Diamondoids and DNA Nanotechnologies

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Abstract
Diamondoids are cage-like saturated hydrocarbons consisting of fused cyclohexane rings. The Diamondoids family of compounds is one of the best candidates for molecular building blocks (MBBs) in nanotechnology to construct organic nanostructures compared to other MBBs known so far. The challenge is to find a route for self-assembly of these cage hydrocarbons and their applications in the bottom-up synthesis. In this paper, a DNA-based self-assembly technique called "DNA Bridge-based Self-assembly" (DBS) is introduced to self-assemble the diamondoid molecules based upon a bottom-up strategy. The results of our computations and simulations with different molecular mechanical force fields (MM+, AMBER, BIO+, and OPLS) and different optimization algorithms (Polak-Ribiere, Fletcher-Reeves, and block-diagonal Newton-Raphson) furthermore confirm the feasibility of the formation of such hybrid nanoarchitecture.
Keywords: *Diamondoids, DNA Bridge-based Self-assembly (DBS), Self-assembly, Bottom-up synthesis, DNA Nanotechnology*

1. INTRODUCTION

1.1. Diamondoids as nanomodules for nanotechnology

Diamondoids are cage-like saturated hydrocarbons consisting of fused cyclohexane rings. The carbon-carbon framework of Diamondoids constitutes the fundamental repeating unit in the diamond lattice structure. This family of organic compounds follows the general chemical formula of $C_{4n+6}H_{4n+12}$. Adamantane is the first compound of the Diamondoids family with n=1. The other members are Diamantane for n=2, Triamantane for n=3, Tetramantane for n=4 and so on (Figure 1). Diamondoid are divided into two major groups accounting their size: lower Diamondoids which include the first three members of Diamondoids and higher Diamondoids containing Tetramantane and other larger family members [1]. Recently, detection and isolation of higher Diamondoids (up to n=11) from certain petroleum fluids were reported and the chemical structures and isomeric forms of higher Diamondoids were studied in detail [2]. The Diamondoids family of compounds is one of the best candidates for molecular building blocks (MBBs) to construct organic nanostructures compared to other MBBs known so far [3-6]. Diamondoids offer the possibility of producing variety of nanostructural shapes. They have quite high strength, toughness, and stiffness compared to other known MBBs. These are tetrahedrally symmetric stiff hydrocarbons that provide an excellent building block for positional (or robotic) assembly as well as for self-assembly. In fact, over 20,000 variants of Diamondoids have been identified and synthesized and even more are possible [3-5], providing a rich and well-studied

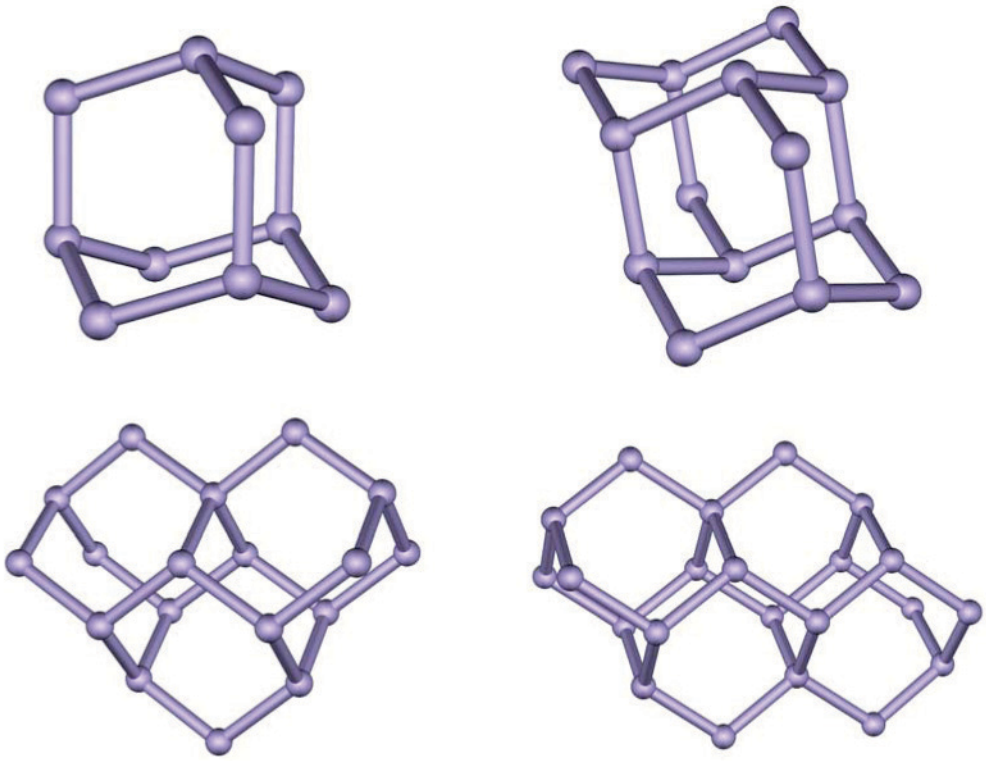


Figure 1: Chemical structures of Diamondoids: the chemical structures of Adamantane (left) and Diamantane (right) are shown in the upper part of the picture. Structures of Triamantane (left) and the Anti- isomer of Tetramantane (right) are represented in the bottom.

