

Using Parametric Mathematical Modeling to Develop a Geometric and Topological Intuition for Molecular Knots

Tahmineh Azizi¹, Jacob Pichelmeyer²

¹Institute of Computational Comparative Medicine, Department of Anatomy and Physiology, Department of Mathematics, Kansas State University, Manhattan, KS, USA

²Department of Mathematics, Kansas State University, Manhattan, KS, USA

Email: tazizi@ksu.edu, jacobpichelmeyer@ksu.edu

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Abstract

Knot theory is a branch of topology in pure mathematics, however, it has been increasingly used in different sciences such as chemistry. Mathematically, a knot is a subset of three-dimensional space which is homeomorphic to a circle and it is only defined in a closed loop. In chemistry, knots have been applied to synthetic molecular design. Mathematics and chemistry together can work to determine, characterize and create knots which help to understand different molecular designs and then forecast their physical features. In this study, we provide an introduction to the knot theory and its topological concepts, and then we extend it to the context of chemistry. We present parametric representations for several synthetic knots. The main goal of this paper is to develop a geometric and topological intuition for molecular knots using parametric equations. Since parameterizations are non-unique; there is more than one set of parametric equations to specify the same molecular knots. This parametric representation can be used easily to express geometrically molecular knots and would be helpful to find out more complicated molecular models.

Keywords

Synthetic Molecular Knots, Parametric Equations, Topology and Knot Theory, Trefoil Knot

1. Introduction

The study of knots started from the 1860s with William Thompson (Lord Kelvin) and his vortex model of the atom. According to Kelvin model, atoms and different chemical elements were formed by different knots. During the past two

decades, different areas in chemistry have been affected by knot theory [1] [2] [3] [4] [5]. Knots and links play a very important role in the molecular structure of certain chemical compounds. Using mathematical methods, researchers can detect and classify knots and links in complex molecular systems [6] [7] [8] [9] [10]. Alexander polynomial is one of the simplest methods to identify knots and it can detect and classify a knot based on the minimum number of crossings in a projection of the chain onto a plane to classify knots [11]. Scientists have been trying to produce synthetic molecular knots for decades. In 1989, Jean-Pierre Sauvage winner of Nobel Prize, conducted a research group which leads to make the first synthetic molecular knot. They created a knot called a trefoil, which consists of two polymer strands intertwined at three cross points. The ends of these strands are joined together, which creates a knot that cannot be unraveled without breaking the strands. One of the well-known examples in molecular knots is cycloparaffins molecule with over 50 carbon atoms which is technically a simple ring or as a knotted ring resembling a trefoil [12]. **Figure 1** and **Figure 2** display three twisted rings were joined at a single atom, and mathematically are known as the Trefoil Knot. The parametric equations corresponding to the trefoil knot has the following form:

$$\begin{cases} x = \sin(t) + 2\sin(2t); \\ y = \cos(t) - 2\cos(2t); \\ z = -\sin(3t); \end{cases} \quad (1.1)$$

and the parametric equations for the trefoil-negative knot has the form:

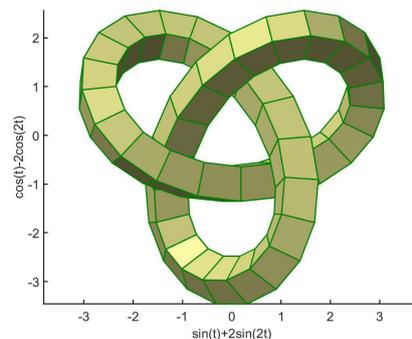


Figure 1. Trefoil, 3_1 .

