Science Education Quarterly, 2025, Vol. **2**, Iss. 4, pp. 226–237 https://doi.org/10.55056/seq.1064

Visualizing DNA dimensions through simplified mathematical models

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Abstract. The mathematical equations that underlie molecular biology experiments are frequently too complicated for efficient K–12 education. By offering a straightforward, yet precise mathematical method for determining important geometrical features of DNA, this work seeks to close this gap. Our approach, which was considered with the teaching methodology in mind, makes it easier for K–12 students and early-stage learners to understand without sacrificing scientific accuracy. In accordance with experimental data, we computed the hydrogen bond length (0.23 nm), the diameter of the DNA double helix (2 nm), and the distance between nitrogenous bases (0.32 nm) using basic geometry. Additionally, we demonstrated that the compact structure of the DNA helix associated practically zero spatial separation between hydrogen bonds in sequential base pairs. In conclusion, our approach facilitates DNA-based education by applying simple mathematical equations for simple presentation of molecular measurement. We also provide a classroom-ready 45–60 minute lesson plan with worked examples and practice items, plus differentiation options for mixed-ability classes (scaffolds for weaker trigonometry backgrounds and extension tasks for advanced students). In addition, we point to free digital tools (e.g., GeoGebra and molecule viewers) that teachers can use to help students visualize the geometry interactively.

Keywords: DNA structure, molecular geometry, K–12 science education, hydrogen bonding

1. Introduction

Over the past several years, there have been multiple interdisciplinary initiatives to incorporate mathematics into biology education, aiming to simplify complex principles and enhance student comprehension [12, 16]. This mathematical–biological integration has proven effective in helping students at various levels better grasp abstract molecular structures such as DNA [4, 7]. In light of recent international calls to strengthen the U.S. scientific enterprise amid global competition and teaching challenges [9], improving foundational STEM education through integrative approaches is more crucial. A number of scientific and medical fields – including genetic testing, drug development, disease research, and forensic science – are fundamentally based on understanding the structure of DNA [1, 11, 22]. Key characteristics of the DNA double helix have been accurately determined over the years: its total length in a single human cell is roughly two meters [21], the vertical separation between two base pairs is approximately 0.34 nm [3], and the diameter of the helix is about 2 nm [22].

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Although these values are well established, explaining how they are measured mathematically remains a challenge in educational contexts, particularly for K–12 and early undergraduate students. This work presents a simplified yet accurate mathematical method to compute key DNA dimensions. Specifically, it demonstrates that the length of a hydrogen bond between nitrogenous bases is approximately 0.23 nm, aligning with experimental data [10]; the spacing between adjacent bases is about 0.32 nm; and the overall diameter of the double helix can be derived as 2 nm, consistent with known structural measurements. Furthermore, we examine the length of a full helical turn, given as 3.4 nm [15], and show that the direct linear distance between hydrogen bonds in consecutive base pairs is effectively zero [8, 18], underscoring the dense packing of the DNA molecule.

By linking mathematics with molecular biology in an accessible way, this study provides both educators and students with a clearer understanding of DNA geometry and demonstrates how theoretical calculations can successfully reflect experimentally validated structures. This work complements prior applications of mathematics to nucleic-acid geometry and energetics (e.g., [5, 19]) by focusing on a minimal, classroom-adaptable pathway that uses only triangle geometry and right-triangle trigonometry while still recovering canonical DNA dimensions. These insights support broader applications in biology, nanotechnology, and science education.

2. Results

2.1. Mathematical measurement of the distance between hydrogen bonds in the adenine–thymine pair

Accurately measuring the distance between hydrogen bonds in the adenine–thymine (A–T) nucleotide pair requires consideration of several key chemical parameters. The length of the double bond between the carbon and oxygen atoms in the carbonyl group of thymine is approximately 121 pm [14], while the single bond between the carbon and nitrogen atoms in thymine measures about 147 pm [17]. The angle formed between these two bonds is roughly 120°, which aligns with the exterior angle of the regular hexagonal structure characteristic of thymine [6].

To determine the distance between the two hydrogen bonds, we construct a geometric model based on the molecular structure of the base pair. Specifically, we form a triangle by connecting the oxygen and nitrogen atoms, using the carbon atom as the vertex. In this triangle, side b represents the bond between the oxygen and carbon atoms, side c represents the bond between the carbon and nitrogen atoms, and side a – the side opposite the vertex carbon atom – represents the distance between the oxygen and nitrogen atoms, which is the target value. The angle included between sides b and c is denoted as α, as illustrated in figure 1.