set of MBBs. Diamondoids are recently named as the building blocks for nanotechnology [2]. Diamondoids have been envisioned to act as the key components in the future Mechanosynthesis design of nanorobots [6] and an artificial red blood cell [7].

The simplest of these polycyclic Diamondoids is Adamantane, followed by its homologues Diamantane, Tria-, Tetra-, Penta- and Hexamantane. The lower adamantologues (i.e. the lower Diamondoids or polymantanes), each has only one isomer. Depending on the spatial arrangement of the adamantane units, higher polymantanes ($n \geq 4$) can have numerous isomers and non-isomeric equivalents. . There are three possible Tetramantane all of which are isomeric. There are seven possible Pentamantanes, six being isomeric ($C_{26}H_{32}$) obeying the molecular formula of the homologous series and one non-isomeric ($C_{25}H_{30}$). For Hexamantane, there are 24 possible structures: among them, 17 are regular cata-condensed isomers with the chemical formula ($C_{30}H_{36}$), six are irregular cata-condensed isomers with the chemical formula ($C_{29}H_{34}$), and one is peri-condensed with the chemical formula ($C_{26}H_{30}$).

When in solid state, Diamondoids melt at much higher temperatures than other hydrocarbon molecules with the same number of carbon atoms in their structure. Since they also possess low strain energy, they are more stable and stiff that resemble diamond in a broad sense. They contain dense, three dimensional networks of covalent bonds, formed chiefly from first and second row atoms with a valence of three or more. Many of the Diamondoids possess structures rich in tetrahedrally coordinated carbon. They are materials with superior strength to weight ratio, as much as 100 to 250 times as strong as titanium, but much lighter in weight. In addition to applications in nanotechnology they are being considered to build stronger, but lighter, rocket and other space components and a variety of other earth-bound articles for which the combination of weight

and strength is a consideration [8, 9]. Due to their unique molecular structures, Diamondoids exhibit a number of superior capabilities promising for nanotechnological implications. Such capabilities are reflected in some of their unique physicochemical properties such as high rigidity, stability, high density, high melting point and low surface energy [1]. Diamondoids show unique properties due to their exceptional atomic arrangements. These compounds are chemically and thermally stable and strain-free. These characteristics make them to have a high melting point in comparison with other hydrocarbons. For instance, the m.p. of adamantane is estimated to be in the range of 266-268 °C and of Diamantane in the range of 241-243 °C.

Adamantane is considered to be an MBB possessing six linking groups, which is an ideal number for molecular building blocks. It has been found that adamantane crystallizes in a face-centered cubic lattice, which is extremely unusual for an organic compound. The molecule, therefore, should be completely free from both angle and torsional strain, making it an excellent candidate for various nanotechnology applications. Adamantane is one of the highest melting hydrocarbons known (m.p. ~ 266-268 °C), yet it sublimes easily, even at atmospheric pressure and room temperature. Because of this, it can have interesting applications in nanotechnology like possibilities for application in molding and cavity formation. Adamantane can be used in molecular studies and preparation of fluorescent molecular probes [10, 11]. Because of its incomparable geometric structure, the adamantane core can impede interactions of fluorophore groups and self-quenching would diminish due to steric hindrance. Hence, mutual quenching would diminish and it becomes possible to introduce several fluorescent groups to the same molecular probe in order to amplify the signals. Such a molecular probe can be very useful in DNA probing and especially in fluorescent-in-situ hybridization (FISH) diagnostics [10].

Adamantane and other light Diamondoids are constituents of petroleum and they deposit in natural gas and petroleum crude oil pipelines causing fouling [8, 12, 13]. Adamantane was originally discovered and isolated from Czechoslovakian petroleum in 1933. The isolated substance was named adamantane, from the Greek for diamond. This name was chosen because it has the same structure as the diamond lattice, highly symmetrical and strain free. The unique structure of adamantane is reflected in its highly unusual physical and chemical properties, which can have many applications in nanotechnology, as do the diamond nano-sized crystals, with a number of differences. The carbon skeletons of Diamondoids comprise a cage structure, which may be used for encapsulation of other compounds. In a broader sense, they may be described as saturated, polycyclic, cage-like hydrocarbons.