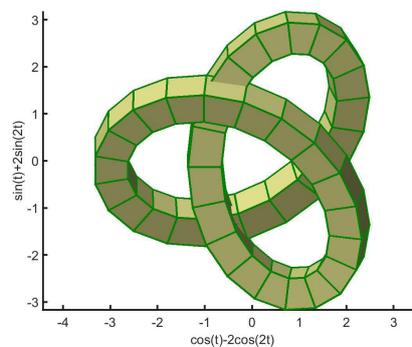


Figure 2. Trefoil-negative, 3_1 .

$$\begin{cases} x = \cos(t) - 2\cos(2t); \\ y = \sin(t) + 2\sin(2t); \\ z = -\sin(3t); \end{cases} \quad (1.2)$$

The trefoil knot has the property of being a Möbius strip (see **Figure 3**). Möbius strip can be constructed by cutting a closed band into a single strip, giving one of the two ends thus produced a half twist, and then re-attaching the two ends. Möbius strips have very complex dynamics and chemists are usually interested to find out the molecules and nanoscale materials can be induced to adopt such a shape, and what would the possible properties of these molecules and materials. A Möbius strip of half-width w with midcircle of radius r and at height $z = 0$ can be demonstrated parametrically by

$$\begin{cases} x = \left[r + \mu \cos\left(t \frac{1}{2}\right) \right] \cos(t); \\ y = \left[r + \mu \cos\left(t \frac{1}{2}\right) \right] \sin(t); \\ z = \mu \sin\left(t \frac{1}{2}\right); \end{cases} \quad (1.3)$$

for μ in $[-w, w]$ and t in $[0, 2\pi)$. In this parametrization, the Möbius strip is a cubic surface with equation

$$-r^2y + x^2y + y^3 - 2rxz - 2x^2z - 2y^2z + yz^2 = 0 \quad (1.4)$$

Chemists make tiny molecular knots in their labs using directed self-assembly techniques. They synthesize these knots and join the fragments rather than tied in a single continuous biomolecular string. Trying to build more complicated knots will assist researchers to better understanding of which materials are better to use for a specific purpose based on strength, flexibility and other features. It can be possible to develop woven knots and forming functional materials with catalyzing properties which are heat-resistant [13]. By weaving the knots in lab, self-assembled structures can be obtained and it can help biophysicists to learn more about synthesized structures such as DNA and RNA, proteins and other molecules which are emerging naturally.

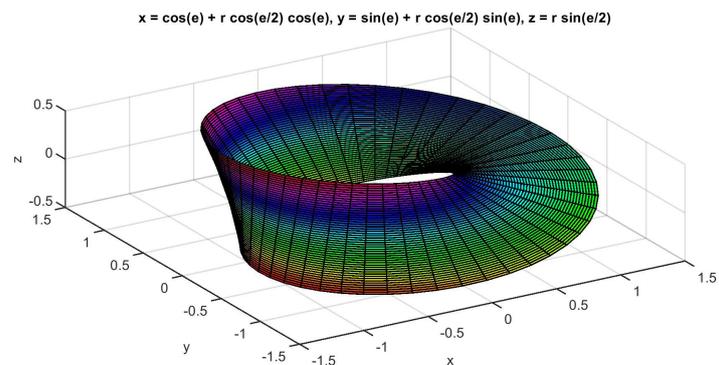


Figure 3. Möbius strip.

In this paper, we study a new way to model synthetic molecular knots. Parametric equations are convenient and helpful to explore more complicated structure of molecular knots. We will provide some mathematical and topological representations for some of the molecular knots. Simplicity of this type of modeling will help biochemists and biophysicists to discover even complicated synthetic molecular knots.

2. A Mathematical Playground

Although it has been proved that Kelvin's theory to be of little physical use, it pushed mathematicians to begin studying of knots in detail. Since Kelvin's theory, mathematicians have developed increasingly different methods for making sense of knots complexity. Mathematicians are interested to determine whether two knots in **Figure 1** and **Figure 4** are the equivalent or not. Two knots called equivalent if one of them can be wiggled around, stretched, tangled and untangled until it coincides with the other one. In this process, cutting and rejoining is not permitted. **Figure 4** can be obtained parametrically by the following equations:

$$\begin{cases} x = (2 + \cos(2t)) \cos(3t); \\ y = (2 + \cos(2t)) \sin(3t); \\ z = 2 \sin(4t); \end{cases} \quad (2.1)$$

