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EDNA: An Interactive Elastic DNA Model for STEM Education and Research

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Abstract

Visualizing and understanding DNA structure and dynamics is a major challenge in science education, especially when introducing students to concepts that bridge biology, chemistry, physics, and engineering. To address this, we have developed EDNA, an interactive elastic DNA model designed to support STEM learning through hands-on exploration.
Unlike traditional rigid DNA models, EDNA is constructed from flexible, elastic materials, enabling learners to physically manipulate the molecule and directly observe its responses to bending, twisting, writhing, and supercoiling. This tactile experience promotes intuitive understanding of DNA mechanics and highlights the interdisciplinary nature of molecular science, making it an ideal resource for STEM classrooms and outreach activities.
Grounded in computational modeling and produced with accessible polymer materials, EDNA serves a dual role as both an educational tool and a research demonstrator. It has been carefully designed to stimulate active learning, curiosity, and creativity in students at multiple levels, while also offering a tangible link between theoretical models and real-world applications.
In this contribution, we present the EDNA model and discuss its broader educational significance, particularly its role in disseminating an accurate representation of DNA structure. More than seventy years after the discovery of the right-handed double helix, incorrect depictions of DNA - most notably left-handed helices - remain widespread in educational materials, scientific graphics, and public media. This problem is further amplified by the rapid proliferation of AI-generated imagery trained on flawed visual sources. By providing a physically accurate, manipulable model of DNA, EDNA offers a timely and effective tool for counteracting such misconceptions and for reinforcing a correct, intuitive understanding of DNA structure and mechanics in contemporary STEM education.

Keywords: *polymer, DNA, model, STEM, science, education*

1. Introduction

DNA carries the genetic information of all living organisms and, as such, is among the most important molecules in nature. Despite this, it is surprisingly difficult to find a three-dimensional model of DNA that can be held in one's hands and that faithfully demonstrates its structural and mechanical properties, as well as the biological and technological consequences arising from their interplay. DNA is not merely an ordinary molecule—it is an asymmetric, chiral, right-handed double helix with elastic properties [1],[2].

1.1 DNA structure

The basic building blocks of DNA are nucleotides - small organic compounds based on nitrogenous bases. DNA contains four types of nitrogenous bases: adenine (A), guanine (G), thymine (T), and cytosine (C). Each base is covalently bound to a sugar molecule, deoxyribose, which in turn is connected via a phosphate group to neighboring deoxyribose molecules, forming a long chain. In this way, the so-called DNA backbone is created, consisting of alternating sugar and phosphate units.

A typical DNA molecule consists of two such strands that wind around each other to form a right-handed double helix, with the strands oriented antiparallel to one another. Complementary nitrogenous bases are paired by hydrogen bonds—adenine with thymine (A–T) and cytosine with guanine (C–G)—which ensure the specificity of base pairing and the faithful storage of genetic information. During DNA replication, the two strands are separated and each serves as a template for

the synthesis of a new complementary strand by DNA polymerases, ensuring the faithful duplication and conservation of genetic information during cell division.

Importantly, the overall thermodynamic stability of the DNA double helix is governed predominantly by stacking interactions between adjacent base pairs, which arise from π–π interactions and hydrophobic effects. While hydrogen bonds determine which bases pair, base stacking contributes the largest fraction of the stabilizing energy of the double-helical structure.

The DNA double helix is a highly regular and symmetric structure, exhibiting both translational symmetry along its axis and rotational symmetry corresponding to approximately 10 base pairs per turn in B-DNA. Rotations of the molecule by integral multiples of ~36° or inversion of its orientation along the helical axis do not alter its appearance. Despite this high degree of symmetry, the geometry of the double helix gives rise to two distinct surface features: the major groove and the minor groove. These grooves arise from the specific symmetry of the DNA double helix, which causes the two sugar–phosphate backbones to be unevenly spaced around the helix, giving rise to a wide major groove and a narrow minor groove.

The major groove is wider and allows easier access for proteins to interact with the DNA bases, making it a key binding site for regulatory proteins and enzymes. Most DNA-binding regulatory proteins, such as transcription factors, recognize DNA via the major groove. This is because differences between base pairs (A–T vs. T–A, C–G vs. G–C) are more readily “read” there. The major groove is more accessible and provides greater opportunities for hydrogen bonding and van der Waals interactions.