1.2. Towards nanostructures; some methods and concepts

Nanofabrication of nanostructures demands appropriate methods and molecular building blocks (MBBs).Vast number of materials have been suggested for this purpose like biomolecular and organic MBBs. MBBs properties will not be discussed here but it is mentioned that the organic MBBs are of more interest in the nanodevice fabrication and bioapplications due to their flexible chemistry and also biomolecules (for instance DNA double helices) for their biocompatibility. Diamondoids, fullerene, graphite and carbon nanotubes are some examples of organic MBBs [14, 15]. As with regard to nanoarchitecture formation two distinct approaches have been proposed [4, 5]: 1- Positional or robotic assembly. 2- Self-assembly.

Positional assembly utilizes a robotic arm (like an AFM tip) to control the steric positions of building blocks. The major difficulty in the positional assembly is overcoming the thermal noises which can cause positional uncertainty. This problem can be solved to some extant by using stiff and rigid MBBs and also lowering the temperature. Some assemblers with robotic arms should be developed in order to gain control over three dimensional and steric orientations. Eric Drexler suggested that a universal assembler must be designed which would be able to build almost any desired nanostructure [16]. However, it seems impossible at first glance unless the simple assemblers are firstly built and these simple assemblers build more complicated

assemblers and so on to the point that we can have the universal assembler. Positional assembly can be used to construct larger MBBs which subsequently self-assemble to the final desired nanostructures. Positional assembly consists of two strategies [5]: Additive synthesis in which MBBs are arranged to construct the desired nanostructure and subtractive synthesis in which small blocks are removed from a large building block or a primitive structure to form an eventual structure (like sculpture). Positional assembly approach has not been advanced because of so many limitations in designing suitable MBBs, robotic arms and technical problems. Instead, more attempts have been focused on the self-assembly.

Self-assembly is a process in which components spontaneously form ordered aggregates. Examples of such a phenomenon can be found from the molecular to the macroscopic levels [17]. The protein folding (second, third or forth structures), DNA double helix, formation of lipid bilayers, colloids [18, 19] and crystals are some instances in which self- assembly is the dominant phenomenon. Self-assembly is largely influenced by the environment. The molecular aggregate which is formed by the self-assembly process, is an ordered array which is thermodynamically the most stable conformation for a macromolecule or number of macromolecules. Self-assembly occurs in liquid medium or near the interface to make it possible dynamic exchanges toward reaching the minimal energy level. Forces involved in the structures formation are mainly weak non-covalent ones (hydrogen bond, electrostatic, Van der Waals, hydrophobic,…) but the number of interactions for formation of each region of molecular conformation are so high that can assure consistence and stability of the macromolecule and whole complex [4, 17] (like hydrogen bonds in the second helical or beta-sheet structures of proteins). The main goal is directed self-assembly, and to design the desired nanostructures, fashions of interactions between MBBs should clearly be understood. Fundamental principles can be founded for the prediction of a nanostructure's steric arrangement according to its MMB composition by inspiration from relationships between the first structure of proteins and the later ones in a biomimetic way. Undoubtedly, to achieve such a degree of knowledge, generating information about the intermolecular interactions and molecular simulations (for determination of interaction patterns between molecules) are of critical importance [20, 21].

Some important self-assembly methods involve DNA directed (self-)assembly on the solid surfaces, self-assembly at the silicon surfaces, strain-directed assembly, lithographically induced self- assembly (LISA) [22], and dynamic combinatorial libraries.

As it was mentioned, construction of a nanostructure according to the bottom-up nanotechnology strategy not only entails appropriate MBBs but also an efficient assembly method [23]. Despite the advantages of Diamondoids for playing an important role in nanotechnology as MBBs, lack of a suitable procedure for their nano-assembly hinders them from formation of nanostructures in the practical nanotechnology. Setting aside the positional assembly of Diamondoids as a practical plan at the moment, one could also seek a consequential self-assembly procedure. Although a number of self-assembly processes have been identified, few are suitable to meet the qualifications required for the bottom-up nano-assembly of structures. Invention of an approach which is a perfect image of an abstract and programmable self-organization to construct large nanostructures still remains a demanding task [24].