Knot theory is a branch of a larger field of pure mathematics called topology which studies knots and links. Topology studies the properties of geometric figures which are unchanged by elastic deformations such as stretching or twisting. To warm up, we present some mathematical definitions which help to understand the topology of the knots. In topology, a surface is connected if every two distinct points on the surface are connected by a path on the surface. A surface is said to be closed if there is no boundary. The sphere and torus are closed and connected. A pair of linked tori is an example of unconnected surface [14] [15] [16] [17] [18]. Examples of surfaces that are not closed are the disc, cylinder and Mobius strip. The torus which has been shown in **Figure 5** and has been demonstrated with θ_1 in **Figure 6** can be generated by the rotation of circle in a

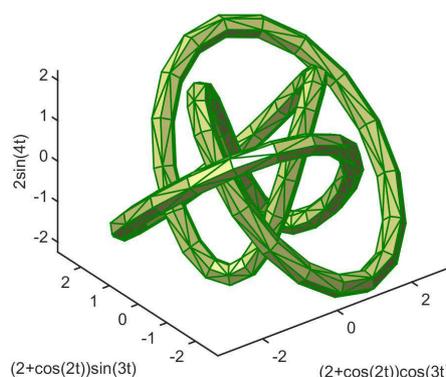


Figure 4. 8 crossings knot.

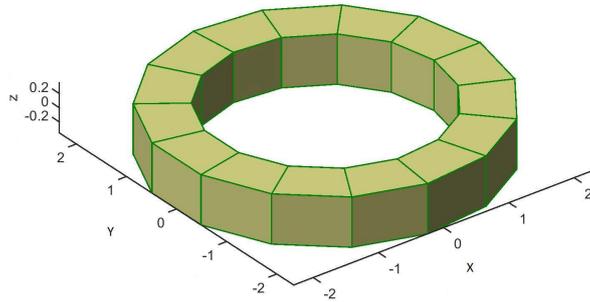


Figure 5. Torus; 0_1 .

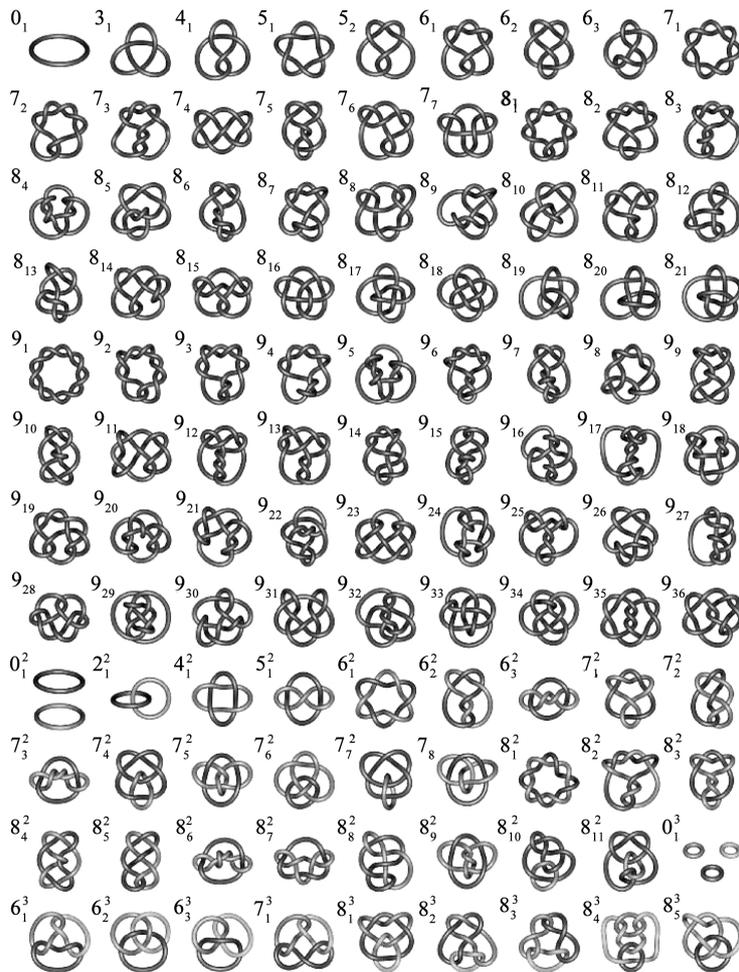


Figure 6. Rob Scharein's knotplot.

circular direction. If we identify the opposite edges of a square with the same direction, we get a torus.