The major groove is wider and more accessible than the minor groove, allowing proteins to distinguish chemical patterns associated with different base pairs. Many DNA-binding proteins, such as transcription factors, recognize specific DNA sequences by interacting with the exposed functional groups in the major groove.

1.2 Mechanical properties of DNA

In its natural environment, DNA is constantly subjected to mechanical stress - whether due to tight packing in the cell nucleus or as a result of biological processes associated with its function [2],[3],[4]. The asymmetric structure of DNA means that mechanical stress leads to irregular deformations. These deformations are linked to the exposure of genetic information. While such exposure can have potentially harmful consequences, it is also essential for the proper functioning of proteins and enzymes [5].

The chemical structure of DNA determines its physical properties, including its mechanical behavior. First and foremost, DNA is a polymer—a long molecule. If fully stretched, the total length of DNA contained in the human genome would be approximately two meters. Due to its double-helical structure, DNA is significantly stiffer and more resistant to mechanical deformation than many natural polymers such as cellulose or starch, as well as common synthetic polymers like polyethylene or polypropylene. The mechanical properties of DNA are primarily characterized by:

Bending stiffness reflects the resistance of DNA to bending and is commonly quantified by the persistence length. For DNA, the persistence length is approximately 150 base pairs (≈50 nm). Directional correlations along the polymer backbone decay over a length scale of two persistence lengths, corresponding to one statistical segment.

Another key property is torsional stiffness, or resistance to twisting. Unlike simple polymer chains, DNA cannot freely rotate around the covalent bonds of its backbone due to its double-helical structure. When twisted, DNA stores torsional stress. To relieve this stress, DNA transitions into so-called supercoiling, in which the double helix itself coils further around its own axis at a higher level of organization [6].

DNA also exhibits stretching elasticity, reflecting its resistance to tensile deformation. Under applied tension, the DNA double helix initially responds by increasing its twist, followed by progressive

unwinding at higher forces, before strand separation or denaturation occurs. This non-trivial coupling between stretching and twisting which is contained only in limited way in the current EDNA model [7].

1.3 DNA models

A model represents a simplified description of a physical object and is used to understand, explain, and predict its behavior. In molecular science today, computer-based molecular modeling and simulations are predominantly used. However, physical molecular model kits have existed since well before the era of high-performance computing.

It is worth noting that Watson and Crick (1953) employed a physical analog model in their groundbreaking research that led to the discovery of DNA's chemical structure [8],[9],[10]. Using metal plates and wires to represent molecular components and their connections, they explored how the constituents of DNA could fit together geometrically. This hands-on modeling approach enabled them to propose the now-famous double-helix structure. While structurally accurate DNA models and kits are available today, they generally lack elastic properties.

Computer models allow DNA behavior to be simulated across multiple scales—from atomic interactions to large-scale folding and supercoiling. These models make it possible to explore the interplay between DNA structure and mechanical properties. However, their major limitation is the need for significant computational power and long simulation times, which makes real-time, interactive demonstrations of DNA deformation impractical.

1.4 Importance of accurate DNA models

The structure of DNA is iconic and is widely used as a symbol of scientific research. DNA imagery—ranging from simple icons and sketches to detailed structural renderings—is commonly employed as illustrative material in education and research in fields such as biology, chemistry, and medicine. Unlike the planetary model of the atom—which is historically important but physically incorrect—the DNA double-helix model represents a structurally accurate description of a real biological molecule. Consequently, inaccuracies in DNA representations are particularly problematic, as they distort an otherwise correct and well-established molecular structure.

The widespread use of such graphics introduces the structure of this life-essential molecule to students and the general public from an early age. As discussed above, DNA possesses several non-intuitive structural features, and it is important for future students to become familiar with them early in their education so that these concepts become firmly embedded in their understanding.

This importance is underscored by the fact that many illustrative representations of DNA—found not only in popular media but even in top-tier scientific publications—depict DNA incorrectly. The most common error is the representation of the DNA double helix as left-handed. Such an incorrect depiction has even appeared on the cover of the journal Nature [11]. Ironically, Nature was also the journal that published Watson and Crick's original paper over 70 years ago [8].

Other common errors include depicting an incorrect number of base pairs per helical turn or an incorrect helical pitch. In its most common form, DNA has 10 base pairs per full helical turn, where a turn corresponds to one complete sinusoidal period. DNA is also frequently illustrated without distinguishing between the major and minor grooves.