1.3. DNA as a self-assembly tool: DNA nanotechnology

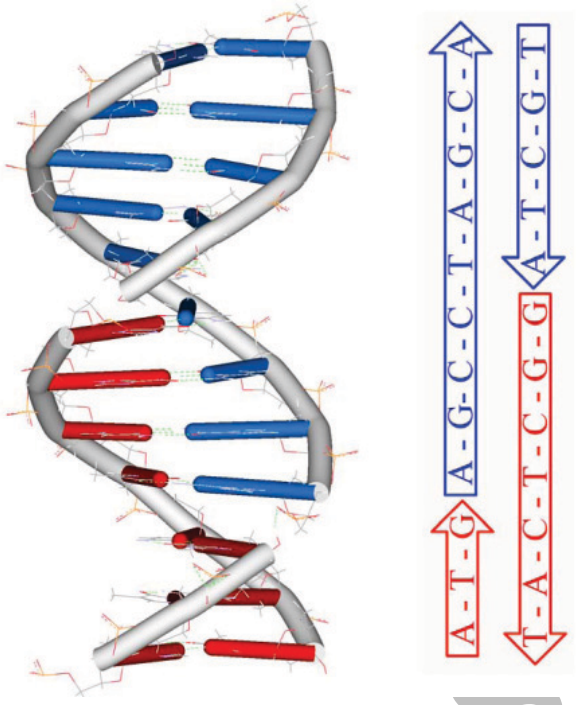
In the early 1980s, Seeman started to publish a series of reports on the construction of immobile nucleic acid junctions in an effort to develop structural DNA nanotechnology [25]. Later several branched DNA motifs were introduced, such as double crossover (DX) [26, 27], triple crossover (TX) [28], paranemic crossover (PX) [29, 30], DNA parallelogram [31], and DX triangle [32-34]. The inspiration to build these DNA motifs stemmed from the Holliday junctions, a mobile junction between four strands of DNA [25, 35-37]. On the other hand, application of sticky ended DNA double strands (Scheme 1) to the nanoassembly process made it possible to construct purely DNA-made nanostructures. Those include the cube-shaped [38-40] and also octahedron-like [39, 41] nanostructures, six helix bundles [42], and

DNA-made nanomechanical devices [43, 44].
Of critical importance is the role of DNA in compositional DNA nanotechnology to assemble different nanomodules [45-47]. The hybridization specificity of two complementary strands and the fidelity of base pairing would assure a full control over assembly process in the DNA-directed assembly (DDA) approach. DNA oligomers can be used for site-selective immobilization of macromolecules to direct self-assembly process on a solid surface via DNA directed immobilization (DDI) [48]. To achieve DDI, at first, the desired site of the molecule is tagged by a DNA strand. Then the complementary DNA strand is fixed on a solid surface. Thus, completely specific DNA hybridization is exploited to immobilize macromolecules with controlled steric orientation. This method has been successfully performed to immobilize gold nanoparticles [48, 49]. The multimeric nucleic acids and nucleic acid-protein conjugates are two instances proving the applicability of DNA to the assembling of nanostructures. They are promising tools to fabricate nanostructured devices, DNA biochips, polymeric aggregates, microcircuts and many other diagnostic kits [46, 50, 51].
Utilization of DNA in the Diamondoid-DNA-made nanoarchitecture takes advantage of the DNA properties based upon which DNA nanotechnology has been underpinned. The bottom-up synthesis of nanostructures entails utilization of those approaches that would make the final three dimensional structures of products predictable. The specificity and fidelity of Watson-Crick base pairing are powerful tools to devise unique DNA sequences. The predictable interactions of these DNA sequences are required when following a predetermined design that would result in a desired three dimensional (3-D) molecular geometry. This is especially the case when one is working with sticky ends which make the double helices accommodate the familiar B-form DNA folding [52-55]. The DNA's persistence length is about 500 Å along which the molecule behaves as an almost rigid rod [52, 53, 55]. Besides structure predictability, the rich nucleic acid chemistry is a motivating factor to propose DNA-incorporated diamondoid-based nanostructures. The given chemistry dates back to the early 1950s, almost at the same time as the magic zip-like and ribbon-shaped model recognized to be in harmony with the prerequisites of cells' genetic contents by Watson and Crick [56]. The automated phosphoramidite chemistry gives us the ability to readily synthesize a wide variety of DNA sequences [56]. Advances in the synthesis of nucleotide analogues [57, 58] open the new avenues toward new derivatives with interesting therapeutic, diagnostic and polymeric properties [59-62]. The use of predictable non-Watson-Crick base pairing patterns seems to be a less explored, and still interesting, possibility in building DNA-based nanostructures [63]. In addition, the DNA-modifying enzymes are also helpful to accompany the chemical modification approaches in the structural DNA nanotechnology [55].
In what follows, the idea of the application of DBS in constructing the Diamondoid-DNA-based nanoarchitecture will be discussed. The efficiencies of different molecular mechanical techniques in computational chemistry are compared to investigate the formation of a cube-shaped nanostructure. The results of computations indicate that the large number of hydrogen bonding between the complementary DNA sequences is very likely to stabilize the 3-D geometry of the nanostructure.

