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Applications of topology in biology

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complementary (i.e. two molecules can base pair with each other by hydrogen bonding and forms a double helix of the type suggested by Watson and Crick [5]. Although the overall features of the dodecamer structure conform closely to those expected of B-form DNA, the molecule shows local sequence- dependent variation [6]. For example, the distance between base pairs varies from 0.314 to 0.356 nm, the average being about 0.33 nm. the DNA base pairs are not all perpendicular to the helix axis and show propeller twist where the purine.

Genetic information is carried in the linear sequence of nucleotides in DNA [7]. Each molecule of DNA is double helix formed from two complementary strands of nucleotides held together by hydrogen bounds between G-C and A-T base pairs. Linking number, writhe and twist: the linkage equation [9]. The linking number Lk for a covalently closed circular DNA molecule is the number of times one strand crosses the other. For a relaxed molecule the Lk can be referred to as Lk_0 . Lk is a topological property of DNA[10].

Lk can be expressed as the algebraic sum of two geometric properties, twist (Tw) and writhe (Wr). Twist refers to the manner in which one strand winds around the second. Writhe refers to the non-planarity of the DNA axis[11].

Lk = Tw + Wr

For relaxed DNA, Wr = 0; or Lk = Tw. That is, twist is equal to the number of turns between the Watson and Crick strands[12].

However, in supercoiled DNA, Lk is not equal to Tw, since Wr is no longer non-zero imagine that you break the strand in a relaxed molecule, and reseal it after taking out 'n' turns (see Fig. 1). The DNA is now under-wound or negatively supercoiled. As a result, the tendency of the axis is to be non-planar [13].

Let us now imagine that by some means, we counteract this force, and keep the axis planar. Hence we impose zero writhe in the molecule as shown. This is one extreme way of accommodating the torsional stress [14]. In the other extreme, we

Abstract

In this paper, the set nitrogenous bases on a single strand can be more than topological space, we have obtained some of topological properties. Then we created a relationship(map) between the nitrogenous bases on the first strand of DNA to the nitrogenous bases on other strand, and we showed topological properties of this map. Then we investigated the aspect, which is that one turns of DNA of simple circular type homeomorphism segment I=[0, 1]. The perfectly circular DNA homeomorphism I.

Keywords: topology, biology, DNA. homeomorphism, Applications

I. Introduction

A typical DNA molecule consists of two complementary polynucleotide chains that are multiply interwound [1], forming a double helix. In the prevailing conformation, called B-DNA, this is a right handed helix with a period of approximately 10.5 base pairs (bp) per turn at physiological condition. The features that distinguish B-DNA from other forms are location of the base paris on the helix axis, the near-perpendicular orientation of the base pairs relative to the helix axis and distinct major and minor grooves (the former in particular allowing easy access to the bases). Some of the helical parameters B-form and other forms of DNA [2].

The helical repeat (base pairs per turn) of maxed-sequence B-form DNA has been determined by a variety of experimental methods and has been found to be clse to 10.5 bp/turn; this value depends on the solution conditions, but is often taken as an average for B-DNA [3]. A number of other parameters are required for a complete description of the conformation of the double helix. In 1980 the structure of B-form DNA molecule was analyses at atomic resolution using X-ray diffraction of single crystal [4]. The molecule used these studies was the dodecamer in d(CGCGAATTCGCG), which selfis



 $X \to Y$ be a map. We say f is continuous if for any $V \in \mathfrak{I}_y, f^{-1}(V) \in \mathfrak{I}_x$.

Definition 2.2.2. Let $f : X \to Y$. We say f is continuous at $x \in X$ if for every open set V in Y with $f(x) \in V$, there exists an open set U in X such that $f(U) \subset V$.

Proposition 2.2.3. *A function* $f : X \rightarrow Y$ *is continuous if and only if it is continuous at every point in X.*

Proof. If the function f is continuous in *X*, then it is obvious that such function is continuous at every point in *X*.