This situation is becoming increasingly urgent due to the proliferation of AI agents capable of generating images from text prompts. This highlights the growing importance of physical reference models in education, which can serve as ground truth for both human learners and future AI-assisted educational tools. Graphic AI systems—such as those integrated into ChatGPT, as well as tools like Leonardo, Midjourney and DALL-E—are trained on existing online images which amplify the dissemination of structurally inaccurate representations. Today, when searching for "DNA helix" in Google, the majority of the most visually appealing images are already structurally incorrect. We would like to note an observation made during the preparation of this manuscript: the logo of the New Perspectives in Science Education conference itself features a left-handed DNA helix (Fig. 1).

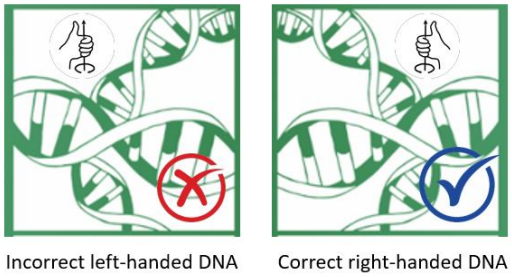

Fig. 1 The DNA double helix is an iconic symbol of science and education and frequently appears in visual identities and educational materials. The figure contrasts a left-handed depiction (left), which is commonly but incorrectly used, with the correct right-handed structure of B-DNA (right).

1.5 Our goal and motivation

The goal of our development was therefore to create a three-dimensional model that correctly reproduces the key structural features of the DNA molecule as well as its mechanical behavior. Through interactive manipulation, such a model can help embed an accurate understanding of DNA in the minds of new generations of students, as well as among scientists and science communicators. This interactive model may help prevent further contamination of both virtual and media spaces by incorrect representations of one of the most fundamental molecules of life.

2. Methods

EDNA represents a simplified physical model of the DNA molecule that enables interactive, real-time demonstration of the interplay between its structure and its reversibly deformable mechanical properties [12].

The model faithfully preserves the key structural features of DNA:

- a right-handed double helix,
- clearly distinguished major and minor grooves,
- correct geometric parameters of the DNA helix (the height-to-width ratio characteristic of B-DNA),
- atomic dimensions translated into a defined physical scale.

At the same time, the model accurately captures the deformational behavior of DNA by incorporating its mechanical properties—bending stiffness, torsional stiffness, and tensile elasticity—through the use of appropriate polymer materials. These materials endow the model with reversible deformability characteristic of the DNA molecule. The model is designed to be robust, reusable, and suitable for repeated handling in classroom and outreach settings.

Students can physically twist, bend, and supercoil the model to observe biologically relevant DNA behaviors associated with bending, twisting, supercoiling, chirality, and topology (knotting and linking), which occur in both biological and technological contexts.

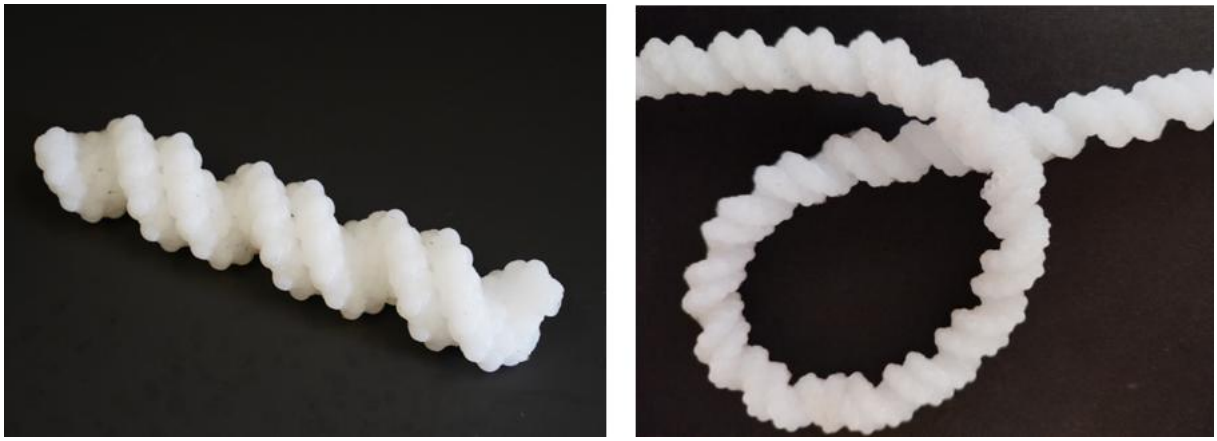

Fig. 2 Variations of the EDNA interactive elastic model (Source [Ref. 13]).