2. COMPUTATIONAL PROCEDURES

2.1. Modeling the nanomodule

The chemical structure of the MBB shown in the figure 2 was built in the Hyperchem software release 7.0. The geometry of the adamantane-derived core was initially optimized using the MM+ force field of molecular mechanics in Hyperchem. The deoxyribonucleic acid residues (nucleotides) were chosen to be in the B-form secondary conformation (right-hand helices) as that is the most prevalent form of DNA under physiological conditions [64]. The pucker of the furanose ring was selected to be 2′ endo consistent with the B-form conformation.
After building the initial models, they were all optimized with the different force fields of molecular mechanics furnished in Hyperchem. Those force fields are MM+ [65], AMBER (Assisted Model Building and Energy Refinement) [66-68], OPLS (Optimized Potentials for Liquid Simulations)



Scheme 1: DNA Sticky ends: Two double helical DNA molecules capable of forming sticky ends are shown in red and blue. Hydrogen bonds between bases are highlighted by the green broken lines. The phosphate-sugar backbones are depicted as arrows oriented from the 5′ to the 3′ terminus.

[69, 70], and BIO+ which is an implementation of the CHARMM (Chemistry at HARvard Macromolecular Mechanics) force field [71, 72] in Hyperchem.

The Polak-Ribiere optimization algorithm was used among the conjugate gradient methods. The optimization was continued until the root mean square (RMS) gradient reached the specified value of 0.1 kCal.mol^{-1}.Å^{-1}. The whole computations were run In Vacuo without adding solvent molecules to the system explicitly. However, the solvent effects are accounted to some extent by setting the effective dielectric constants. Different energies including bond, angel, dihedral, bending, and electrostatic were recorded for comparison and data analysis.

2.2. Simulation of the nanostructure

The hybridization of DNA single stranded linkers of each set of two MBBs with their complementary single stranded bridge was investigated using the Autodock Tools 3.0 software working under the Linux operating system. Two linker sequences of the neighboring MBBs were introduced to Autodock Tools as a macromolecule and the bridge sequence was designated to be the ligand. The software calculated the docking parameters and yielded the docked double helix structures. Each double helix corresponds to one of the cube's edges. The twelve edges of the cube were thus simulated separately and then attached together in the Hyperchem software according to the blueprint (in scheme 3). The nanostructure assembled manually in Hyperchem was finally optimized using the MM+ force field of Hyperchem until the RMS gradient of 0.5 kCal.mol^{-1}.Å^{-1} was achieved. Three different optimization algorithms were used to minimize the nanostructure energies including Polak-Ribiere, Fletcher-Reeves, and block-diagonal Newton-Raphson algorithms. The results of energy minimization by the aforementioned optimizers were recorded for further comparison and studied for monitoring hydrogen bonds.

3. RESULTS AND DISCUSSION

3.1. A case study: the DNA Bridge-based self-assembly (DBS) concept

The main idea in DBS is to incorporate DNA strands into a diamondoid molecule to act as linkers [73].

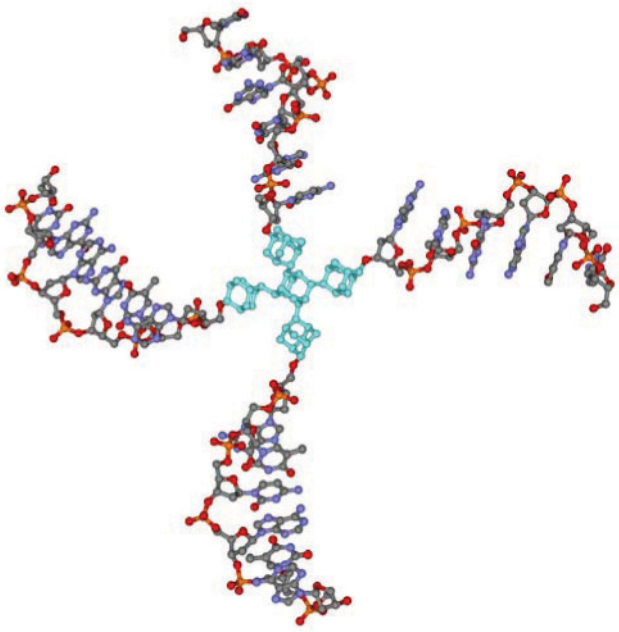
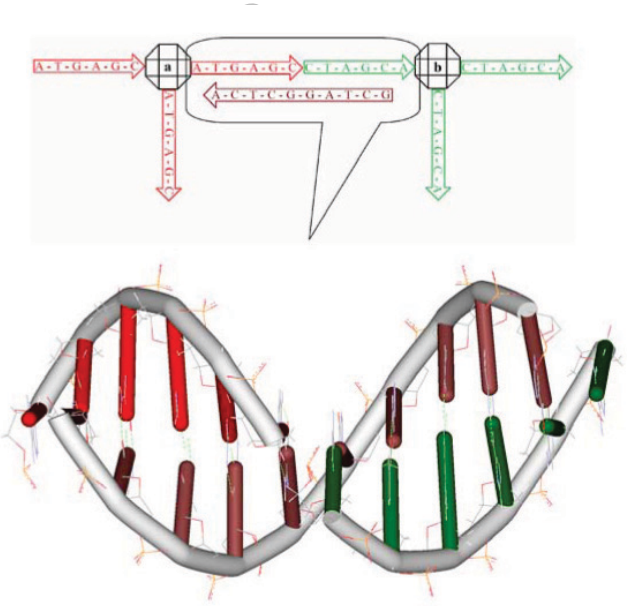


Figure 2: The chemical structure of a nanomodule made of a Diamondoid-derived core and four DNA linkers.



