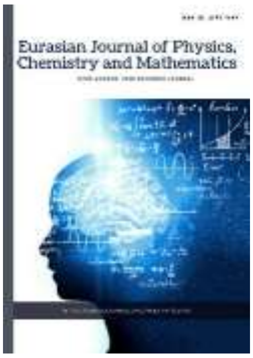

Application of Topology in Variety Fields

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ABSTRACT

Topology although one of the recently invented sciences in mathematics, it is widely used in many areas of human life. In this paper we discuss some applications in various fields of Science and Technology, like applications to Biology, Robotics, GIS, Error-coding and Genetics. Being a part of theoretical mathematics, the laws of topology are finding more and more application in various types of human activities that are described by rules and laws of topology.

Keywords: topology, genotypes, genotype-phenotype relationship, phenotype space, chains, sequences, digital topology, digital domain, pixels, closed set, odd and even integers, metric, configuration space, kinematics map, GIS, intersection, distance, codewords, Hamming distance.

Introduction

At the turn of the XIX-XX centuries, a completely new field separated from geometry - topology, which, in fact, determined the development of mathematics of the XX century. Those geometric structures that turned out to be the most fundamental, simplest and most related to physics of the XX century have gone into topology. The merit in this belongs primarily to the great French mathematician Henri Poincaré, who identified topological structures and who developed the language to describe them. If we talk about the difference between geometry and topology, then distance plays a major role in geometry [1-4].

Topology is a Greek word which means the study of place. This well-defined branch of mathematics emerged in the initial.

Furthermore, topology became popular not least because it has found its application in physics. Just at the turn of the century, physics ceased to be linear. It turned out that the Newtonian world, in which our space is equally extended and evenly in all directions, is not a sufficiently accurate tool for describing reality. Because of this, Poincaré took a decisive part, made our world curved, twisted. And so, to describe the non-flat world, topology turned out to be the most suitable tool [5-9].

For example, the shape of the Earth we know through the simplest astronomical observations that simply describe the shadow from the Earth during a lunar eclipse. The shadow cast by our planet is round. And we can conclude from here that the Earth itself is round. If we were in more difficult conditions, we would have simple topological means to understand which planet we live on. To do this, it would be enough to simply divide the Earth into triangles, triangulate it and calculate the number of triangles involved in the partition, the number of their vertices and their sides.

And then the famous Euler formula, obtained by him long before the results of Poincaré, would allow people to say the topological nature of the surface of the planet on which they live [10-14].

Nowadays, mathematicians and scientists use topology to model and comprehend the real-world occurrences. Topology basically has emerged out of geometry, expanding some notions and losing some of the erections appearing therein, where the concept of distances and angles are excluded. Here objects are taken and treated as if they are made of rubber which one can stretch, crumble, twist and even deform but without cutting and pasting. In topology, the objects we take are called topological spaces. From the topological perspective, circle and square are same, which are totally different in other perspectives. Topologically, we can deform a circle into a square and vice versa, we call them topologically equivalent. Consequently, a sphere cannot be deformed into torus and vice versa, and hence they are not topologically equivalent. In topology, the properties that remain preserved during deformations are taken into consideration and are called as topological invariants. Topologists cannot distinguish between a circle and a square, sphere and a cube, because they share topological properties throughout the deformation mathematically called homeomorphism. The properties that remain unchanged during homeomorphism are what we call topological properties or topological invariants [15-19]. In this paper we describe some applications of topology in other fields of Science and technology. We discuss applications to Biology, Robotics, GIS, Computer Sciences, and Engineering. Topology has influenced the world of Science and technology with much great effects.

The basis of Topology is the classical set theory. A topological space is an ordered pair (X, τ) consisting of a set X and topology τ on X and satisfies the following: topology on a set is the collection τ of the subsets of the set X such that τ contains the empty set, the set itself, and which is closed under finite intersection and arbitrary unions. The elements of this collection are called open sets [20-24]. There are many ways of defining topology on a set, as in Subspace topology, product topology, order topology. We usually find a basis to generate topology on a set. Basis for a topology τ on a set X is the collection of subsets B of subsets of X such that (if for each $x \epsilon X$, there exists at least one basis element B containing x. (ii) If x belongs to the intersection of two basis elements B_1, B_2, then there is a basis element B_3 containing x such that $B_3 \subset B_1 \cap B_2$.

Topology has expanded its boundaries and crossed almost every other field like Robotics, Chemistry, Computer Sciences, Geography, Biology and etc. Now we describe various applications of topology and try to understand its influence [25-29].

