

DNA Double Helix and Chromosome Compaction

Astonishing Parallels to T0-Torus Geometry

From Molecular Winding to Highest Information Density

Biological Geometry Analysis

February 6, 2026

Abstract

This paper examines the astonishing structural parallels between the DNA double helix, its hierarchical compaction into chromosomes, and the 4D torsional structure of T0 theory. The analysis reveals: Both systems use **the same geometric trick – double helices winding around tori, which in turn fold hierarchically** – to store maximum information in minimum volume. The study identifies **ten astonishing parallels**: (1) **Double helix as basic structure**, (2) **Winding numbers determine properties**, (3) **Hierarchical compaction across levels**, (4) **Toroidal geometry at each level**, (5) **Singularity avoidance through minimum radii**, (6) **Information maximization with volume minimization**, (7) **10,000-fold compression without loss**, (8) **Fractal self-similarity**, (9) **Topological stability**, (10) **Dynamic unfolding when needed**. DNA compaction is not an evolutionary accident, but rather the **biological solution to the same fundamental geometric problem** that also structures physics at all scales.

Contents

1 Introduction: The Packaging Problem

1.1 DNA: 2 Meters in $6\text{ }\mu\text{m}$

Every human cell faces an astonishing geometric problem:

How does one pack ~ 2 meters of DNA into a nucleus of $\sim 6\text{ }\mu\text{m}$ diameter?

This corresponds to a **compression factor of $\sim 10,000$!**

1.2 T0: Universal Information in Space

T0 theory faces an analogous problem:

How does one encode maximum physical information in finite space without singularities?

1.3 The Common Solution

The Universal Principle

Both use the same geometric strategy:

Double helices \rightarrow wind around **tori** \rightarrow which **fold hierarchically** \rightarrow and **dynamically unfold** when needed

This is the **optimal solution for information storage!**

2 The DNA Hierarchy

2.1 Level 1: The Double Helix (Molecular)

Structure:

- Two antiparallel polynucleotide strands
- Right-handed helix
- Turn: 360° per 10.5 base pairs
- Diameter: $\sim 2\text{ nm}$
- Pitch: $\sim 3.4\text{ nm}$ per turn

Geometry:

$$\text{Winding number } w = \frac{n_{\text{base pairs}}}{10.5} \approx \frac{L}{3.4 \text{ nm}} \quad (1)$$

2.2 Level 2: Nucleosomes (Histones)**Structure:**

- DNA wraps 1.65 times around histone octamer
- Histone core diameter: $\sim 11 \text{ nm}$
- 147 base pairs per nucleosome
- "Beads on a string"

Compression: ~ 6 -fold**Geometry – TORUS!:**

$$R_{\text{Histone}} \approx 5.5 \text{ nm}, \quad r_{\text{DNA}} \approx 1 \text{ nm} \quad (2)$$

The DNA forms a **toroidal loop** around the histone core!

2.3 Level 3: 30-nm Fiber (Solenoid)**Structure:**

- Nucleosome chain folds into **solenoid**
- 6 nucleosomes per turn
- Diameter: $\sim 30 \text{ nm}$
- "Fiber of fibers"

Compression: ~ 40 -fold (cumulative)**Geometry – HELIX of TORI!****2.4 Level 4: Higher Loops ($\sim 300 \text{ nm}$)****Structure:**

- 30-nm fiber forms loops
 - Loops attached to protein scaffold
 - Diameter: $\sim 300 \text{ nm}$
- Compression:** ~ 400 -fold (cumulative)

2.5 Level 5: Condensed Chromatin

Structure:

- Further folding of loop domains
- Diameter: ~ 700 nm
- **Compression:** $\sim 1,000$ -fold (cumulative)

2.6 Level 6: Metaphase Chromosome (Maximum Compaction)

Structure:

- Highest condensation during cell division
- Length: ~ 1 – $10 \mu\text{m}$
- Diameter: $\sim 1 \mu\text{m}$
- X-shaped structure (two sister chromatids)
- **Compression:** $\sim 10,000$ -fold!