Scheme 2: The concept of DBS: A DNA bridge (brown) attaches two linkers from nanomodules (a) and (b).

Application of sticky-ended DNA segments to the assembly of Diamondoids seems to be impractical. DNA is a macromolecule about 20 A° in width [52, 55] while Diamondoids are single and small organic molecules. Diamondoids are much smaller than a core bearing several sticky-ended DNA double strands as linking groups. Consequently, introduction of DNA double strands to the diamondoid cores sounds implausible due to the steric hindrance and size limitations. Nonetheless, DNA single strands might be capable of inclusion in the Diamondoid nucleuses. DNA-directed immobilization and assembly of nanostructures is a well-established practice proved many times to be effective in different circumstances (such as assembly of gold nanoparticles and peptides). However, those self-assemblies essentially demand solid surface immobilization techniques to control the assembling process [23, 47-50].

In this paper, we propose DBS as a bottom-up approach to self-aggregate a predetermined supramolecular structure already devised as a blueprint. Hence, it may become possible to control the nano self-assembly procedure in the liquid medium. The stereoselective nature of MBBs, their sequential addition, and utilization of DNA bridges assure the placement of MBBs near one another in a proper and specified fashion. An MBB required for DBS consists of a Diamondoids-derived nucleus and three or four DNA sequences as linkers (See figure 2).

As a case study, assume that one is going to construct a cube-shaped nanostructure using DBS. The first step would be to draw a blueprint assigning the exact positions of MBBs with respect to each other. Here, the term "blueprint" refers to a molecular design depicting the structural details of a nanostructure at the theoretical level.

Eight MBBs, each endowed with three DNA single strands as linkers (scheme 2), are necessary to form a nanostructure with the connectivity of a cube. The Diamondoids-derived nucleus of each MBB is placed in one of the cube's corners and the DNA strands correspond to the edges connecting the corners.

A bridging DNA sequence should be designed in such a way that its first half is complementary to one of the linkers of the MBB "a" and its second half is complementary to one of the linkers of the neighbor MBB, let us say the MBB "b", as represented in scheme 2. The DNA bridge is comprised of 10 nucleotides to bridge the two linkers and attach them together by formation of DNA double strands. Each linker consists of six nucleotides and thus the two successive linkers ranged in row create a gap of 12 nucleotides between two neighboring nucleuses. Only five out of six nucleotides of each linker would participate in DNA hybridization / double strand formation with the DNA bridge. The first nucleotide of each linker is supposed to play the role of a spacer separating the double helix structure and nucleus in order to avoid steric congestions (Scheme 2).

To complete the blueprint the next assignment would be to select the appropriate linkers for each MBB. Some considerations are to be made regarding the selection rules. Firstly, the linkers should not be complementary on their own. Secondly, the linkers are supposed to be adopted in such a way that only one interacting sequence exists for attachment to the nearby MBB. In other words, the bridging sequences used to attach an MBB to its neighbors should not be identical. Otherwise, it is not possible to manage the three dimensional extension of the nanostructure.

The blueprint showing the detailed description of our cube-like nanostructure is reflected in scheme 3.

In order to materialize a devised blueprint a two-step cycle is to be followed repeatedly:

1) Addition of the neighboring MBBs to the solution (For example, addition of «b» to «a»).

2) Addition of the related DNA bridge to the mixture of two MBBs (for instance, addition of ba21 bridging sequence to the solution containing the MBBs «a» and «b»).

The aforementioned cycle should be repeated for the introduction of a new MBB to the nanostructure. Therefore, by repeating the cycle MBBs would be positioned at their place one by one based upon a sequence of stepwise self-assembly procedures.

3.2. Simulation of the diamondoid-DNA-made nanomodule

The potential energy surfaces (PESs) calculated for the MBB by different force fields were then compared at the RMS gradient of 0.1 kCal.