Applications to Biology

Topology besides being a very different branch of mathematics, it plays a very good role in Biology. Since genotypes-phenotypes are primary important in biology, we see how topology is even useful in sequencing the right nucleotides in DNA strand. Genotypes are the internally veiled and inheritable information of a living being while as phenotypes are the physical appearances of that information. Topology solves one most important problem in DNA research. As we know that DNA is composed of four nucleotides: Adenine, Cytosine, Guanine and Thymine. These are arranged in a manner that they resemble a sequence. The sequence of nucleotides on every single chain of DNA decides the sequence of the other chain. The problem found in DNA research is in the comparison of distinct DNA sequences. The genotype-phenotype relationship is of fundamental importance in biology. The genotype is internally coded, inheritable information possessed by all living organisms, while the phenotype is the physical realization of that information. For instance, the collection of genes responsible for eye color in a particular individual is a genotype. The observable eye coloration in the individual is the corresponding phenotype. A model of evolutionary proximity established by defining a topology on a set of phenotypes. Molecular biologists propose this model as a means for formally defining continuous and discontinuous evolutionary change, providing a mathematical framework for understanding evolutionary processes.

The idea of phenotype space via an example involving ribonucleic acid (RNA) molecules. Strands of RNA are formed from smaller molecules, called nucleotides, that bond together to make strong, flexible chains. There are four different nucleotides in RNA: guanine (G), cytosine (C), adenine (A) and uracil (U). Nonadditive nucleotide pairs undergo additional bonding, contorting the chain into a more complicated folded arrangement as:

GUGAUGGAUU AGGAUGUCCU ACUCCUUUGC UCCGUAAGAU AGUGCGGAGU UCCGAACUUA CACGGCGCGC GGUUAC

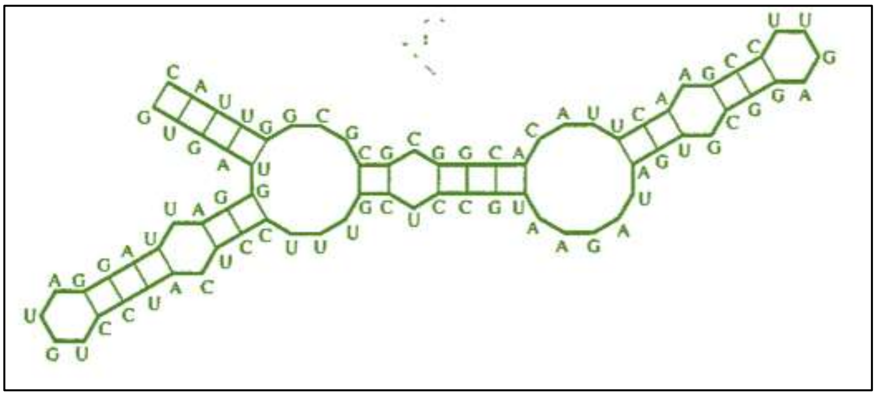

Figure. 1.

Pairing of guanines with cytosine and adenine with uracil contribute the most to folding, though guanine and uracil can also pair. In theory, there are many ways that a particular nucleotide chain can fold and bond, but only the most energetically favorable of these are likely to occur. For simplicity, we assume that this bonding occurs in a unique way. Here, we consider only relatively short nucleotide chains to illustrate the structures and the topological model. RNA molecules in living cells can be anywhere from tens to thousands of nucleotides in length.

For a particular RNA molecule, the associated unfolded nucleotide chain is called the primary structure. We represent the nucleotide chain by a sequence of C's, G's, A's and U's called the genotype sequence for the molecule.

Given a genotype sequence, its bonding diagram is an unlabeled diagram depicting the bonding that occurs in the resulting RNA molecule. The dots on the diagram refers to the location of the first nucleotide in the sequence, and the rest of the sequence wraps counterclockwise around the perimeter of the diagram. The bonding diagram is the phenotype in the model: it is also referred to as the RNA shape or secondary structure for the RNA molecule. The phenotype spaces we introduce are sets of RNA shapes on which a topology is defined.

Application in DNA sequence

DNA is a long thin molecule made up of millions of atoms. Within its structure lies the code that determines our genetic makeup. RNA, DNA is composed of nucleotides. While an RNA molecule consists of a single chain of nucleotides, a DNA molecule consists of two chains wound together to form the familiar double helix. The nucleotides in DNA come in four types: adenine (A), cytosine (C), guanine (G), and thymine (T). In our introduction to RNA we showed that nucleotides in a chain tend to pair together, contorting the chain into a folded shape. Nucleotides in a DNA chain also pair, but do so with their neighbors on the opposite chain (adenine pairs with thymine, and guanine pairs with cytosine). In fact, the two chains are constructed such that every nucleotide on one chain pairs with its neighbor on the other. Thus, the sequence of nucleotides on one chain determines the sequence on, he opposite chain, and we can represent part or all of a DNA molecule with a sequence of the letters A, C, G, and T, corresponding to the sequence of nucleotides found in one of the two chains.