If we show the radius from the center of the hole to the center of the torus tube be ρ_1 , and the radius of the tube be ρ_2 . Then the equation in Cartesian coordinates for a torus symmetric about the z -axis is

$$\left(\rho_1 - \sqrt{x^2 + y^2}\right)^2 + z^2 = \rho_2^2 \tag{2.2}$$

and the parametric equations are

$$\begin{cases} x = (\rho_1 + \rho_2 \cos(\phi)) \cos(\theta); \\ y = (\rho_1 + \rho_2 \cos(\phi)) \sin(\theta); \\ z = \rho_2 \sin(\phi); \end{cases} \quad (2.3)$$

where, $\phi, \theta \in [0, 2\pi)$.

A knot is a closed curve in space without self intersections means that a knot is a simple closed curve [3]. In other words, a knot is defined as a topological state of a closed loop which we cannot untie it without being spliced. This is equivalent to say that that knots cannot be defined in open chains. However, there are many knots in biological systems which are open chains. For a simple linear string, we can consider it knotted if it does not disentangle itself after being pulled at both ends. One can apply this idea in open chains and it is similar to their ends being unambiguously connected with a loop to make a corresponding closed curve. Recognizing knots in topologically complex systems is complicated and it is not often straightforward and needs some mathematical methods to both discover and divide them into different knot types. To distinguish knotted structures, a variety of algorithms can be applied. One of the simplest knot exploring algorithms, known as the Alexander polynomial, can discover and categorize a knot according to the minimum number of crossings in a projection of the chain onto a plane [5]. The crossing number $c(K)$ of a knot K is defined as the minimal number of crossings in any diagram of that knot which is a natural measure of complexity. Also, a minimal diagram of K is one with $c(K)$ crossings. Each knot type can be labeled based on the Alexander Briggs notation, where the first number demonstrates the crossing number which measures the complexity of knots and the subscripted index number describes the knot's order amongst all knots considering that crossing number. For example, a simple ring with zero crossings is referred to as the unknot 0_1 or the trivial knot (Figure 5) while the simplest knot type which is not trivial knot type is the trefoil knot 3_1 with three crossings (Figure 1 and Figure 2).

In addition to the Alexander polynomial, there are two more advanced algorithms, the Jones and HOMFLY polynomials, which can be used to distinguish between different complex knots [5]. There are many kinds of knots called chiral knots which are not equivalent to their mirror images. The mirror image K^- of a knot K can be achieved by reflecting it in a plane in \mathbb{R}^3 . All such reflections are equivalent.

The simplest chiral knot which we have already discussed about it is the trefoil knot (Figure 1 and Figure 2). In contrast, trivial 0_1 in Figure 5 is achiral knot which can be converted to their mirror images.

There is another family of knots called torus knots which can be drawn as closed curves on the surface of a torus and have been demonstrated in Figure 1 and Figure 2.

One of the disadvantages of using polynomials to analyze the knots is that

they are working well for simpler knots without many crossings, however, when we have complicated knots with many crossings, they cannot be computationally effective and cannot recognize complicated knots as simpler ones. To solve this problem, researchers have been developed an alternative smoothing algorithm, sometimes referred to as the KMT reduction, was developed such that complex knotted structures are simplified by omitting regions of the chain unnecessary for maintaining the knot [19] [20]. In this method, highly reduced configurations of the original chain would be produced which leads to efficient computation of the polynomials [5]. Indeed, for protein structures this reduction algorithm is very useful for demonstrating the knotted chain in a simplified manner so that knots can be recognized directly and can be easily visualized [21] [22].

One of the interesting topic for topologist about knot theory is how we can produce an unknot like **Figure 5**. In the process of constructing a knot, it is always possible to turn it into a diagram of the unknot only by changing some of its crossings. In another word, there is always a way to build an unknot by allocating the crossings such that we get an unknot. The unknotting number $u(K)$ of a knot K is the minimum number of crossing changes required to turn into an unknot. In other words, by passing the knot through itself, we can reduce it to the unknot. Here, the question is how many times we need to let it cross itself. For example, the unknot in **Figure 5** is the only knot with unknotting number $u = 0$. Also, the trefoil in **Figure 1** and **Figure 2** has $u = 1$.