Assume *f* is continuous at every point $x \in X$, so for every point *x* with $f(x) \in V$ where *V* is an open set in *Y* we have $f(U_x) \subset V$ with $x \in U_x$. Thus $U_x \subset f^{-1}(V)$, we can write

$$f^{-1}(V) = \bigcup_{\substack{x \in f^{-1}(V) \\ V \in V}} U_x$$

since the chosen open set V is arbitrary, we see that the function f is continuous in X. \Box

Definition 2.2.4. A continuous bijective map $f: X \rightarrow Y$ is called a homeomorphism if

 $f^{-1}: Y \to X$ is continuous as well.

Remark. If there exists a homeomorphism between *X* and *Y*, we say *X* and *Y* are homeomorphic.

2.2 Connected and Path-Connected

Definition 2.2.1. Given a topological space *X*. We say *X* is connected if whenever $X = U \cup V$ where *U* and *V* are disjoint open sets, we have $\{U, V\} = \{\emptyset, X\}$. If there exist other disjoint open sets $\{U, V\}$ such that $X = U \cup V$, then we call *U*, *V* the separation of *X*.

Remark. X is connected if and only if the only separation of X is $\{\emptyset, X\}$.

Proposition 2.3.2. A space X is connected if and only if the only sets that are both open and closed are \emptyset and X.

Proof. Suppose X is connected and U is a subset of X which is both closed and open but not \emptyset and X, so V = X - U is both open and closed but not \emptyset and X. Thus $\{U, V\}$ provides a separation of X. Here is a contradiction, so there must be no such U and V. The reverse implication is trivial.

Definition 2.3.3. Given a continuous map $f : [a, b] \rightarrow X$ and $x, y \in X$ where *X* is a topological space. Then f is called a path from x to y if f(a) = x, f(b) = y. A space X is called *path-connected* if given any two points $x, y \in X$, there exists a path between x and y

let the stress to be counteracted entirely by coiling (non-planarity) of the axis, that is, entirely by writhe [15]. In reality, supercoiled DNA consists of all possible dynamic conformations ranging from the one shown at the left (no writhe) to that shown at the right (no change in twist). Or, supercoiling which is a change in Lk, can be partitioned into Tw and Wr in amyriad ways. Let us illustrate supercoiling with a simple example as follows. Imagine a relaxed DNA circle with a 1000 bp. We assume that there are 10 bp per every turn of DNA. Or this molecule contains a 100 turns, or its $Lk_0 = 100$.

Lk = Tw + Wr;

In our relaxed molecule, Wr = 0.

$$Lk_0 = 100 = Tw + 0$$

Let us remove 20 turns from this molecule by breaking a strand and resealing it. Now there are only 80 turns in this molecule, or Lk = 80.

 $\mathbf{L}\mathbf{k} = \mathbf{80} = \mathbf{T}\mathbf{w} + \mathbf{W}\mathbf{r}.$

If we force the axis to be planar, thus keeping Wr = 0.

80 = Tw + 0

This twist is now 80, and therefore the pith of the helix changes it is no longer 10 bp per turn, rather 1000/80 or 12.5 bp per turn. This is the case illustrated in Fig. 1 at the left now, let us keep the twist the same (100 turn; 10 bp per turn), and partition the negative supercoiling entirely into writhe[16].

II. Topological space

Definition 1.1.1 A topological space to be a nonempty set \varkappa and a collection \Im of sets in \varkappa . The collection \Im will serve as the topology of \varkappa . In order that it be sensible to regard the sets in \Im as the 'open sets 'of \varkappa we require that \Im satisfy the conclusions of theorem

(i) $\emptyset \in \mathfrak{J}, X \in \mathfrak{J}$.

(ii) Any union of sets in \Im is in \Im .

(iii) Any finite intersection of sets in \Im is in \Im . [book2]

Remark. A space X with a topology \Im is called a topological space.