This triangular configuration allows us to compute the hydrogen bond distance A using the law of cosines [2]:

$$a^2 = b^2 + c^2 - 2bc\cos(\alpha)$$

Substituting the known values:

- $b = 121$ pm
- $c = 147$ pm
- $\alpha = 120^\circ$ with $\cos(120^\circ) = -\frac{1}{2}$

$$a^2 = 121^2 + 147^2 - 2 \cdot 121 \cdot 147 \cdot \left(-\frac{1}{2}\right)$$

$$a^2 = 14641 + 21609 + 17743.5 = 53993.5$$

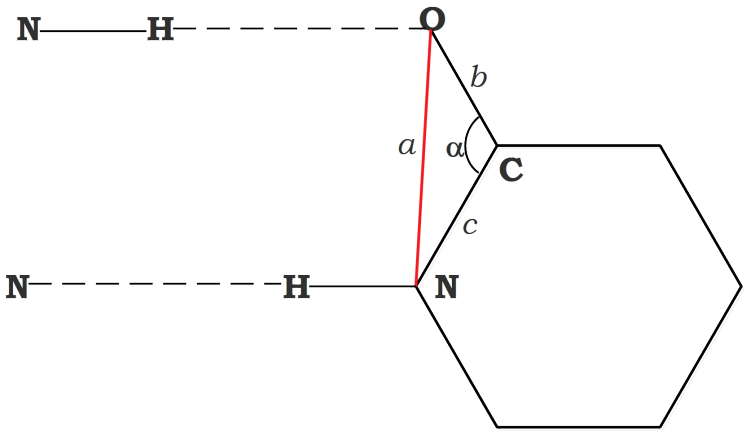

Figure 1: OCN triangle used to obtain the O–N separation. Sides: b = OC = 121 pm (length of C=O bond), c = CN = 147 pm (length of C–N bond), included angle $\alpha = 120°$. Target side a = ON is computed via the law of cosines.

$$a = \sqrt{53993.5} \approx 232 \text{ pm}$$

This distance is not vertical because the triangle $\triangle OCN$ is not isosceles. The length of side b is 121 pm, while the length of side c is 147 pm. Subtracting the two gives a difference of 26 pm, which results in angle $\angle ONC = 26°$ and $\angle CON = 34°$, since the interior angles of a triangle sum to 180°, as illustrated in figure 2.

By drawing a straight line from point M to the hydrogen atom H, we bisect the internal 120° angle of the thymine hexagon into two equal 60° angles. Thus:

$$\angle MNC = 60° + 26° = 86°$$

$$\angle HNC = 94°$$

(since the straight line forms a 180° total with the angles).

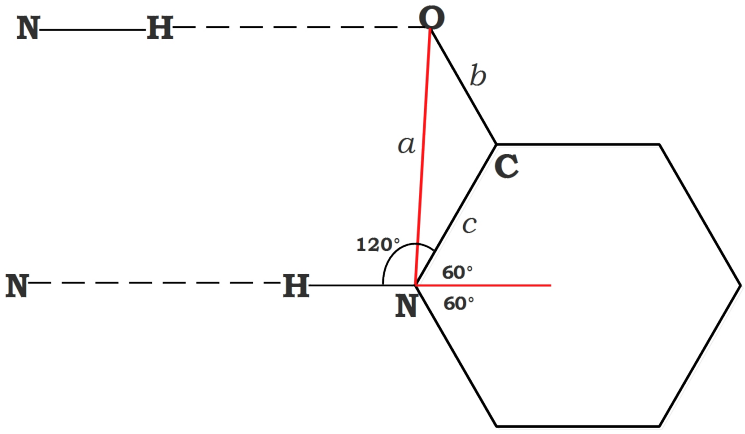

Figure 2: Hydrogen-bonding geometry in A–T pair. The 120° hexagon angle at c is bisected (60° + 60°); due to $b \neq c$ the triangle is scalene with $\angle ONC \approx 26°$ and $\angle CON \approx 34°$.

By drawing a vertical line from point O to point U, which lies on line MH, we form a right-angled triangle. The line OU is the vertical distance between the two hydrogen bonds (see figure 3).

Using the sine rule:

$$\sin(\angle ONU) = \frac{\text{length of } OU}{\text{length of } ON}$$

$$\sin(86^\circ) = \frac{OU}{232} \implies OU = 232 \times \sin(86^\circ) \approx 231.7 \text{ pm} \approx 0.23 \text{ nm}$$

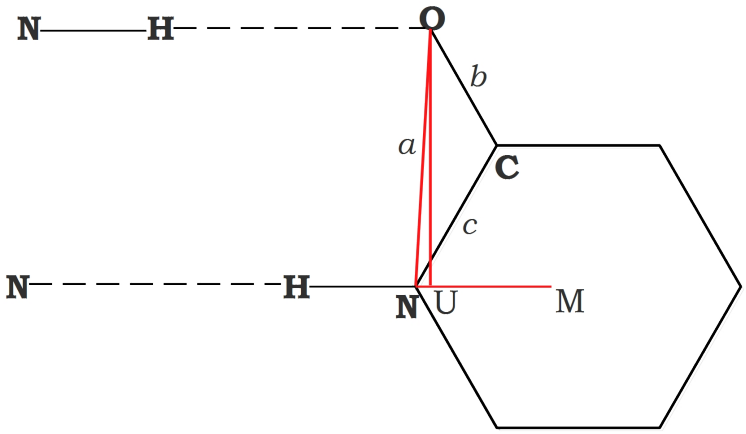

Figure 3: Right-triangle projection to obtain the vertical H-bond distance. Dropping a perpendicular from O to U along MH forms $\triangle ONU$ with $\angle ONU \approx 86^\circ$, giving $OU \approx 232 \times \sin(86^\circ) \approx 0.23$ nm.