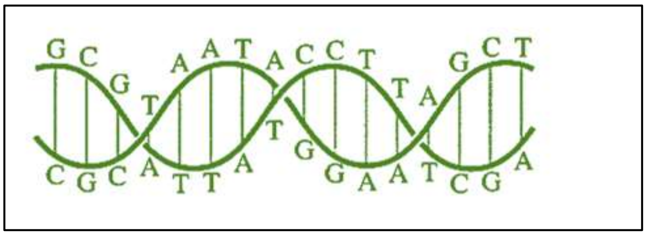

Figure 2.

One of the most important problems in DNA research is how to compare distinct DNA sequences. How different is one sequence of DNA from another? In some sense, this is a measure of the evolutionary distance between the two sequences. When a species splits into two new species, resulting in a fork in the evolutionary tree, the species' initially identical DNA sequences begin to accumulate unique changes. Measuring the distance between the two sequences as a function of these differences provides insight into the nature of the evolutionary history of each species. During the course of evolution, DNA sequence differences arise in a variety of ways. One of the most common is nucleotide substitution, the apparent replacement of a letter in one DNA sequence relative to the original sequence. If this is the only type of change that has occurred between two sequences, then the Hamming distance provides a useful measure of the distance between them. Another commonly occurring change in DNA is the insertion or deletion of nucleotides, realized as the insertion or deletion of letters in the corresponding DNA sequence. In this case, all of the subsequent letters in the altered sequence appear offset relative to the original sequence. This results in a large Hamming distance between the two DNA sequences, when in reality they are quite similar. To deal with this problem, we introduce another metric that is useful in making comparisons.

Let x and y be two sequences of the letters A, C, G, and T. we measure distance between x and y by determining how many operations on x are necessary to turn it into y. We allow three types of operations on x: We can insert any letter into x, we can delete any letter in x, and we can replace any letter with a different letter. For our particular x and y, we can use a sequence S of these operations to turn x into y. Let i_S represent the number of insertions in the sequence, d_S the number of deletions, and r_S the number of replacements. So, the total number of operations to turn x into y is $i_S + d_S + r_S$. But of course, there are many different choices of sequences of operations to turn x into y, and therefore we define the distance between x and y as follows: The Levenshtein distance between sequences x and y is given by $D_L(x,y) = \min_S\{i_S + d_S + r_S\}$, where the minimum is taken over all sequences S that turn x into y.

Applications to Digital Image Processing

The main purpose of Digital Topology is the study of topological properties of discrete objects which are obtained digitizing continuous objects. Digital Topology plays a very important role in computer vision, image processing and computer graphics. A digital image is an object in the computer screen where the smallest elements are pixels or, more abstractly, compact topological cells such that they only have intersection in their borders. So it is natural to abstract the screen model as a graph whose vertices corresponding to the pixels and the edges represent the adjacency between the pixels.

In the initial development of the field of digital topology, work focused on defining and studying digital analogs of topological concepts (for example, connectedness and continuity) without having an underlying topology on the model of the digital image display. The 1979 paper, "Digital Topology," by Azriel Rosenfeld (1931—2004), was one of the first introductions to these ideas. Later, topological spaces were found that appropriately model the digital image display, enabling topological concepts to be used directly in the digital domain.

The digital image display contains a rectangular pixel array. In digital topology, this array is modelled by what is known as the digital plane.

Example 1.1. for each $n \in Z$, define

$$B(n) = \begin{cases} \{n\} \text{ if n is odd} \\ \{n-1, n, n+1\} \text{ if n is even} \end{cases}$$

The collection $B = \{B(n) | \, n \in Z\}$ is a basis for a topology on Z. The resulting topology is called the digital line topology.

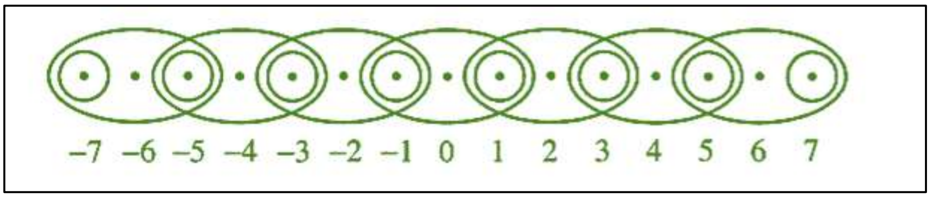

Figure 3.