2 meters DNA \rightarrow $6 \mu\text{m}$ nucleus

3 The T0 Hierarchy

3.1 Level 1: Fundamental (Sub-Planck)

Structure: 4D torsional crystal

- Double loop – analogous to DNA double strand
- Toroidal + poloidal circulation
- Winding number $w = n_\phi / n_\theta$
- Minimum radius: $r_{\min} = 21\ell_P$

3.2 Level 2: Particles ($\sim 10^{-15}$ m)

Structure: Elementary particles as torus resonances

- Electrons, quarks = stable windings
- Toroidal structure on Compton scale
- Spin from winding number

3.3 Levels 3–6: Scale-Invariant Hierarchy

Further torus structures on all scales up to cosmic:

- Atoms $\sim 10^{-10}$ m
- Planets $\sim 10^6$ m
- Stars $\sim 10^9$ m
- Galaxies $\sim 10^{20}$ m

Compression: ~ 60 orders of magnitude with $D_f = 3 - \xi$!

4 The Ten Astonishing Parallels

4.1 Parallel 1: Double Helix as Basic Structure

4.1.1 DNA

The **double helix** is the fundamental structure:

- Two strands wound around each other
- Right-handed
- Complementary (A-T, G-C)
- Stability through **both** strands

4.1.2 T0

The electron model (Williamson & van der Mark, 1997) shows **double helix / double loop**:

- Two circulations: toroidal + poloidal
- Circularly polarized field
- Winding over Compton wavelength λ_C
- Stability through **both** circulations

First Parallel

Double Circulation / Double Helix

Both use **two intertwined components**:

- DNA: Two nucleotide strands
- T0: Toroidal + poloidal flow

The **factor 2** is fundamental for stability!

4.2 Parallel 2: Winding Numbers Determine Properties

4.2.1 DNA

The **number of turns** determines:

- Helix length
- Number of base pairs
- Topological properties (linking number)
- Supercoiling behavior

Example: Plasmid with 4,000 base pairs has ~ 380 helix turns

4.2.2 T0

The **winding number** $w = n_\phi/n_\theta$ determines:

- Spin: $w = 1/2 \rightarrow$ fermions
- Spin: $w = 1 \rightarrow$ bosons
- Charge from flux quantization
- Mass from resonance

Second Parallel

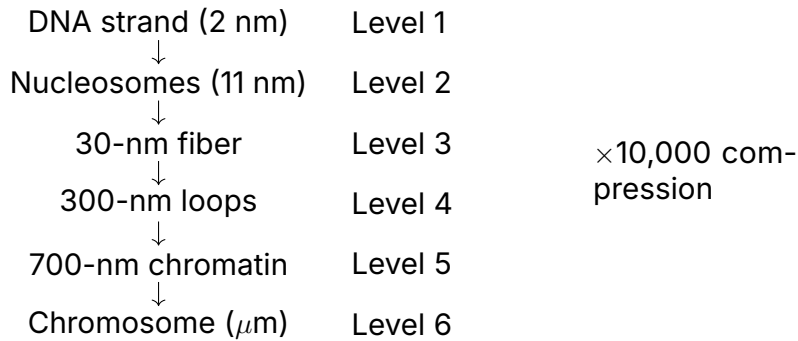
Winding Number = Quantum Number

DNA	T0
Number of turns determines length	Winding number determines spin
Linking number topological	Winding number topological
Supercoiling energy	Field energy

4.3 Parallel 3: Hierarchical Compaction

4.3.1 DNA

6 Hierarchy Levels:



4.3.2 T0

60+ Hierarchy Levels:

From Sub-Planck (10^{-39} m) to Cosmic (10^{26} m)

Third Parallel

Both use **hierarchical folding across multiple scales**:

DNA: 6 levels, 10,000-fold compression

T0: 60+ levels, self-similar with $D_f = 3 - \xi$

4.4 Parallel 4: Toroidal Geometry

4.4.1 DNA

Torus at every level:

Level 2 (Nucleosomes): DNA wraps **1.65 times around histone core**

$$\text{Torus : } R = 5.5 \text{ nm}, \quad r = 1 \text{ nm} \quad (3)$$

Level 3 (Solenoid): Nucleosome chain forms **helix** (torus-like)

Level 4+: Loop domains attached to central axis = **toroidal arrangement**

4.4.2 T0

Torus on EVERY scale:

- Sub-Planck: Fundamental 4D torus
- Particles: Torus resonances
- Macro: Magnetic fields, plasmatoroids
- Cosmic: Galactic spirals, cosmic web

Fourth Parallel

The torus is the universal geometry

Why? Because it:

- Is closed (no boundaries)
- Enables two independent circulations
- Stores energy/information efficiently
- Is topologically stable (genus = 1)

4.5 Parallel 5: Singularity Avoidance

4.5.1 DNA

Minimum radii prevent collapse:

- DNA helix cannot go below ~ 1 nm radius
- Nucleosomes have fixed core diameter
- 30-nm fiber has minimum bending
- Too strong compression \rightarrow DNA damage

Reason: Steric hindrance, Van der Waals radii, hydrogen bonds

4.5.2 T0

Minimum torus radius:

$$r_{\min} = 21\ell_P \approx 3.4 \times 10^{-34} \text{ m} \quad (4)$$

Reason: Fractal dimension $D_f = 3 - \xi$ prevents singularity

Fifth Parallel

Both have fundamental lower limit

	DNA	T0
Minimum radius	~ 1 nm	$21\ell_P$
Cause	Chemical	Geometrical
Consequence	DNA stability	No singularity

4.6 Parallel 6: Information Maximization

4.6.1 DNA

Problem: 3 billion base pairs of information in $\sim 6 \mu\text{m}$

Solution: Hierarchical folding

Result:

- Information density: $\sim 10^9$ bits / μm^3
- Highest known information density in biology!
- Access when needed through local unfolding

4.6.2 T0

Problem: Maximum physical information in finite space

Solution: Fractal torus folding

Result:

- Holographic principle: Information on surface
- Folding maximizes surface area
- Torus has maximum surface area for given volume

Sixth Parallel

Both maximize $\frac{\text{Information}}{\text{Volume}}$

The folding is the **solution to an optimization problem!**

4.7 Parallel 7: Compression Factor

4.7.1 DNA

Quantitative:

Stretched DNA : $\sim 2 \text{ m}$ (5)

Chromosome : $\sim 6 \mu\text{m}$ (6)

Compression factor : $\frac{2 \text{ m}}{6 \mu\text{m}} \approx 333,000$ (7)

Considering diameter: **$\sim 10,000$ -fold**

4.7.2 T0

Quantitative:

$$\text{Planck scale : } 10^{-35} \text{ m} \quad (8)$$

$$\text{Hubble scale : } 10^{26} \text{ m} \quad (9)$$

$$\text{Orders of magnitude : } 61 \quad (10)$$

With $\xi = 1.33 \times 10^{-4}$: Scaling factor $\sim 1/\xi \approx 7500$ per level!

Seventh Parallel

Both achieve enormous compression without information loss

DNA: 10,000-fold (6 levels)

T0: 7500^{60} (60 levels) = unimaginable!

4.8 Parallel 8: Fractal Self-Similarity

4.8.1 DNA

Self-similar structure:

- Helix (Level 1) \rightarrow winds into solenoid (helix of helices, Level 3)
- Nucleosomes (tori, Level 2) \rightarrow arranged on helix (Level 3)
- 30-nm fiber \rightarrow folds into loops (Level 4) \rightarrow into chromatin (Level 5)

Each level is a folded version of the previous one!

4.8.2 T0

Strict self-similarity:

$$\frac{R_{\text{Level } n+1}}{R_{\text{Level } n}} = \frac{1}{\xi} \approx 7500 \quad (11)$$

The ratio R/r remains constant across scales!