Therefore, the vertical and accurate distance between the two hydrogen bonds is approximately 0.23 nm.

2.2. Validation of the mathematical method

To validate the proposed method, it is applied to calculate the DNA molecule's diameter, a dimension that has been experimentally confirmed to be approximately 2.0 nm for B-DNA. This serves as a benchmark, allowing comparison between theoretical predictions and empirical observations. The calculation is based on the additive bond lengths across complementary nucleotide pairs.

2.3. Mathematical calculation

The following molecular measurements are used in the calculation: the length of the hydrogen bond connecting adenine and thymine is approximately 232 pm (value 1), the bond length between the hydrogen and nitrogen atoms within the adenine nucleotide is 101 pm (value 2), and the corresponding bond length within thymine is also 101 pm (value 3).

To estimate the contribution of the nucleotide ring structures to the overall DNA diameter, we calculate the diameter of the hexagonal rings present in both adenine and thymine. Each ring has a side length of 147 pm, and its diameter is approximated as twice that value:

$$\text{Diameter}_{\text{Adenine}} = 2 \times 147 \text{ pm} = 294 \text{ pm (value 4)}$$

$$\text{Diameter}_{\text{Thymine}} = 2 \times 147 \text{ pm} = 294 \text{ pm (value 5)}$$

These calculated distances, when summed appropriately, correspond closely to the known DNA diameter, thus supporting the mathematical method introduced in this study. A visual representation of the hexagonal diameter estimations is provided in figure 4.

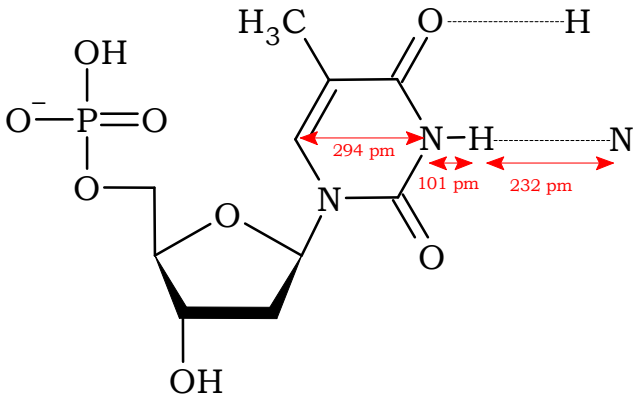

Figure 4: Calculation of the diameter of the hexagonal ring structures in adenine and thymine.

2.4. Calculation of vertical distance

To determine the vertical distance between the carbon atom of the hexagonal ring and the nitrogen atom of the pentagonal ring in the adenine molecule, we apply a geometric approach based on trigonometry.

Consider a right-angled triangle $\triangle K$, in which the hypotenuse represents the bond between the carbon atom in the hexagon and the nitrogen atom in the pentagon. This bond has a length of approximately 147 pm. To resolve this bond vector into its vertical component, we must first calculate the angle between the two rings.

The internal angle of a regular pentagon is 108°, while the exterior angle of a regular hexagon is 120°. The difference between these angles gives us the tilt angle between the atoms involved in bonding:

$$\angle NCD = 120^\circ - 108^\circ = 12^\circ$$

This geometric configuration is illustrated in figure 5.

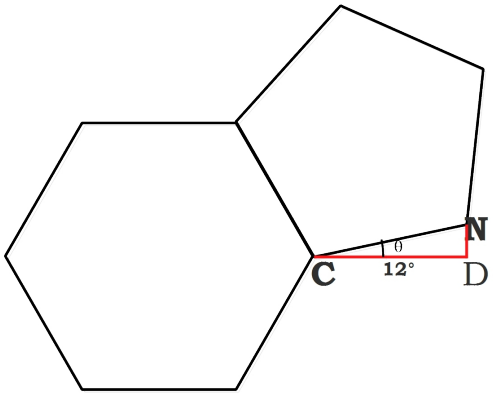

Figure 5: Diagram illustrating the right-angled triangle used to calculate the vertical distance between the carbon atom of the hexagon and the nitrogen atom of the pentagon in adenine.