Definition 2.1.2. A space X with topology \Im is called **Hausdorff** if for any $x, y \in X$ with $x \neq y$, there exist two open sets $U, V \in \Im$ and $x \in U$, $y \in V$ such that $U \cap V = \emptyset$.

Remark. A Hausdorff space is a space where we can separate points by open sets [17].

a. Continuity And Continuous Function

Definition 2.2.1. Given two topological spaces *X*, *Y* with topologies \mathfrak{I}_x and \mathfrak{I}_y respectively, let f:



Definition 2.5.2. A partition A of a set X is a collection of subsets $\{U_i\}_{i \in I}$, such that

$X = \bigcup_{i \in I} U_i$ and $U_i \cap U_j = \emptyset$ if $i \neq j$.

Definition 1.5.3. Let X be a topological space and A a partition of X. Let $f : X \to Y$ be a surjective map provided that $f(x_i) = U_i$ where U_i is an element of A which uniquely contains x_i . If we let T_A denote the quotient topology on A arising from the quotient map f, then we call A the quotient space of X with respect to A.

III. Knot Theory

A knot is an embedding of the circle S^1 into R^3 . Two knots are equivalent if there exists an ambient isotopy between them.

Proposition: The two strand of close-circular DNA molecule are knots are equivalent because ambient isotopy between them. It is clear that by definition knots.

3.1 Reidemeister Moves

There are certain continuous deformations which leave the topological properties of knots invariant. These are called the Reidemeister moves.

2.3 Compactness

Definition 2.4.1 Let *X*be a space and $\{U_i\}$ a collection of open sets. $\{U_i\}$ is called an open cover of *X* if $X = \bigcup_{i \in I} Ui$. The space *X* is compact if every open cover contains a finite subcover (i.e. U_1 , U_2 , ..., $U_n \in \{U_i\}$ such that $X = U_1 \cup U_2 \cup ... \cup U_n$) [18].

Proposition 2.4.2. Every closed subset of a compact space is compact.

Proof:

Given a compact set X, suppose Y is a closed subset of X. Let $\{U_i\}$ be any open cover of Y. Let $U' = \{Ui\}, \{X - Y\}$, we can tell that U' is an open cover of X so it has finite subcover $U_1', U_2', ..., U_n'$. If $\{X - Y\}$ is among any U_i' , throw them out. Hence Y is compact.

Proposition 2.4.3. Every compact subset of a Hausdorff space is closed.

Proposition 2.4.4. Let $f: X \rightarrow Y$ be a continuous map. If X is compact, then f(X) is compact as well.

2.4 Quotient Map and Quotient Space

Definition 2.5.1. Given two topological spaces *X* and *Y*. Let $f : X \to Y$ be a surjective map. We call *f* a quotient map provided that $U \in T_Y$ if and only if $f^{-1}(U) \in T_X$.

Definition 3.1.1. The Reidemeister moves are local continuous deformations of knots that appear as such:



Figure 1: The equivalence relation on diagrams generated by all Reidemeister moves is called an ambient isotopy.

if $X = \{A, T, C, G\}$ then there exist a topology \Im on X, such that $\Im = \{\emptyset, X, \{A, T\}, \{G, C\}\}$. proof:

1) Ø

- 1) $\emptyset, X \in \mathfrak{J}$
- 2) Any union of sets in \Im is in \Im i. e. $(\emptyset \cup X = X \in \Im, X \cup \{A, T\} = X \in \Im, X \cup \{C, G\} = X \in \Im, \{A, T\} \cup \{G, C\} = X \in \Im, ... etc.$

3) Any finite intersection of sets in \Im is in \Im . $\emptyset \cap X = \emptyset \in \Im, \{A, T\} \cap \{G, C\} = \emptyset \in \Im$

Propositions of topology ℑ I.ℑis not Hausdorf topology The equivalence relation on diagrams generated by all Reidemeister moves is called an ambient isotopy.