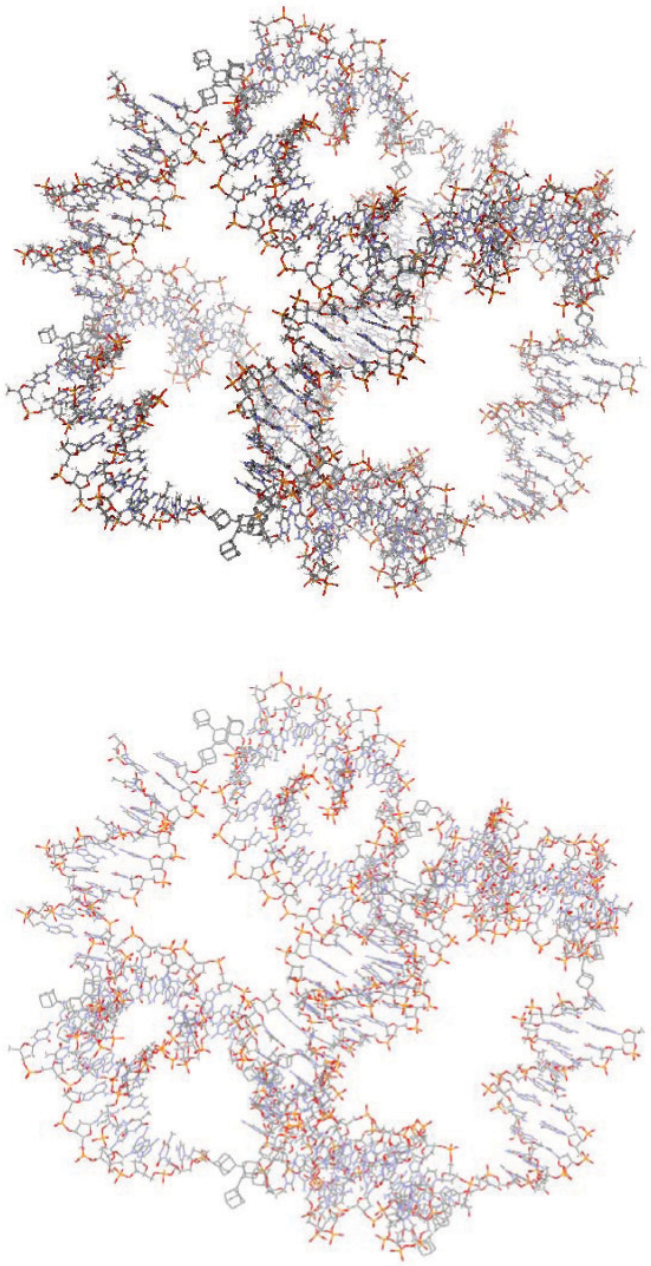


Figure 3: A simulated cube-shaped nanostructure assembled by connection of eight nanomodules (depicted in the figure 2) using DBS with (in the top) and without (in the bottom) the "Depth Cue" rendering technique. Both pictures have a perspective angle of 15 º but in the top one, the parts of the supramolecule which are much further (in the depth of the plane) faded.

Table 1: Computed energies (kCal.mol-1) for the MBB shown in the figure 2: A comparison among different force fields of molecular mechanics.

	MBB						
	Bond	Angel	Dihedral	van der Waals	Electrostatic	Stretch-bend	PES
OPLS	8.10	111.58	236.15	-269.70	-202.41	—	-116.28
AMBER	14.43	118.41	307.94	-227.65	-104.43	—	108.70
BIO+	119.67	449.14	821.16	277.19	-151.55	—	1515.61
MM+	69.89	749.28	437.48	72.98	-250.94	-112.94	965.75

Table 2: Docking energies: Different energies (kCal.mol-1) calculated for docking two DNA linkers and their related DNA bridge by the Autodock Tools software. Two numbers in each cell of the first column specify the names of two linkers (for instance, 1+4 means attachment of linker 1 to the linker 4 via their corresponding DNA bridge).

Names of the two linkers	(1) Final Intermolecular Energy	(2) Torsional Free Energy	Estimated Free Energy of Binding = (1) + (2)
1+1	-9.97	16.81	6.84
1+2	-12.72	16.81	4.09
1+3	-11.77	16.50	4.72
1+4	-11.42	16.50	5.08
2+1	-8.85	16.81	7.96
2+2	-12.58	16.50	3.92
2+3	-11.09	16.19	5.09
2+4	-10.61	16.50	5.89
3+1	-8.67	16.50	7.83
3+2	-12.26	16.19	3.93
3+3	-10.92	15.88	4.95
3+4	-10.55	16.19	5.63
4+1	-11.15	16.50	5.35
4+2	-14.08	16.50	2.42
4+3	-13.02	16.19	3.17
4+4	-12.88	16.19	3.31

Table 3: Comparison of different energy optimization algorithms: Results of energy (kCal.mol-1) minimization obtained from different optimizers for the cube-like nanostructure using the MM+ force field of Hyperchem.