To determine the vertical distance between the carbon atom of the hexagonal ring and the nitrogen atom of the pentagonal ring in the adenine molecule, we apply the cosine rule within a right-angled triangle. The cosine rule is defined as:

$$\cos(\theta) = \frac{\text{Adjacent side}}{\text{Hypotenuse}}$$

In this context, the angle θ is 12°, the hypotenuse (bond CN) is 147 pm, and the vertical distance to be calculated is the adjacent side, denoted as CD. Substituting the known values into the formula:

$$\cos(12^\circ) = \frac{CD}{147}$$

Solving for CD:

$$CD = 147 \cdot \cos(12^\circ) \approx 147 \cdot 0.978 = 143.7 \text{ pm}$$

Thus, the vertical distance CD between the carbon atom of the hexagon and the nitrogen atom of the pentagon in adenine is approximately 143.7 pm.

In addition to this, relevant bond lengths involved in the hydrogen bonding between thymine and adenine are as follows:

- The bond between the carbon and hydrogen atoms in thymine is 109 pm (value 7).
- The bond between the hydrogen and carbon atoms in adenine is also 109 pm (value 8).

The hydrogen atom in thymine aligns vertically with the oxygen atom in the sugar ring structure. Since the oxygen atom in the sugar occupies the midpoint of the pentagon's diameter, the radius of the pentagon is taken as 109 pm (value 9). Similarly, the corresponding radius on the adenine side of the sugar molecule is also 109 pm (value 10), due to the symmetrical placement of the sugar's oxygen atom.

These measurements are illustrated in figure 6.

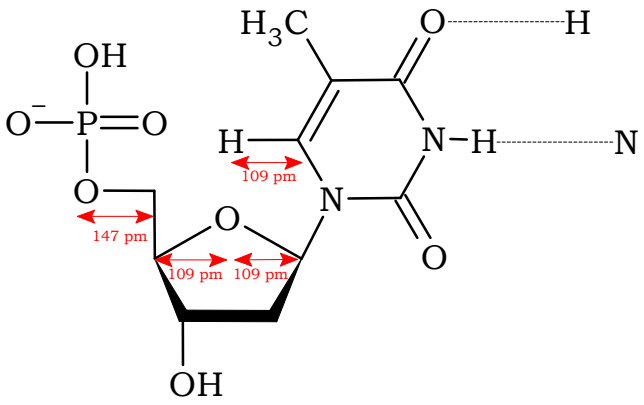

Figure 6: Diagram illustrating the vertical distance and bond lengths associated with adenine and thymine.

2.5. Bond lengths and calculation of DNA diameter

The bond lengths for the DNA molecule are as follows:

- The bond between the carbon atom of the sugar and the oxygen atom of the phosphate group on the thymine side is 147 pm (value 11). This bond length is identical on the adenine side (value 12).

To determine the diameter of the DNA molecule, we sum the lengths of all bonds:

$$\begin{aligned}\text{Diameter of DNA} = 232 + 101 + 101 + 294 + 294 + 143.7 + 109 + 109 + 109 + \\ + 109 + 147 + 147 = 1895.7 \text{ pm}\end{aligned}$$

Performing this calculation:

$$\text{Diameter of DNA} = 1.9 \simeq 2 \text{ nm}$$

This diameter of 2 nm is consistent with the experimentally measured diameter of DNA, confirming the accuracy of this mathematical method.

2.6. Calculation of the distance between hydrogen bonds between base pairs

In DNA samples, a full turn consists of varying base sequences, but there is no measurable distance between consecutive base pairs when the number of hydrogen bond distances is 15 or more. However, when the number of distances is less than 15, very small distances of no more than 0.05 nm can be observed between consecutive base pairs because the number of distances don't less than 12 distance in the complete turn. This suggests that the distances between consecutive base pairs are nearly zero, indicating the compact and tightly packed nature of DNA.

The distance between hydrogen bonds connecting Adenine to Thymine and Guanine to Cytosine can be calculated as follows:

$$\text{Distance} = \frac{\text{Length of the DNA fragment}}{\text{Number of distances between the hydrogen bonds}}$$

Given that the length of the DNA fragment is 3.4 nm and the number of distances between the hydrogen bonds is 15, we have:

$$\text{Distance} = \frac{3.4 \text{ nm}}{15} = 0.226 \text{ nm} \approx 0.23 \text{ nm}$$

This calculated distance of 0.23 nm corresponds to the distance between the two hydrogen bonds connecting Adenine to Thymine and Guanine to Cytosine. Therefore, the 15 distances, each equal to 0.23 nm, are present within the DNA fragment, and no additional distances of length 3.4 nm are found within the fragment.

2.7. Mathematical determination of the length of the hydrogen bond

By drawing a vertical line from the hydrogen atom in adenine to a point S, this line is opposite and equal to the OU line, with a length of 232 pm.