Mathematically, there are three common methods to study the knots. Algebraic methods are a part of the theory of the fundamental group, algebraic topology, and so on. Geometric methods are from arguments that are essentially rigorous visual proofs. Combinatorial proofs are mostly very hard to describe in topological point of view [18].

A table of the simplest knots and links has been demonstrated in **Figure 6**. This table came from Rob Scharein's Knotplot site. It shows the 72 simplest knots, and 36 of the simplest links [8].

According to this table, the knots are given names like 5_1 ; 5_2 which imply to the first 5-crossing knot and the second one. The table doesn't list knots which are connect-sums of simpler ones and just prime knots are included. The table also does not list mirror images. Most knots are distinct from their mirror images. There are examples of amphichiral, which are equivalent to its mirror. In the table, there is asterisk or symbol which is placed next to the diagrams of the amphichiral knots to demonstrate their unusual property. We usually consider the crossing number as a measure of the complexity of a knot or link, simply implies that it is drawable using a small number of crossings.

3. Molecular Knots

The beginning of building synthetic molecular was in the late 1980s when synthetic molecular trefoil was made. In the last few years, many complex synthetic molecule knots have been build. By imposing steric restrictions on molecular

strands result in knotting impart significant physical and chemical properties, including chirality, strong and selective ion binding, and catalytic activity [9]. Technically, increasing complexity of molecular knots, make them more effective for chemist and other disciplines. In 2018, M. Marenda, E. Orlandini, and C. Micheletti proposed a Monte Carlo sampling and molecular dynamics simulations tool for thermodynamically and kinetically accessible knot types made of helical templates [7].

Beside synthetic molecular, we have another well-known application of knot theory in biology, DNA, RNA and proteins. DNA, RNA and proteins are three major classes of biopolymers and play an important role in the structural, dynamical properties of the biological systems [3] [5] [7] [9]. The DNA or deoxyribonucleic acid is a molecule which forms a 200 kilometer long double-stranded filament tightly knotted to encode the genetic information which is necessary for developing and functioning of all living organisms. The second copy of the DNA would be created after division of cell and this copy is tangled up with the first one while they are pulled apart from each other. Breaking and rejoining the strands of DNA need enzymes called topoisomerases which allow the molecules to pass through one another [3] [5]. Biologists are interested to know more about these enzymatic actions and to explore the changes these enzymes make, they need to get help from knot theory. Mathematics help biologist to compare the knottedness of two molecules. From the beginning of arrival of knot theory in biology in the 1860s when William Thompson (Lord Kelvin) proposed his vortex model of the atom, many changes occurred in the study of molecular knots [1]-[10].

The DNA follows a complex structure and it has indispensable topology. In all organisms, each contains a family of naturally occurring enzymes that change cellular DNA in order to interfere the replication, transcription and recombination process of cellular life. In order to investigate enzyme binding and mechanism, molecular biologists have brought a topological approach to enzymology, which is a protocol obtained experimentally in which we do a reaction between small artificial circular DNA substrate molecules and purified enzyme *in vitro* [3] [5]. Technically, the role of these enzymes can be divided into two different categories: geometrically, these enzymes affect the DNA substrate by supercoiling and topologically, they are effective in knotting and linking of the DNA molecules. After applying the changes in topology of the DNA molecules, mathematicians can discover the structure of the active DNA-protein complex and also different changes in that structure which is caused by enzyme mechanism [3] [5] [7] [9].