Eighth Parallel

Fractal repetition of the same pattern

DNA: Qualitatively self-similar (helix \rightarrow solenoid \rightarrow loops)

T0: Quantitatively self-similar ($D_f = 3 - \xi$, fixed scaling ratio)

4.9 Parallel 9: Topological Stability

4.9.1 DNA

Topological invariants:

- **Linking number** (Lk): Number of intertwinings
- **Twist** (Tw): Local turns
- **Writhe** (Wr): Supercoiling

Fundamental relationship:

$$Lk = Tw + Wr \quad (12)$$

These numbers are **topologically invariant** – change only through cutting!

4.9.2 T0

Topological quantum numbers:

- Winding number $w = n_\phi / n_\theta$
- Flux quantization $\Phi = n \cdot h/e$
- Charge, spin, color charge from topology

These are **topologically protected** – change only at phase transition!

Ninth Parallel

Topological stability

Both use **topological invariants** for stability:

DNA: Linking number preserves structure

T0: Winding number preserves quantum numbers

4.10 Parallel 10: Dynamic Unfolding

4.10.1 DNA

Unfolding when needed:

- **Transcription:** Local unfolding for RNA polymerase
- **Replication:** Complete unfolding during S-phase
- **Recombination:** Temporary unfolding for repair
- **Regulation:** Acetylation → loose structure → accessibility

The compaction is **reversible** and **regulatable**!

4.10.2 T0

Dynamic processes:

- Energy flows in torus variable
- Torsion waves propagate
- Particle creation = excitation
- Phase transitions possible

The structure is **static**, but energy is **dynamic**!

Tenth Parallel

Static structure, dynamic processes

	DNA	T0
Structure	Chromosome (static)	Torsion crystal (static)
Dynamics	Local unfolding	Energy flows
Reversible?	Yes	Yes (excitations)

5 Why These Parallels?

5.1 Universal Optimization Problem

The Fundamental Question

Both biology (DNA) and physics (T0) face **the same challenge**:

How does one store maximum information (sequence / physical states) in minimum space without:

- Knotting (topology problems)
- Singularities (infinite energies)
- Information loss (entropy)
- Inaccessibility (must remain readable)

The **answer is universal: Hierarchical torus folding with double helices!**

5.2 Mathematical Necessity

The parallels are not coincidental but follow from:

1. Topology:

- Torus (genus = 1) is simplest non-trivial closed surface
- Enables two independent circulations
- Topologically stable

2. Geometry:

- Helix is natural curve in 3D
- Double helix maximizes stability
- Winding around torus is optimum

3. Information theory:

- Holographic principle: Information on surface
- Folding maximizes surface area
- Hierarchy allows logarithmic compression

5.3 Evolution vs. Fundamentality

The Deep Insight

Did evolution “discover” torus geometry?

NO!

Evolution **had to** use this geometry because it is the **only optimal solution** to the information storage problem!

Just as physics **had to** use the same geometry for fundamental structure!

DNA compaction is **not a random biological invention**, but rather the **manifestation of a universal geometric truth!**

6 Quantitative Comparisons

6.1 Compression Factors

System	From	To	Factor
DNA	2 m (stretched)	6 μm (chromosome)	333,000×
T0	10^{-35} m (Sub-Planck)	10^{26} m (cosmic)	10^{61}

Table 1: Compression factors

6.2 Hierarchy Levels

System	Levels	Factor/Level	Geometry
DNA	6	$\sim 2-6\times$	Helix + Torus
T0	60+	$\sim 7500\times$	Torus + Fractal

Table 2: Hierarchical structure

6.3 Characteristic Lengths

DNA Level	Length	T0 Analog	Length
Double helix	2 nm	Sub-Planck	10^{-39} m
Nucleosome	11 nm	Particle	10^{-15} m
30-nm fiber	30 nm	Atom	10^{-10} m
Loop	300 nm	Molecule	10^{-9} m
Chromatin	700 nm	Macro	10^0 m
Chromosome	1 μm	Cosmic	10^{26} m

Table 3: Scale comparison (qualitative)