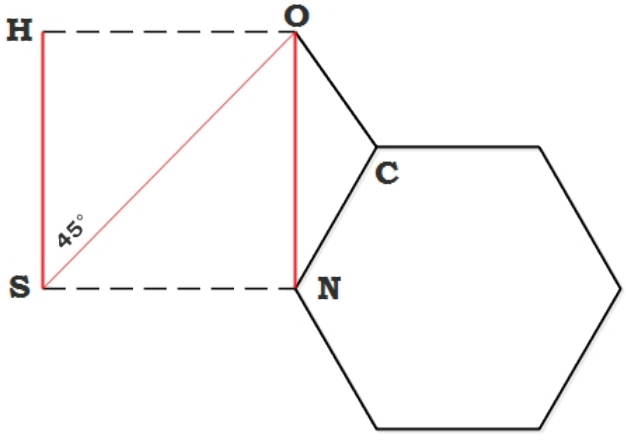

Figure 7: Instructional hydrogen-bond length. The projected H-bond distance is $OH = OS\sin(45) = 0.23$ nm in our 2D teaching model.

The angle $\angle OHS = 90°$ and $\angle USH = 90°$. By drawing the line OS, which bisects the angle $\angle HSU$ into two equal parts of 45°, we find that $\angle OSH = 45°$ (see figure 7).

We can compute the length of the line OS, which is the hypotenuse of the right triangle OHS, using the cosine rule:

$$\cos(45^\circ) = \frac{232}{OS}$$

$$OS = \frac{232}{\cos(45^\circ)} = 328 \text{ pm}$$

Next, we calculate the hydrogen bond length OH using the sine rule:

$$\sin(45^\circ) = \frac{OH}{328}$$

$$OH = \sin(45^\circ) \times 328 = 232 \text{ pm} = 0.23 \text{ nm}$$

Therefore, the length of the hydrogen bond is equal to the distance between the two hydrogen bonds.

2.8. Mathematical measurement of the distance between consecutive base pairs and full helical turn in DNA

The vertical spacing between DNA base pairs stems from the phosphate–oxygen bonds of the backbone, which, due to the double-stranded structure, contribute twice per pair.

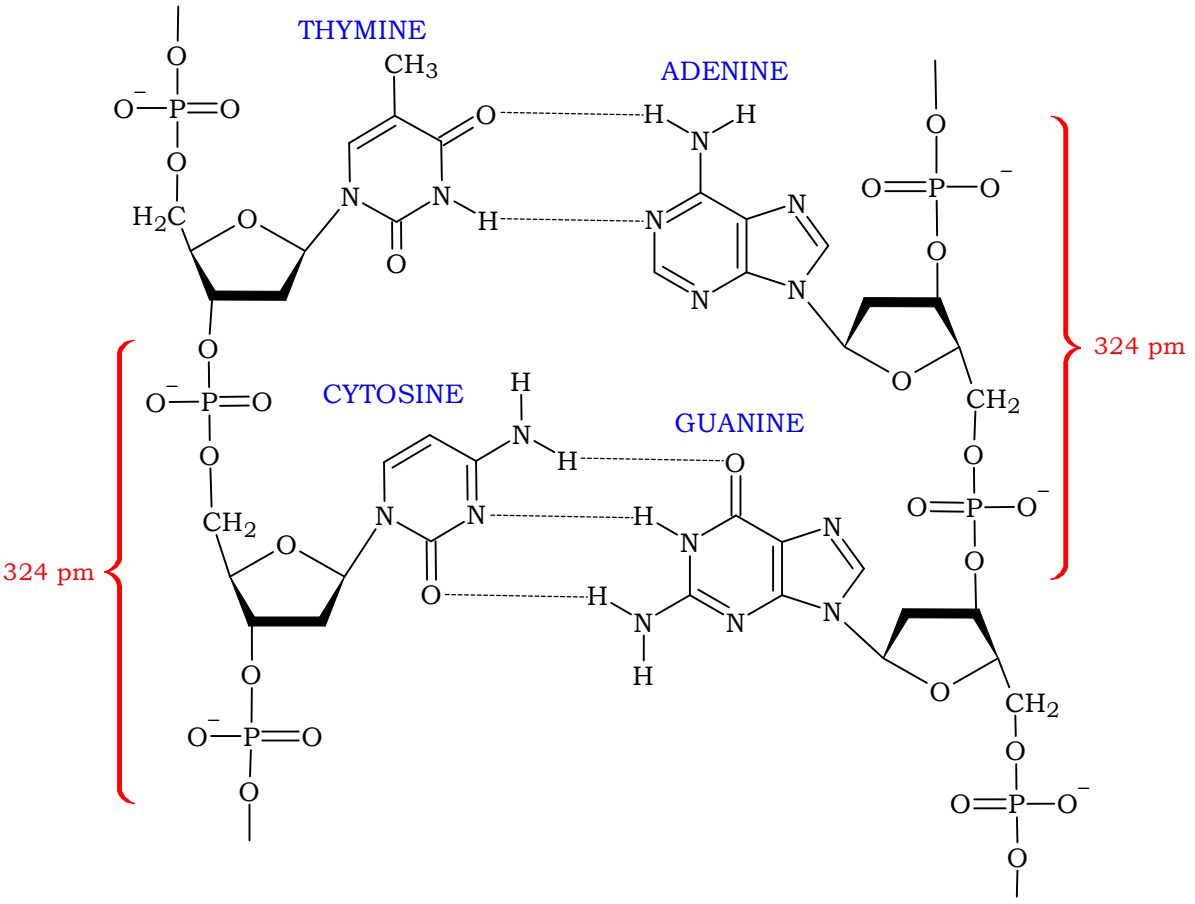

Figure 8: Two phosphate–oxygen links of ≈ 162 pm each yield a vertical rise ≈ 0.324 nm per base pair.