The EDNA model is intended as an educational and didactic tool that allows students and researchers to better understand the relationship between DNA structure, mechanical properties, and biological function.

In designing the model, we based its dimensions on what is practical for interactive manipulation. The size of the DNA model should allow it to be comfortably held in a child's hand, while its mechanical properties should permit twisting, bending, and stretching without the application of excessive force.

As practical dimensions, we selected model diameters ranging from approximately 1.5 cm to 10 cm. The thickness of the model also determines its mass, which in turn limits the practical length of the model at a given diameter. For the thinner variant, we found it practical to produce a model approximately half a meter in length, corresponding to 470 base pairs. For the thicker variant, four helical turns correspond to 40 base-pairs. The weight of the mentioned EDNA models is approximately 200 grams.

The thinner model is advantageous for demonstrating DNA deformation over longer length scales and for illustrating phenomena such as DNA wrapping around proteins like histones, or DNA wrapping around itself during supercoiling generated by biological processes such as transcription.

The thicker model can be used to provide a more detailed visualization of the interplay between DNA structure and mechanical stress during twisting, stretching, and bending, for example in teaching DNA mechanics to students of biophysics.

The structural fidelity of our DNA model, together with its mechanical properties, was achieved by combining our expertise in molecular modeling, materials engineering, polymer chemistry, and 3D printing.

3. Results and Discussion

In the following, we present several examples of how our interactive DNA model can be used to demonstrate the coupled structural and mechanical behavior of the DNA molecule. These examples are suitable for use in school education, scientific presentations, and science-popularization events. This demonstration is particularly effective in classroom discussions of transcription, replication, and DNA topology.

3.1 Torsional deformations

When DNA is subjected to torsional stress, it may become overwound or underwound relative to its relaxed double-helical state. These torsional deformations alter the helical twist and lead to changes in groove geometry and mechanical stress distribution along the molecule.

An elastic DNA model with four helical turns clearly illustrates how torsional stress alters the three-dimensional arrangement of the double helix: the major and minor grooves narrow and widen unevenly during deformation, influencing how regulatory proteins interact with DNA.

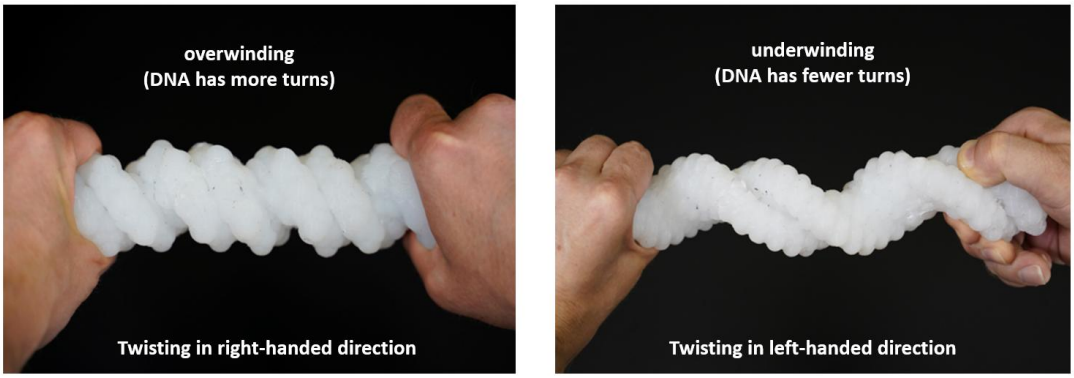

Fig. 3 Interplay between structure and mechanical deformations during overwinding and underwinding of DNA (Source [Ref. 13]). This figure allows students to directly experience correct and incorrect DNA chirality and understand why handedness matters.

In most cells, underwinding is biologically favorable because it loosens the DNA structure and facilitates unwinding of the double helix during replication and transcription. Overwinding, on the other hand, excessively tightens and twists DNA, hindering protein access to the template and potentially stalling replication or transcription. Cells therefore employ topoisomerases to balance torsional stress—removing harmful positive supercoils and maintaining a moderate level of negative supercoiling as the natural, functional state of DNA.

3.2 Nucleosome

The nucleosome is the fundamental unit of chromatin organization, in which a segment of DNA (~147 base pairs, corresponding to approximately 15 helical turns) is tightly wrapped around a core of histone proteins. This arrangement enables compact DNA packing, regulates gene accessibility, and provides the basis for higher levels of chromosomal structure.

