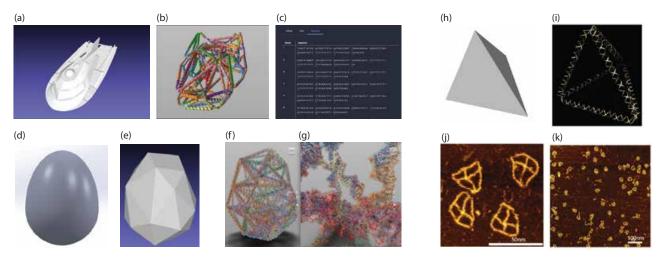
## Computational design of 3D wire-frame nano-structures with DNA oligos

Byoungkwon An\*1, Daniel Fu<sup>1</sup>, Dongran Han<sup>3,4</sup>, Gaetan Bellot<sup>5</sup>, Bryan Wei<sup>6</sup>, John Reif<sup>1</sup>, Peng Yin<sup>3,4</sup>, Yonggang Ke<sup>2</sup>

- 1. Department of Computer Science, Duke University, Durham, NC 27708, USA.
- 2. Wallace H. Coulter Department of Biomedical Engineering, Georgia Institute of Technology and Emory University, Atlanta, GA 30322, USA.
- 3. Department of Systems Biology, Harvard Medical School, Boston, MA 02115, USA.
- 4. Wyss Institute for Biologically Inspired Engineering at Harvard, Boston, MA 02115, USA.
- 5. Institut de Génomique Fonctionnelle, CNRS UMR 5203, INSERM U1191, F-34000 Montpellier, France.
- 6. School of Life Sciences, Tsinghua University, Beijing, 100084, China.
- \*. dran@cs.duke.edu, www.drancom.com

We introduce an automated design method for DNA oligo-based frame-structures (Fig. 1). The input is an arbitrary 3D graph (also known as a wire-frame) with 3D coordinates for each vertex and edges between pairs of vertices. The edges may be either be specified straight or with a given curvature. Such 3D graph models have been used for computer graphics and mechanical design work and can represent complex frame-structures with many studied theorems and software tools. Given input, the design algorithm first determines the routing of the frame-structure. Then, it determines branches and helical structures. The edges may be designed as helical bundles with specified curvature. Next, the bases' locations, complementary pairs and strands geometry is determined. After assigning ATCG code, the algorithm outputs DNA sequences of the oligos. OxDNA [1] may be used to determine an approximation to the resulting 3D structure, and further design iterations may be made. We have implemented the design algorithm as a web-based design software. Fig. 1 (h)-(k) and Fig. 2 include experimental results, including AFM and Cryo-EM images.



**Fig. 1: Three DNA frame-structures**<sup>1</sup>. (a)-(c) Fantastic Voyage Submarine frame-structure. (a) Input model, (b) Molecular model of the DNA frame-structure. (c) DNA sequences; (d)-(g) Egg frame-structure. (d) Input model (e) Frame Model (f) Molecular model of the DNA frame-structure. (g) Zoomed model of joint; (h)-(k) Asymmetry simple (four-face) frame-structure. (h) Input model. (i) Rribbon view. (j),(k) AFM images.

\_

<sup>&</sup>lt;sup>1</sup> Visualization tools [2, 3, 4] are used.

To control the stiffness, we add or remove various edges. The DNA frame models shown in Fig. 1 (b), (f), (g) and Fig. 2 (a),(b) contains inner edges, which are added automatically by existing tessellation algorithms, such as Netgen [5]. An extreme case can be that the structure is completely filled by additional inner edges possibly resulting in a lack of room for any helix to move, so the structure becomes too rigid. If the algorithm removes too many edges, the stiffness may be reduced, but in an extreme case of removing too many edges may result in a structure that is not structurally stable. Hence a trade-off is made between structural stability and flexibility.

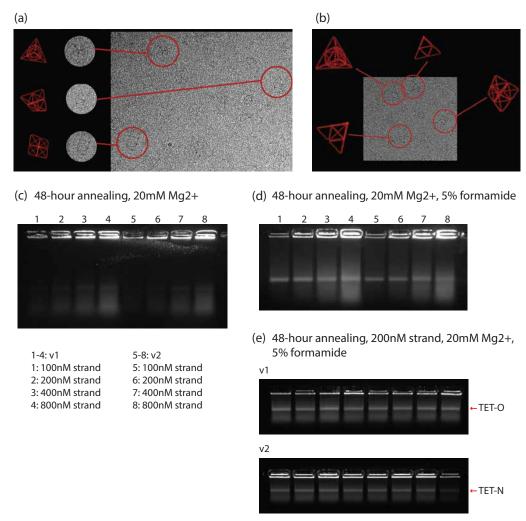


Fig 2. Cryo-EM image. (a)-(b) and GEL experiments. (c)-(e) of tetrahedron having interior edges.

- [1] T. E. Ouldridge, et al., Structural, mechanical, and thermodynamic properties of a coarse-grained DNA model, The Journal of Chemical Physics, 134, 8, 2011.
- [2] P. Cignoni et al., *MeshLab: an Open-Source Mesh Processing Tool*, Sixth Eurographics Italian Chapter Conference, pages 129-136, 2008.
- [3] M. Wang et al., Autodesk Molecule Viewer, https://moleculeviewer.lifesciences.autodesk.com, 2017.
- [4] E.F. Pettersen et al., *UCSF Chimera--a visualization system for exploratory research and analysis.*, Journal of Computational Chemistry, 25(13):1605-12. 2004.
- [5] J. Schöberl, *NETGEN An advancing front 2D/3D-mesh generator based on abstract rules*, Computing and Visualization in Science, 1(1), pages 41-52, 1997.