To determine this spacing, we applied our proposed geometric method using experimentally established bond lengths. The bond between the phosphate and oxygen atoms in the backbone measures:

$$\text{Bond length} = 162 \text{ pm}.$$

Since this bond occurs on both sides of a base pair, the total vertical distance between two adjacent base pairs is:

$$\text{Distance} = 162 \text{ pm} + 162 \text{ pm} = 324 \text{ pm} = 0.324 \text{ nm}$$

This result (see figure 8) corresponds closely with the well-documented vertical rise of 0.34 nm per base pair in the DNA helix, reinforcing the validity and precision of our approach.

Our method, based purely on atomic bond lengths and spatial geometry, not only matches experimental observations but can also be adapted to model structural variations in mutated or synthetic DNA, analyze conformational changes under different biological conditions, and enhance science education by helping students visualize nucleic acid structure through accessible mathematical reasoning. For teaching, the constructions above are straightforward to replicate with GeoGebra (dynamic angle sliders) and entry-level molecular viewers (e.g., JSmol) to map computed segments onto base-pair schematics. We include teacher notes indicating which measurements are user-entered versus model-derived [13].

2.9. Classroom implementation and lesson plan

We designed a 45–60 minute lesson aligned to typical Grades 10–12 learning goals (right-triangle trigonometry; interpreting scientific diagrams).

Materials: teacher slides, a one-page worksheet, and an optional GeoGebra file.

Sequence:

1. *Hook* (2–3 min): show a DNA double helix and ask students to estimate key distances.
2. *Mini-lesson* (10–12 min): review the law of cosines and angle relations used in the base-pair triangle.
3. *Guided example* (10–12 min): compute the hydrogen-bond projection (≈ 0.23 nm) step-by-step from given bond lengths.
4. *Partner practice* (12–15 min): students use the same workflow to derive the 0.32–0.34 nm inter-pair rise.
5. *Share/reflect* (5 min): compare with accepted values and discuss sources of error/approximation.

Differentiation: For students with weaker backgrounds, we provide a diagram – first scaffold with all angles labeled and a calculator-allowed track; for advanced students, we include an extension that explores how small angle/length perturbations change the results.

Pilot experience: We piloted the activity with two Grade 11 sections (n = 26). Informal exit tickets indicated improved comfort with multi-step geometry in a biology context and correct order-of-magnitude estimates for the three target distances.

3. Discussion and conclusion

This study introduces a simplified mathematical framework designed to quantify key structural distances within the DNA molecule – specifically, the length of hydrogen bonds between complementary nucleotide bases and the vertical spacing between consecutive base pairs. The primary goal is to make these molecular measurements conceptually accessible to K–12 students by demonstrating how basic geometry and trigonometry can be used to derive values that typically require experimental techniques. By translating complex molecular dimensions into step-by-step geometric

models, this approach supports early science education and bridges the gap between abstract theory and observable biological structure.

On hydrogen-bond length: Many crystallographic and spectroscopic sources report typical N–H$\cdots$O hydrogen-bond distances for base pairs in the range 0.28–0.30 nm. Our classroom calculation yields ≈ 0.23 nm because it models a 2D geometric projection built from idealized bond lengths and ring angles, rather than a full 3D heavy-atom–to–heavy-atom distance with thermal/disorder effects. In practice, adding a small angular deviation (± 5) or using heavy-atom baselines shifts the computed value upward toward the literature range. We therefore present 0.23–0.30 nm as an instructional band, noting that the simplified geometry reliably recovers the correct order of magnitude and the accepted diameter (≈ 2.0 nm) and inter-pair rise (≈ 0.34 nm [20]).

The calculated hydrogen bond length connecting adenine to thymine (A–T) and guanine to cytosine (G–C) was approximately 0.23 nm (or 232 pm), as shown in figure 9. This value was derived using trigonometric identities applied to a geometrically constructed triangle based on atomic bond lengths and angles, and it aligns with experimentally reported data – validating the method's reliability. Additionally, the vertical spacing between two consecutive base pairs, determined from the length of the phosphate–oxygen bonds in the DNA backbone (each 162 pm), totals 324 pm or 0.324 nm. This closely matches the widely accepted helical pitch of 0.34 nm, reinforcing the accuracy of the method.