This example shows a one-dimensional digital image display. We assume that we have an infinite line of pixels, each of which corresponds to an odd integer. For each odd integer we have a basis element $B(n) = \{n\}$. Subsequently, each individual pixel is an open set in the digital line topology. Each even integer n represented the boundary between the pixels at $n-1$ and $n+1$. In addition to this, we should admit, that in the digital line, every odd integer is an open set, and every even integer is a closed set.

So, the digital line as a set of open pixels corresponding to the odd integers, along with the set of closed boundaries between the pixels corresponding to the even integers.

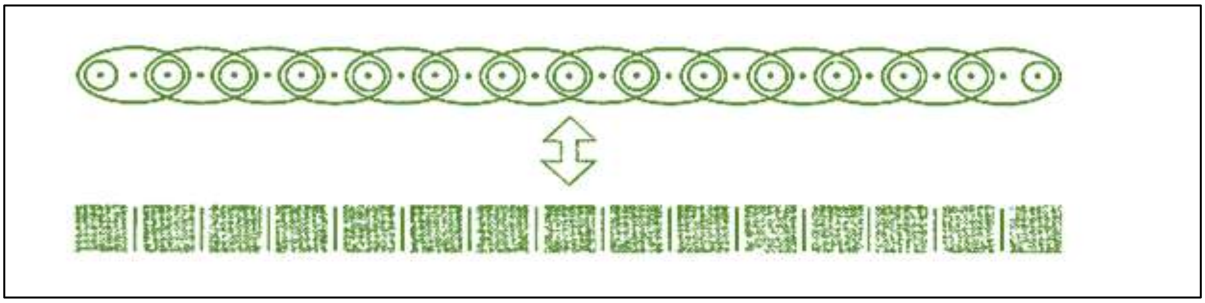

Figure 4.

Application to Robotics

Topology and physics have a very deep connection. It requires the most advanced knowledge of topology to study the most sophisticated applications in other fields. One of the modern fields nowadays become robotics. Topology enters robotics through the notion of configuration space. Any mechanical system R determines the variety of all its possible states X which is called the configuration space of R. Usually a state of the system is fully determined by finitely many real parameters; in this case the configuration space X can be viewed as a subset of the Euclidean space R^k. Each point of X represents a state of the system and different points represent different states. The configuration spaces X comes with the natural topology (inherited from R^k) which reflects the technical limitations of the system. Many problems of control theory can be solved knowing only the configuration space of the system. Peculiarities in the behavior of the system can often be explained by topological properties of the system's configuration space. We will discuss this in more detail in the case of the motion planning problem. We will see how one may predict the character of instabilities of the behavior of the robot knowing the cohomology algebra of its configuration space. If the configuration space of the system is known one may often forget about the system and study instead the configuration space viewed with its topology and with some other geometric structures, e.g., with the Riemannian metric. In this field of robotics can be defined by continuous function that is called the forward kinematics map, which plays a role in motion planning for linkages, robot arms and other similar mechanisms. The linkage presented in pic. 3 had two rods. We assume that rod B is shorter than rod A. the configuration space for system is the torus, $S^1 \times S^1$, where the first S^1 corresponds to the circle of angles θ_A through which rod A can turn about its fixed end, and the second S^1 corresponds to the circle of angles θ_A through which B can turn about its end that is fixed to rod A.

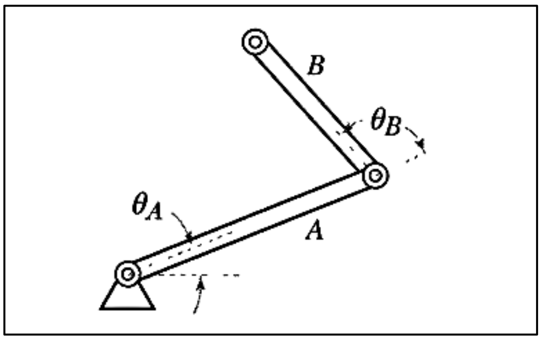

Figure 5.

The operational space for the linkage is the space traced out by the end of rod B and the resulting operational space is an annulus.

In general, in studying the design of a machine or robot arm, we are interested in a particular point on the mechanism where there is a tool that serves a specific function, such as spraying the end effector and the operational space is the space traced out by the end effector.