Figure 7 displays one of the synthesized molecules called 8_{19} , which has been making through chemistry. The 8_{19} knot in **Figure 7** can be obtained by the following parametric equations:

$$\begin{cases} x = \sin(t) + 2\sin(3t); \\ y = \cos(t) - 2\cos(3t); \\ z = \sin(2t); \end{cases} \quad (3.1)$$

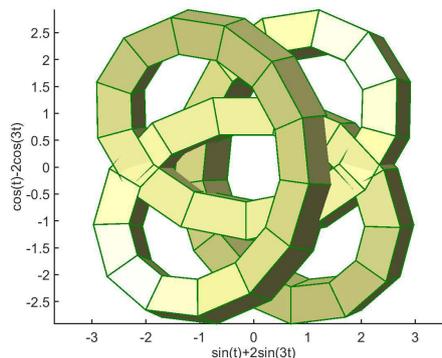


Figure 7. 8_{19} knot.

The knot 8_{19} has been made with polymer strands of carbon, hydrogen, nitrogen and oxygen. Afterward, these polymer strands would be composed with iron and chlorine ions in a solvent liquid which is used to foster chemical interactions. Then, this compound would be heated to 266 degrees Fahrenheit for 24 hours, which would make the iron ions to bind to the polymer strands in particular locations. Particularly, four iron ions which each one has been bound to three polymer strands near their intended cross points, hold the strands together so that the knot could form.

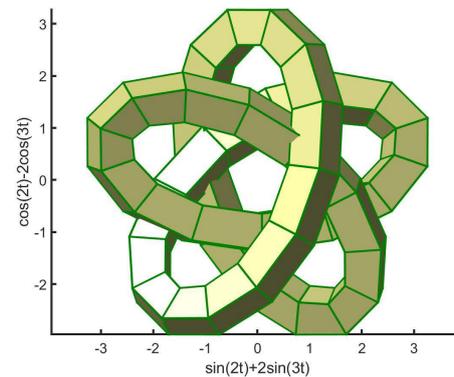
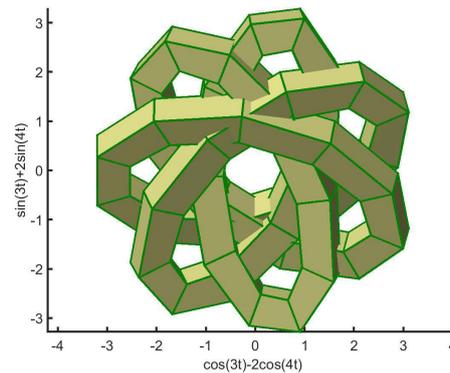
It is always possible to change the reaction conditions by adding in a new catalyst, modulating the temperature, or changing the solvent as needed. Applying each of these changes make the polymer strands to braid around the metal ions and become more possible forming the 8_{19} knot. These steps are sometimes longer than a day and finally synthesizing of a 8_{19} knot would be completed. 8_{19} knot has one chlorine ion in the center, and four iron ions at the polymer cross points. After 30-minute chemical reaction these metal ions would be removed and the result is a pure 8_{19} knot consisting of only the three polymer strands. The final knot has only 192 atoms long and it is a hundred times smaller than a mammalian cell. So far, 8_{19} knot is the most complicated molecular knot which has been synthesized in the laboratory and researchers are looking for the techniques involved in its building to incorporate other molecular knots with three or more polymer strands.

The 5_1 knot with 5 minimal crossings, in **Figure 8** can be obtained by:

$$\begin{cases} x = \cos(2t) - 2 \cos(3t); \\ y = \sin(2t) + 2 \sin(3t); \\ z = \sin(2t); \end{cases} \tag{3.2}$$

Other molecular knot, 7_1 with 7 minimal crossings, cyclic symmetric realisations of knots requires more templates than prime knots with 8 crossing such as 8_{19} [7]. The 7_1 knot in **Figure 9** can be obtained parametrically by:

$$\begin{cases} x = \cos(3t) - 2 \cos(4t); \\ y = \sin(3t) + 2 \sin(4t); \\ z = \sin(2t); \end{cases} \tag{3.3}$$

Figure 8. 5_1 knot.Figure 9. 7_1 knot.