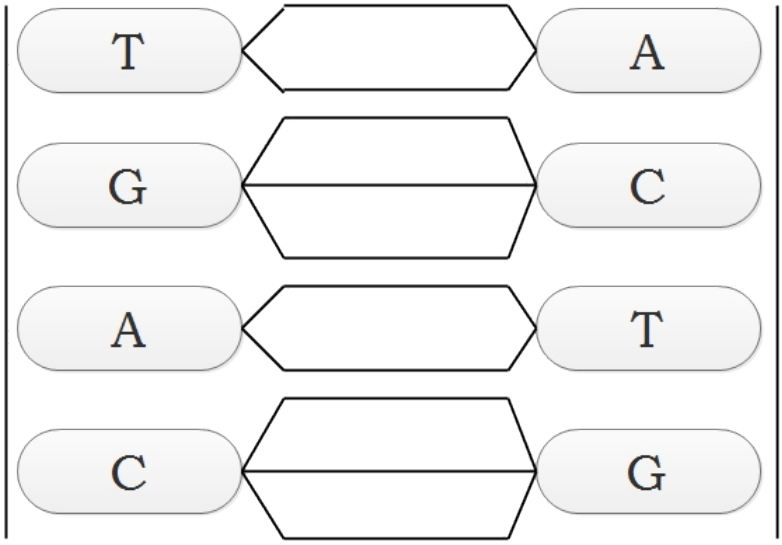

Figure 9: Average instructional H-bond distance annotated as 0.23 nm; caption cross-references literature values (0.28–0.30 nm) as discussed in the highlighted note in the Discussion.

These findings also highlight DNA's dense structural packing: the minimal linear distance between hydrogen bonds of neighboring base pairs reflects the compact and stable nature of the double helix, which is essential for genetic information storage. Moreover, the strong correlation between the calculated values – such as hydrogen bond lengths, vertical stacking, and overall helix diameter – and established experimental data supports the use of geometric reasoning to validate molecular structures without instrumentation.

Beyond its value as an educational tool, this framework may also have diagnostic applications. By analyzing subtle variations in bond lengths between healthy and

diseased DNA – such as those found in cancer or inherited disorders – it may be possible to identify molecular anomalies that serve as early indicators of disease. Such nanoscale precision could open new pathways in biotechnology, nanomedicine, and molecular diagnostics.

In conclusion, this method not only simplifies the modelling of DNA geometry for K–12 education but also demonstrates the power of foundational mathematics in exploring complex biological systems. By equipping students and educators with tools to connect theory with biological reality, it fosters both scientific literacy and a deeper appreciation for the structure of life at the molecular level.

Acknowledgments: This study was partially supported by the Academy of Science and Research Technology (ASRT), Egypt through the project entitled "Analysis of cellular and molecular signature for memory cells post-vaccination of COVID-19" for Prof. Mohamed Labib Salem, the PI of the project. The authors would like to express their sincere gratitude to Shaimaa Gamal from the chemistry department for her invaluable assistance in using ChemDraw during the preparation of this work.

References

[1] Alberts, B., Johnson, A., Lewis, J., Raff, M., Roberts, K. and Walter, P., 2002. *Molecular Biology of the Cell*. 4th ed. Garland Science.

[2] Barry, P.D., 2015. *Geometry with Trigonometry*. 2nd ed. New York, NY: Academic Press / Woodhead Publishing. Available from: http://ndl.ethernet.edu.et/bitstream/123456789/24493/1/212.Patrick%20D.%20Barry.pdf.

[3] Berg, J.M., Tymoczko, J.L., Gatto, Jr., G.J. and Stryer, L., 2015. *Biochemistry*. 8th ed. W. H. Freeman and Company. Available from: https://dn790008.ca.archive.org/0/items/JeremyM.BergJohnL.TymoczkoGregoryJ.GattoJr.LubertStryerBiochemistry_201708/Jeremy%20M.%20Berg%2C%20John%20L.%20Tymoczko%2C%20Gregory%20J.%20Gatto%20Jr.%2C%20Lubert%20Stryer%20Biochemistry.pdf.

[4] Bialek, W., 2012. *Biophysics: Searching for Principles*. Princeton, NJ: Princeton University Press. Available from: https://www.princeton.edu/~wbialek/PHY562/WB_biophysics110918.pdf.

[5] Clauvelin, N., Olson, W.K. and Tobias, I., 2012. Characterization of the Geometry and Topology of DNA Pictured As a Discrete Collection of Atoms. *Journal of Chemical Theory and Computation*, 8(3), pp.1092–1107. Available from: https://doi.org/10.1021/ct200657e.

[6] Drew, H.R., Wing, R.M., Takano, T., Broka, C., Tanaka, S., Itakura, K. and Dickerson, R.E., 1981. Structure of a B-DNA dodecamer: conformation and dynamics. *Proceedings of the National Academy of Sciences of the United States of America*, 78(4), pp.2179–2183. Available from: https://doi.org/10.1073/pnas.78.4.2179.

