

# DNA Double Helix and Chromosome Compaction

Astonishing Parallels to T0-Torus Geometry

From Molecular Winding to Highest Information Density

Biological Geometry Analysis

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## 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 $6 \mu\text{m}$

Every human cell faces an astonishing geometric problem:

**How does one pack  $\sim 2$  meters of DNA into a nucleus of  $\sim 6 \mu\text{m}$  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** → wind around **tori** → which **fold hierarchically** → 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:  $360^\circ$  per 10.5 base pairs
- Diameter:  $\sim 2$  nm
- Pitch:  $\sim 3.4$  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:**  $\sim 6\text{-fold}$ **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:**  $\sim 40\text{-fold}$  (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:**  $\sim 400\text{-fold}$  (cumulative)

## 2.5 Level 5: Condensed Chromatin

**Structure:**

- Further folding of loop domains
- Diameter:  $\sim 700$  nm

**Compression:**  $\sim 1,000$ -fold (cumulative)

## 2.6 Level 6: Metaphase Chromosome (Maximum Compaction)

**Structure:**

- Highest condensation during cell division
- Length:  $\sim 1\text{--}10 \mu\text{m}$
- 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 ( $\sim 10^{-15} \text{ m}$ )

**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:**  $\sim 60$  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  $\lambda_C$
- 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  $\sim 380$  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

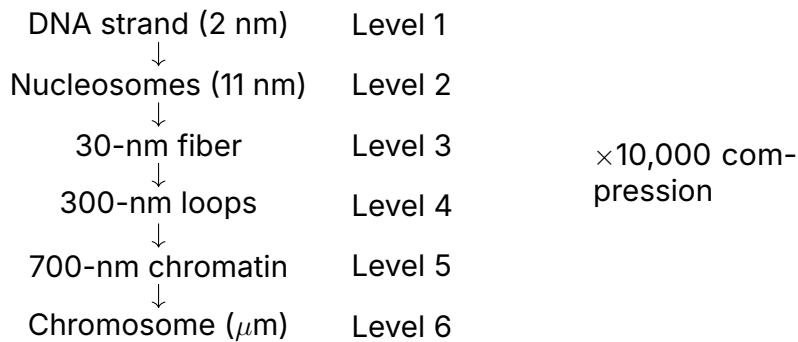
##### Winding Number = Quantum Number

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  $\sim 1$  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	$\sim 1$ 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:  $\sim 10^9 \text{ bits} / \mu\text{m}^3$
- 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:**

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

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

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

Considering diameter: **~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) → winds into solenoid (helix of helices, Level 3)
  - Nucleosomes (tori, Level 2) → arranged on helix (Level 3)
  - 30-nm fiber → folds into loops (Level 4) → 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 → solenoid → 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:

$$\text{Lk} = \text{Tw} + \text{Wr} \quad (12)$$

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 $\mu\text{m}$ (chromosome)	333,000 $\times$
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	$\sim 2\text{--}6 \times$	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 $\mu\text{m}$	Cosmic	$10^{26}$ m

**Table 3:** Scale comparison (qualitative)