In principle, because of Reidemeister's Theorem (which states that two strand of B-DNA are equivalent because their diagrams can be connected by a sequence of Reidemeister moves), we can classify all (B-DNA) by the diagrams generated by any sequence of Redemeister moves on a given knot. Remember that genetic information is carried in the linear sequence of nucleotides in DNA. Each molecule of DNA is double helix formed from two complementary strands of nucleotides held together by hydrogen bounds between G-C and A-T base pairs [19]. Lemma 1:



one. The following topological criterion is a more 4 appropriate equivalence relation on knots. [20].

Curves and continua

The focus our attention on R^2 . we have seen that lines and circles separate R^2 into distinct components. What can be said about other curve?

First, something needs to be said about curves in general.

Definition

A curve in \mathbb{R}^2 to be the image f(I) of a compact interval I under a continuous function $f: I \to \mathbb{R}^2$. Definition

Let I = [0, 1] and let S be the square $[0, 1] \times [0, 1]$. For each $n \in N$, Hilbert constructed a continuous function $f_n: I \to S$. The curves f_1 , f_2 and f_3 are illustrated a continuous in the diagram below

The sequence $\langle f_n \rangle$ of function converges uniformly to continuous function $f: I \to s$. AS IS Evident from the construction, the curve f(I) passes through every point of S i.e. f(I) = S. We say that f(I) is a space-filling curve'.Simple curve . The shall say that a curve C is a simple arc if it is topologically equivalent to the compact interval [0, 1]. This means that there exist a homeomorphism $f: [0,1] \to C$. A curve C will be called a Jorden curve (or simple ' closed ' curve) if it is topologically equivalent to the unit circle U in R^2

 $A \neq T$ there is no exist two open sets $U, V \in \mathfrak{T}$ and $A \in U$, $B \in V$ such that $U \cap V = \emptyset$. II. Let $f: X \to X$ such that f(A) = T, f(T) =A, f(C) = G, f(G) = C, then f is continuous. Proof: $f^{-1}(\{A,T\}) = \{T,A\}.$ $f^{-1}(\{C,G\}) = \{G,C\}.$ $f^{-1}(\emptyset) = \emptyset.$ $f^{-1}(X) = X.$ *f* : is quotient map III. The map $f: X \to X$ is a homeomorphism. **Proof:** f isclear continuous bijective map and $f^{-1}: X \rightarrow X$ X is continuous as well.by definition the end. VI. A topological space X is separation. Proof: $\{A, T\} \cup \{C, G\} = X \text{ and } \{A, T\} \cap \{C, G\} = \emptyset$ V. A topological space X is compact.

Proof: $[A, T] \cup [G, C]$ is finite open cover of X for any open cover of X.

IV. f(X) is compact by proposition (because X is finite set)

-Now the B-DNA is a Reidemeister moves because the properties which is have it.

Usually homeomorphic space is considered equivalent in topology. Since all knots homeomorphic to the unit circle, they are all homeomorphic to one another. Therefore, homeomorphism type is an uninteresting equivalence relation on knots and a rather unnatural



Figure 2: curve C will be called a Jorden curve

IV. Conclusions

The set nitrogenous bases on a single strand can be more than topological space. They have obtained some of topological properties. Then we created a relation (map) between the nitrogenous bases on the first strand of DNA to the nitrogenous bases on other strand, and we showed

Proposition

Let C a relaxed B-DNA is a simple curve then it is a topologically equivalent to a compact interval [0, 1] this mean that there exist a homeomorphism $f: [0,1] \rightarrow C$ then C is Jorden curve U in \mathbb{R}^2 . Proof:

Since B-DNA is circular ,then it is topologically equivalent to the unit circle U in R^2 .



methods

and

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topological properties of this map. The investigated the aspect, which is that one turns of DNA of simple circular type homeomorphism segment I=[0, 1].Let C a relaxed B-DNA is a simple curve then it is a topologically equivalent to a compact interval [0, 1] this mean that there exist a homeomorphism $f: [0,1] \rightarrow C$ then C is Jorden curve U in \mathbb{R}^2 .

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