	Results using the MM+ force field						
	Bond	Angel	Dihedral	van der Waals	Electrostatic	Stretch-bend	PES
Polak-Ribiere	753.68	8428.52	4422.77	41.42	-2937.28	-1244.27	9464.82
Fletcher-Reeves	758.14	8412.93	4376.58	15.81	-2981.75	-1256.66	9325.06
Block-Diagonal Newton-Raphson	964.17	8573.64	4487.43	266.76	-2936.66	-1491.05	9864.28

$mol^{-1}.Å^{-1}$. The OPLS force field gives the minimal energy when comparing with the other force fields and for the same molecule (Table 1).

3.3. The diamondoid-DNA-made nanostructure

The docking energies calculated confirms the anticipation that those complementary sequences match together according to the proper pattern of Watson-Crick base pairing (Table 2). From the minimization point of view, the conjugate gradient optimizers (Polak-Ribiere and Fletcher-Reeves) calculated improved energies for the nanostructure in comparison with the block-diagonal Newton-Raphson algorithm (Table 3). The hydrogen bonding patterns and fidelity of base pairing are still persistent after geometry optimization by MM+ (Figure 3). Each face of the cube has approximate dimensions of 40 X 50 Å.

4. CONCLUSION

Application of DBS to the organization of custom-made MBBs would pave the way to establish a new type of hybrid nanoarchitecture. The bases for the fabrication of the discussed nanoarchitecture would be laid using the state-of-the-art combination of diamondoid-derived nucleuses with the DNA nanotechnology. The ease with which the MBBs could be self-assembled through programmable and algorithmic DBS has many advantages. The results of our computations demonstrate that the predictability, periodicity, and bottom-up synthesis are unique merits of the aforementioned emerging nanoarchitecture.

In view of the fact that Diamondoids are rigid molecules and the DNA's persistence length is about 500 Å, utilization of DNA double strands about 40 to 70 Å in length (less than two turns) is very likely to lead to the rigid nanostructures with well-founded and predictable geometries. The proposed hybrid diamondoid-DNA nanoarchitecture could have a wide variety of applications. They range from self-assembly of nanoelectronic components to acting as the 3-D scaffolds for crystallography of biomolecules, as molecular cages for drug delivery purposes, and also as elements in molecular manufacturing of nanorobotic machinery parts, just to name a few.

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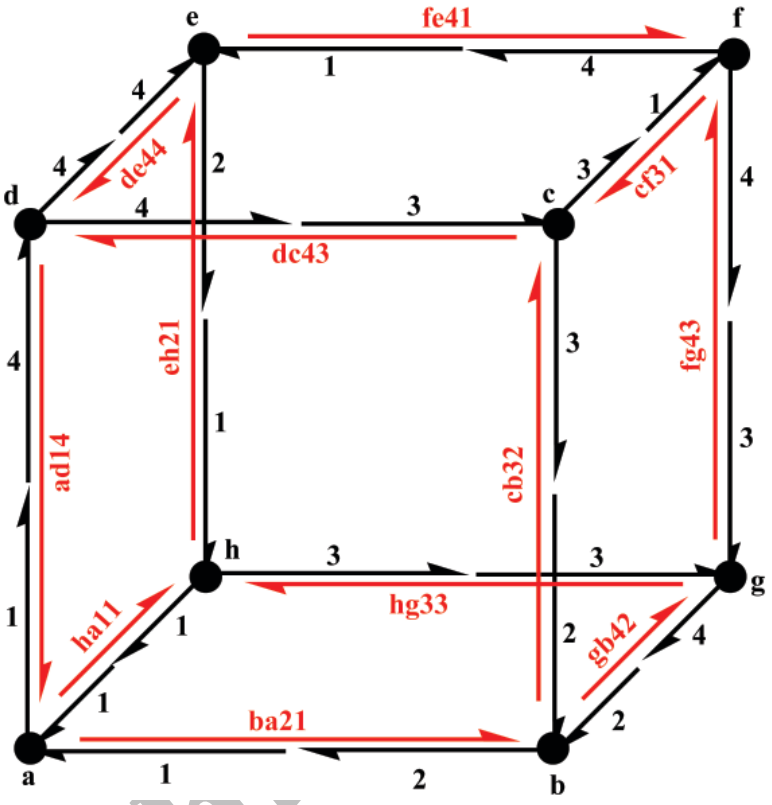

Scheme 3: An example of a molecular blueprint used for designing a nanostructure based on a bottom-up strategy. The apexes of arrowheads show the 3′ termini of the DNA sequences. The solid spheres at the corners correspond to the positions of the Diamondoid-made nucleuses. The white arrowheads are representatives of the linkers. The bridging sequences (drawn in red) are specified by two letters and two numbers (for instance ba21): the letters stand for the MBBs that a bridging sequence attaches together when they are read from the 5> to the 3> terminus and the left number is the name of linker attached to the nucleus from its 5′ terminus and the right number is suggestive of the second linker attached to its nucleus through its 3′ terminus.

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