Because the persistence length of DNA (~50 nm) is much larger than the bending radius in a nucleosome (~4–5 nm), the double helix is bent extremely strongly in this context. Uneven deformations of the major and minor grooves during wrapping allow histones to form specific contacts: the major groove opens outward at certain positions, facilitating access for regulatory proteins, while the minor groove provides precise anchoring points. In this way, mechanical deformation of DNA is directly linked to its biological regulation.

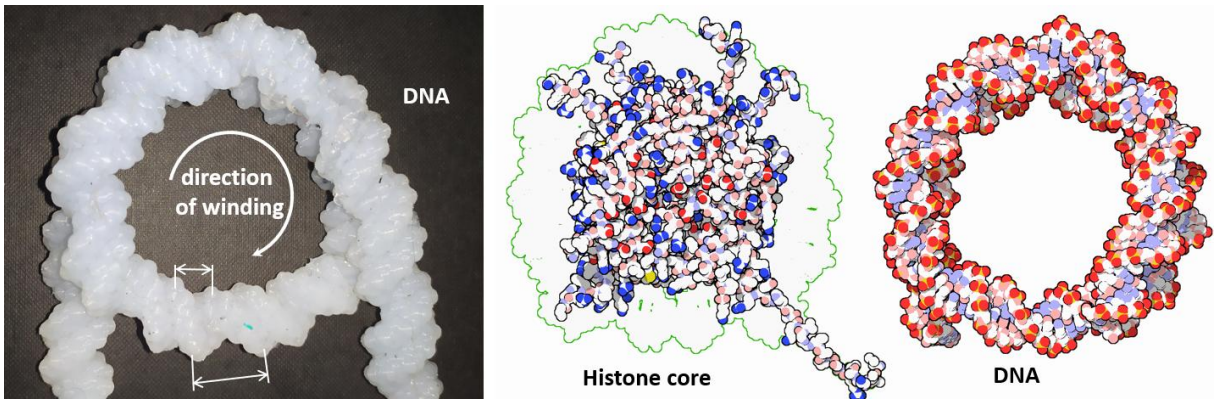

Fig. 4 Structure of DNA in nucleosomes and structural deformations induced by tight winding of DNA around the core protein complex (Source [Ref. 13] and right part of the figure is partially adopted figure from [Ref. 14]).

3.3 Plectonemes

When torsional stress exceeds a critical threshold and DNA is constrained, overwinding or underwinding can be converted into supercoiling, in which the DNA axis itself coils in three-dimensional space. Supercoiling is an additional level of twisting of DNA beyond its fundamental winding into a double helix. Underwinding relaxes the double helix, facilitating strand separation and protein access during replication and transcription. In contrast, overwinding further compacts DNA and reduces its accessibility. Supercoiling is therefore a key mechanism in the regulation of biological processes and genome organization [3],[4].

Plectonemes play a key role in the compact organization of the bacterial chromosome by enabling superhelical arrangements of DNA and its packaging into the confined cellular space. They form when excess torsional stress in the DNA double helix is released through spatial rearrangement of the helix, leading to the formation of loops and intertwined, spiral-like structures.

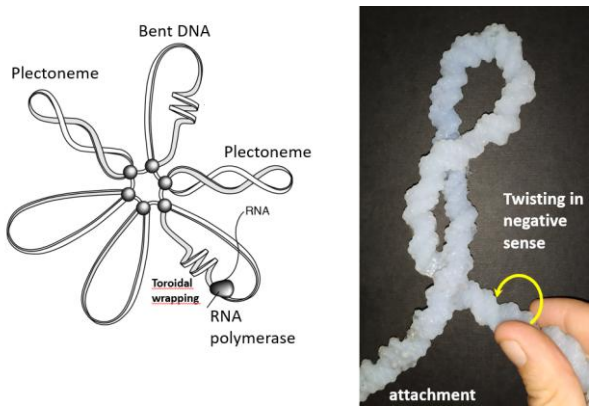

Fig. 5 Spontaneous structural transition and formation of plectonemes in torsionally stressed DNA (Source [Ref. 13]; the left panel of the figure is partially adopted from [Ref. 15]).

The stability and dynamics of these supercoiled structures are regulated by the enzyme DNA gyrase (topoisomerase II), which actively introduces negative supercoils and thereby maintains DNA in a state suitable for replication and transcription. Antibiotics from the quinolone family (e.g., ciprofloxacin) act by binding to the gyrase–DNA complex and blocking the re-ligation of cleaved DNA strands, leading to the accumulation of DNA breaks and ultimately halting cell division.