The 9_1 knot with 9 minimal crossings in Figure 10 can be obtained by:

$$\begin{cases} x = \cos(4t) - 2\cos(5t); \\ y = \sin(4t) + 2\sin(5t); \\ z = \sin(2t); \end{cases} \quad (3.4)$$

The $T(4,3)$ knot in Figure 11 can be obtained by:

$$\begin{cases} x = \cos(t) - 3\cos(3t); \\ y = \sin(t) + 3\sin(3t); \\ z = \sin(2t); \end{cases} \quad (3.5)$$

The $T(5,4)$ knot in Figure 12 can be obtained by:

$$\begin{cases} x = \cos(t) - 3\cos(4t); \\ y = \sin(t) + 3\sin(4t); \\ z = \sin(2t); \end{cases} \quad (3.6)$$

4. Conclusion and Future Work

During the past 3 decades, many progresses have been made by chemist for making molecular trefoil knots, using different synthetic processes. However, there are many synthetic molecular knots that remain as a challenge in chemistry. Increasing the number of molecular knot topologies helps chemists to discover the

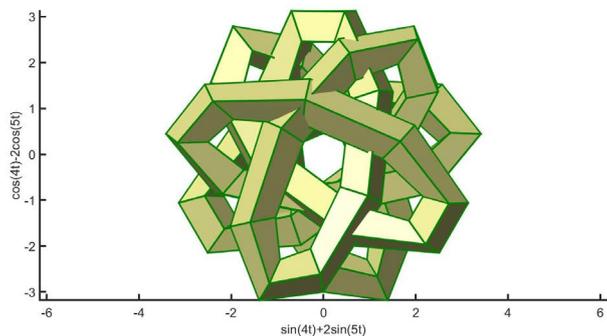


Figure 10. 9_1 knot.

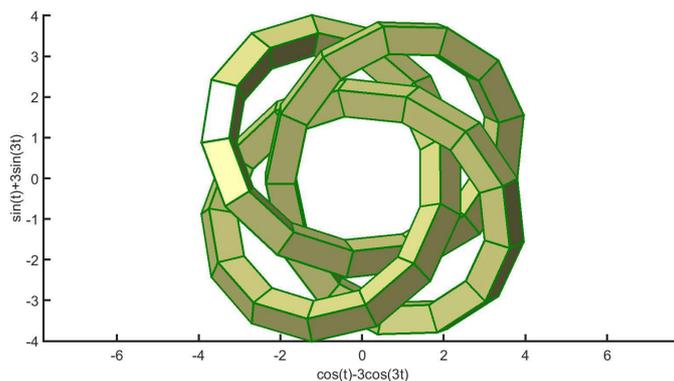


Figure 11. Torus knots; $T(4,3)$.

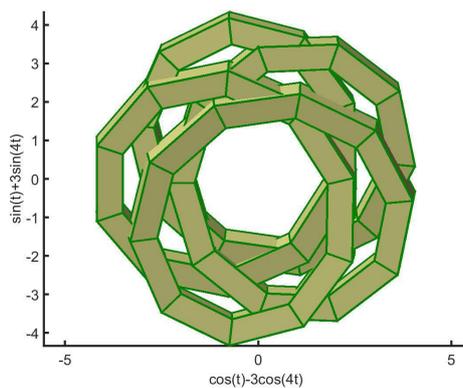


Figure 12. Torus knots; $T(5,4)$.

properties of synthetic molecular knots. The rigorous theories of knot theory in mathematics can help to discover more about synthetic molecular knots. By combining different array of knots in the lab, it can be possible to explore some of the properties such as self-assembling and other synthesized strands properties. Then, biophysicists can understand about knots actions in DNA, proteins or other naturally made molecules. In this paper, we provided a mathematical and topological view of this complicated world. Using parametric modeling, we can study rigorously different synthetic molecular knots. We have represented different knots using parametric equations which help to visualize a variety of syn-

thetic molecular knots. Mathematically, this parametric representation or parameterization can be used to express a geometric object such as a curve or surface. Since parameterizations are non-unique; there is more than one set of parametric equations to specify the same molecular knots. Parametric equations are convenient for describing different synthetic molecular knots and can be considered as manifolds and algebraic varieties of higher dimension. It is always possible to convert a set of parametric equations to a single implicit equation through implicitization which can be done easily by eliminating the variable t from the equations. This study brings more mathematical intuitions in studying the synthetic molecular knots and will help chemists and biophysicists to discover more complicated properties of them.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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