[7] Ellington, R., Wachira, J. and Asamoah Nkwanta, A., 2010. RNA Secondary Structure Prediction by Using Discrete Mathematics: An Interdisciplinary Research Experience for Undergraduate Students. *CBE—Life Sciences Education*, 9(3), pp.348–356. Available from: https://doi.org/10.1187/cbe.10-03-0036.

[8] Ferris, M.M., Yan, X., Habbersett, R.C., Shou, Y., Lemanski, C.L., Jett, J.H., Yoshida, T.M. and Marrone, B.L., 2004. Performance Assessment of DNA Fragment Sizing by High-Sensitivity Flow Cytometry and Pulsed-Field Gel Electrophoresis. *Journal of Clinical Microbiology*, 42(5), pp.1965–1976. Available from: https://doi.org/10.1128/jcm.42.5.1965-1976.2004.

[9] Galvin, M., 2025. NAS President Marcia McNutt to Deliver Second State of the Science Address on June 3. Available from: https://tinyurl.com/rn888638.

[10] García de la Torre, J. and Hernández Cifre, J., 2020. Hydrodynamic Properties

of Biomacromolecules and Macromolecular Complexes: Concepts and Methods. A Tutorial Mini-review. *Journal of Molecular Biology*, 432(9), pp.2930–2948. Integrative Biophysics: Protein Interaction and Disorder. Available from: https://doi.org/10.1016/j.jmb.2019.12.027.

[11] Glick, B.R., Pasternak, J.J. and Patten, C.L., 2010. *Molecular Biotechnology: Principles and Applications of Recombinant DNA*. 4th ed. Herndon, VA: ASM Press. Available from: https://ia802904.us.archive.org/30/items/BiotechnologyByBernard/biotechnology%20by%20bernard.pdf.

[12] Gross, L.J., 2004. Interdisciplinarity and the undergraduate biology curriculum: Finding a balance. *Cell Biology Education*, 3(2), jun, pp.85–87. Available from: https://doi.org/10.1187/cbe.04-03-0040.

[13] Hanson, R.M., 2010. Jmol – a paradigm shift in crystallographic visualization. *Journal of Applied Crystallography*, 43(5), pp.1250–1260. Available from: https://doi.org/10.1107/S0021889810030256.

[14] Lesyng, B., Jeffrey, G.A. and Maluszynska, H., 1988. A model for the hydrogen-bond-length probability distributions in the crystal structures of small-molecule components of the nucleic acids. *Acta Crystallographica Section B: Structural Science*, 44(2), pp.193–198. Available from: https://doi.org/10.1107/S0108768187011170.

[15] Lodish, H., Berk, A., Matsudaira, P., Kaiser, C.A., Krieger, M., Scott, M.P., Zipursky, L. and Darnell, J., 2000. *Molecular Cell Biology*. 5th ed. New York: W. H. Freeman and Company. Available from: https://www.mustafaaltinisik.org.uk/s-molecularcellbiology.pdf.

[16] May, R.M., 2004. Uses and abuses of mathematics in biology. *Science*, 303(5659), pp.790–793. Available from: https://doi.org/10.1126/science.109444.

[17] Meysman, P., Marchal, K. and Engelen, K., 2012. DNA Structural Properties in the Classification of Genomic Transcription Regulation Elements. *Bioinformatics and Biology Insights*, 6, pp.155–168. Available from: https://doi.org/10.4137/BBI.S9426.

[18] Nakhle, J., Özkan, T., Lněničková, K., Briolotti, P. and Vignais, M.L., 2020. Methods for Simultaneous and Quantitative Isolation of Mitochondrial DNA, Nuclear DNA and RNA from Mammalian Cells. *BioTechniques*, 69(6), pp.436–442. Available from: https://doi.org/10.2144/btn-2020-0114.

[19] Swigon, D., 2009. The Mathematics of DNA Structure, Mechanics, and Dynamics. In: C.J. Benham, S. Harvey, W.K. Olson, D. Sumners and D. Swigon, eds. *Mathematics of DNA Structure, Function and Interactions*, *IMA Volumes in Mathematics and its Applications*, vol. 150. New York, NY: Springer, pp.293–320. Available from: https://doi.org/10.1007/978-1-4419-0670-0_14.

[20] Tabernero, L., Bella, J. and Alemán, C., 1996. Hydrogen Bond Geometry in DNA–Minor Groove Binding Drug Complexes. *Nucleic Acids Research*, 24(17), Sep, pp.3458–3466. Available from: https://doi.org/10.1093/nar/24.17.3458.

[21] Wang, J.C., 2002. Cellular roles of DNA topoisomerases: a molecular perspective. *Nature Reviews Molecular Cell Biology*, 3(6), Jun, pp.430–440. Available from: https://doi.org/10.1038/nrm831.

[22] Watson, J.D. and Crick, F.H.C., 1953. Molecular Structure of Nucleic Acids: A Structure for Deoxyribose Nucleic Acid. *Nature*, 171(4356), pp.737–738. Available from: https://doi.org/10.1038/171737a0.