3.4 DNA knotting

The primary biological role of topoisomerases is to permit the segregation of newly replicated DNA molecules by enabling controlled strand passage events. Mechanistically, topoisomerases transiently cleave one or both DNA strands, allow intra- or intermolecular passage of DNA segments, and subsequently reseal the break.

In the highly crowded intracellular environment, this essential mechanism can inadvertently lead to the formation of DNA knots or links, even though topoisomerases also play a key role in their removal. The probability of spontaneous DNA knotting further increases with DNA length, approaching unity for genome sizes on the order of 10^7 base pairs and above.

A long-standing question in biology is how topoisomerases are able to maintain DNA in an unknotted state. This problem bridges the fields of biology, biophysics, and mathematics [16],[17],[18].

From a mathematical perspective, knots are topological objects formed when a curve wraps around itself and its ends are joined. A fundamental characteristic of a knot is the number of crossings, or self-intersections, of the curve. Knots are further classified by knot type, and the number of distinct knot types increases rapidly with the number of crossings.

Knots are topological entities that depend not only on the number of crossings but also on how those crossings are arranged. The manner of crossing partially determines the direction of self-wrapping, which is related to chirality. Most knots are chiral; only 20 knots with up to 11 crossings are known to be achiral. Because DNA itself is chiral, the structure of the knot and the chirality of DNA influence each other, and DNA knots tend to occur in a single predominant chiral form.

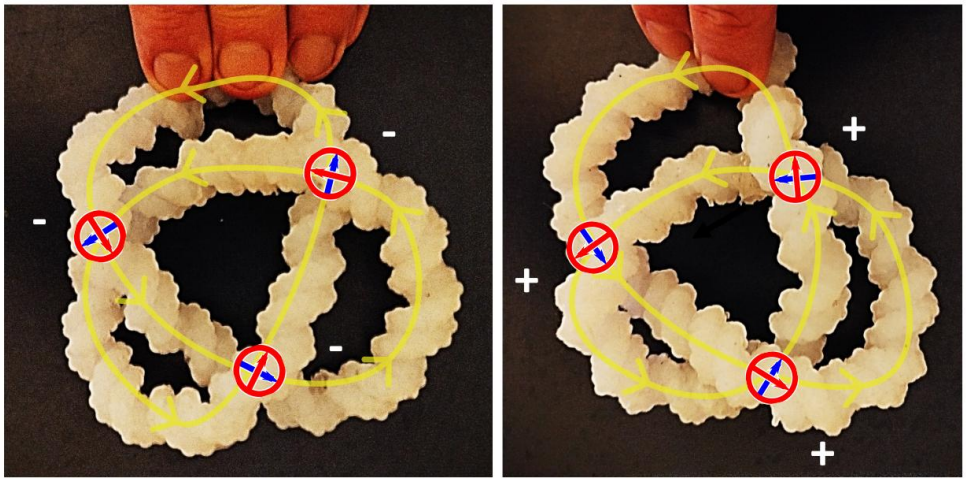

Fig. 6 Interplay of chiralities in knotted DNA double-helix (Source [Ref. 13]).

4. Conclusions

In this work, we introduced EDNA, an interactive elastic model of DNA designed to bridge the gap between molecular theory and hands-on exploration. Unlike conventional rigid models, EDNA faithfully reproduces the right-handed double helix, distinguishes the major and minor grooves, and incorporates the mechanical properties of DNA, including bending, twisting, and tensile elasticity. By allowing real-time manipulation, EDNA demonstrates biologically relevant behaviors such as supercoiling, nucleosome wrapping, formation of plectonemes, and knotting. These features make it a versatile tool for STEM education, outreach, and scientific demonstrations, providing a tangible link between molecular structure, mechanics, and biological function. By combining physical interaction with scientific accuracy, EDNA supports modern STEM education that emphasizes inquiry, intuition, and interdisciplinary thinking.

Looking forward, EDNA offers broad potential for educational and scientific applications. It can enhance students' intuitive understanding of DNA mechanics, support interactive teaching across disciplines, and help prevent the perpetuation of incorrect DNA representations in educational and digital media. Further development may extend the model to illustrate complex chromatin structures, DNA–protein interactions, or the influence of molecular topology on gene regulation, providing an engaging platform for active learning and interdisciplinary scientific exploration.

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