To each point in the configuration space of a mechanism, we associate the corresponding end-effector point in the operational space. Thus, a function f is defined; it is called the forward kinematics map for the mechanism. It is natural to assume that the forward kinematics map is continuous because points close together in the configuration space correspond to points clothe in the operational space. In the case of our two-rod linkage, f is a continuous map from the torus to the annulus.

An important question in the field of robotics is whether a given path in the operational space of a mechanism can be traced by the end effector. In the given example, we can ask if there is a way to manipulate the configuration space variables θ_A and θ_B to yield a given path in the operational space annulus.

An application to Geographic Information Systems

A geographic information system (GIS) is a computer system capable of assembling, storing, manipulating and displaying geographically referred data. To date are often used for solving complex planning and management problems. To analyze spatial information, users select data from GIS by submitting queries. Typical GIS queries incorporate spatial relations to describe constraints about spatial objects to be analyzed or displayed. For example, in studying wetland protection within a state's recreation areas, a GIS user might ask for a display of all wetlands that lie partially or entirely within the state's parklands. The GIS would search for wetland areas and state parkland areas and examine the relationship of each to the other in order to return all wetlands that satisfied the specified requirements.

Evidently, in a GIS there is a need to be able to distinguish different ways that land regions can lay in relation to each other. For a mathematician, it often suffices to know if two sets intersect or not, but in a GIS a classification finer than intersect/not-intersect is needed. For example, in Figure 6, while sets

A and B and sets A' and B' intersect, there is an obvious difference in the nature of their intersections. There is a need to make these distinctions precise.

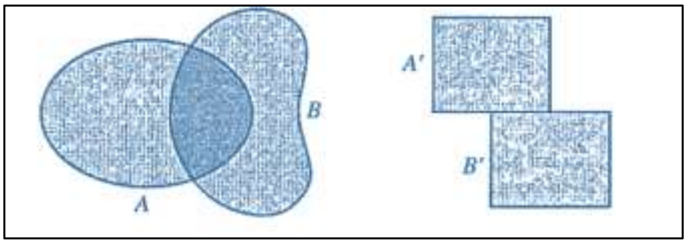

Figure 6.

Furthermore, in Figure7, while the initial view of sets C and D suggests that they intersect, after zooming in it is obvious that they do not. Information stored in a GIS regarding the relationship between such sets should not depend on how the sets appear in a particular picture. Thus, by storing the information C and D do not intersect, the GIS ensures that the nature of the relationship between the two sets is independent of potentially misleading pictorial representations of them, particularly those characterized by poor resolution.

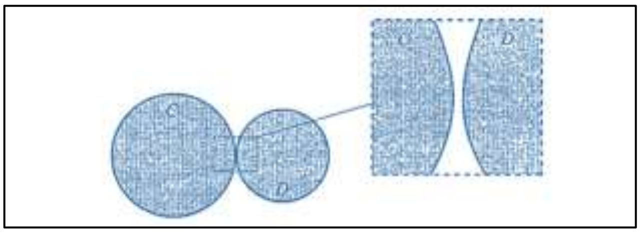

Figure 7.

Application in error-coding

With the incredible amounts of information being transmitted over phone lines, through the internet, or from satellites in space to Earth, it is extremely important to know whether a given message has arrived intact. We expect that there will be some errors in transmission due to electrical surges, cosmic radiation, or a variety of other factors. We want to be able to recognize when this occurs and to correct the faulty message. This brings us to the theory of error-correcting codes.

Suppose that we want to send a certain message. We assume that the message has been encoded in a binary code, which is to say that our message consists of a finite sequence of 0s and 1s, say n of them, which we call a word. We also assume that in transmission, some number of 0s may be turned into is and vice versa. We do not allow for lost entries or additional entries, so the word that arrives also has length n. Note that what we call a word here could consist of a few words, as we normally think of them, making up a particular message. Each word of length n can be thought of as a vector of length n, with all entries either 0s or 1s, we write the set of all these possibilities as $\mathrm{V}^{\mathrm{n}} = \{(\mathrm{a}_1, \dots, \mathrm{a}_\mathrm{n}) \big| \, \mathrm{a}_\mathrm{i} \in \{0,1\}\big\}$. So V^{n} is the product of n copies of the set $\{0,1\}$. We now put a metric on this set. The Hamming distance $\mathrm{D}_\mathrm{H}(\mathrm{x}, \mathrm{y})$ between two words of length n is the number of places in which the words differ. A code of length n is any subset C of V^{n}. the elements of C are called the codewords.

If the sender and receiver have agreed on a particular code, then when a word arrives that is not one of the codewords, the receiver knows that at least one error has occurred in transmission. Let C be a code of length n. define the minimum distance of the code C to be the least Hamming distance between two codewords in the code.

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