermat's last theorem. *Ann. Math.* **1995**, *141*, 443–551.
13. Silverman, J.H. *The Arithmetic of Elliptic Curves*, 2nd ed.; Springer-Verlag: New York, NY, USA, 2009.
14. Birch, B.J.; Swinnerton-Dyer, H.P.F. Notes on elliptic curves. II. *J. Reine Angew. Math.* **1965**, *218*, 79–108.
15. Gross, B.H.; Zagier, D.B. Heegner points and derivatives of *L*-series. *Invent. Math.* **1986**, *84*, 225–320.
16. Fibonacci anyons. Available online: https://en.wikipedia.org/wiki/Fibonacci_anyons (accessed on 1 January 2024).
17. LMFDB, the LMFDB collaboration. The *L*-functions and modular forms database. Available online: https://www.lmfdb.org (accessed on 1 August 2025).
18. Franklin, R.; Gosling, R.G. Molecular Configuration in Sodium Thymonucleate. *Nature* **1953**, *171*, 740–741.
19. Wilkins, M.H.F.; Stokes, A.R.; Wilson, H.R. Molecular structure of deoxypentose nucleic acids. *Nature* **1953**, *171*, 738–740.
20. Arnott, S.; Hukins, D.W. Optimised parameters for the ribonucleotide helix. *Biochem. Biophys. Res. Commun.* **1972**, *47*, 1504–1509.
21. Depew, D.E.; Wang, J.C. Conformational fluctuations of the DNA helix. *Proc. Natl. Acad. Sci. USA* **1975**, *72*, 4275–4279.

22. Mandelkern,M.; Elias, J. G.; Eden,D.; Crothers, D. M. The dimensions of DNA in solution,*Journal of Molecular Biology* **1981**, *152*, 153–161.
23. Wang, J.C. Helical repeat of DNA in solution. *Proc. Natl. Acad. Sci. USA* **1979**, *76*, 200–203.
24. Strick, T.R.; Allemand, J.-F.; Bensimon, D.; Bensimon, A.; Croquette, V. Twisting and stretching single DNA molecules. *Science* **1996**, *271*, 1835–1837.
25. Drew, H.R.; Dickerson, R.E. Structure of a B-DNA dodecamer: Conformation and dynamics. *Proc. Natl. Acad. Sci. USA* **1981**, *78*, 2179–2183.
26. Olson, W.K.; Gorin, A.A.; Lu, X.J.; Hock, L.M.; Zhurkin, V.B. DNA sequence-dependent deformability deduced from protein-DNA crystal complexes. *Proc. Natl. Acad. Sci. USA* **1998**, *95*, 11163–11168.
27. Hearst, J.E.; Vinograd, J. A calorimetric study of the denaturation of DNA. *Proc. Natl. Acad. Sci. USA* **1961**, *47*, 999–1004.
28. Gray, D.M. Conformation of nucleic acids in solution. III. Light-scattering study of sodium deoxyribonucleate. *Biopolymers* **1967**, *5*, 117–134.
29. Sosnick, T.R.; Wang, J.C. Hydrodynamic measurements of short DNA fragments. *Biochemistry* **1993**, *32*, 3051–3059.
30. Langowski, J.; Kapp, U.; Klenin, K.K.; Vologodskii, A.V. Solution structure and dynamics of DNA topoisomers: Dynamic light-scattering studies and Monte-Carlo simulations. *Biopolymers* **1994**, *34*, 639–646.
31. Jiang, L.Y.; Jiang, H.Q.; Posner, J.D.; Vogt, B.D. Atomistic-based continuum constitutive relation for microtubules: Elastic modulus prediction. *Nanotechnology* **2008**, *19*, 355704.
32. Gu, Y.; Zhao, Y.; Ichikawa, M.; et al. Tektin makes a microtubule a micropillar. *Cell* **2023**, *186*, 2726.
33. Andreu, J.M.; Díaz, J.F. Synchrotron X-ray scattering and electron microscopy of taxol microtubules. *J. Mol. Biol.* **1992**, *226*, 1161–1173.
34. Mandelkow, E.M.; Herrmann, M.; Rühl, U. Tubulin domains probed by limited proteolysis and subunit-specific antibodies. *J. Mol. Biol.* **1986**, *185*, 311–327.
35. Chrétien, D.; Fuller, S.D. Microtubules switch occasionally into unfavorable configurations during elongation. *J. Struct. Biol.* **2000**, *131*, 115–122.
36. Roostalu, J.; et al. Structure and Dynamics of *Caenorhabditis elegans* Tubulin Reveal the Mechanistic Basis of Microtubule Growth. *Dev. Cell* **2018**, *44*, 555–567.e5.
37. Alberts, B.; et al. Structure and Organization of Actin Filaments. In *Molecular Biology of the Cell*, 6th ed.; Garland Science: New York, NY, USA, 2015.
38. Planat,M.; Amaral, M. M. What ChatGPT Has to Say About Its Topological Structure: The Anyon Hypothesis *M. Mach. Learn. Knowl. Extr.* **2024**, 6, 2876–2891.
39. Culler, M.; Shalen, P.B. Varieties of group representations and splitting of 3-manifolds. *Ann. Math.* **1983**, *117*, 109–146.
40. Ashley, C.; Burelle, J.P.; Lawton, S. Rank 1 character varieties of finitely presented groups. *Geom. Dedicata* **2018**, *192*, 1–19.
41. Planat, M.; Amaral, M. M.; Fang, F.; Chester, D.; Aschheim, R.; Irwin, K. Character Varieties and Algebraic Surfaces for the Topology of Quantum Computing. *Symmetry* **2022**, *14*, 915.
42. Python Code to Compute Character Varieties. Available online: http://math.gmu.edu/~slawton3/Main.sagews (accessed on 1 May 2025).
43. Planat, M.; Aschheim, R.; Amaral, M M.; Fang, F.; Irwin, K. Complete quantum information in the DNA genetic code. *Symmetry* **2020**, *12*, 1993.
44. Maclachlan, C.; Reid, A.W. *The Arithmetic of Hyperbolic 3-Manifolds*; Springer-Verlag: New York, NY, USA, 2002.
45. Planat, M. Quantum computing thanks to Bianchi groups. *EPJ Web Conf.* **2019**, *198*, 00012.
46. Davies, P.C.W. Does quantum mechanics play a non-trivial role in life? *Biosystems* **2004**, *78*, 69–79.
47. Planat, M. Baryonic matter, Ising anyons and strong quantum gravity, *Int. J. Topol.* **2025**, 2, 4.
48. M. Planat, Neutrino mixing matrix with $SU(2)_4$ anyon braids, *Quantum Rep.* **2025**, 7, 30.
49. Noosphere. Available online: https://en.wikipedia.org/wiki/Noosphere (accessed on 1 April 2025).
50. M. Planat, A. Gaj, T. Guy, "Topological Quantum Field Theory and Neutrino Mixing: Exploring Connections via $SU(2)_k$ Modular Categories," in preparation (2025).