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Holliday Triangle Hunter (HolT Hunter): Efficient Software for Identifying Low Strain DNA Triangular Configurations

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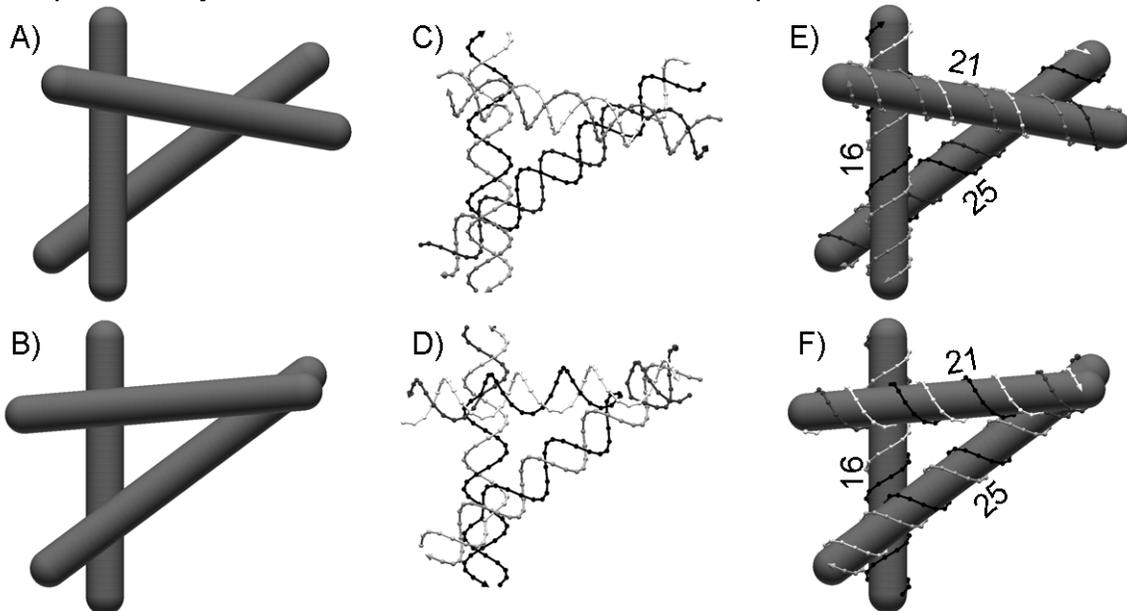
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Synthetic DNA nanostructures are typically held together primarily by Holliday junctions. One of the most basic types of structures possible to assemble with only DNA and Holliday junctions is the triangle.^{1, 2} To date, however, only equilateral triangles have been assembled in this manner – primarily because it is difficult to figure out what configurations of Holliday triangles have low strain. Early attempts at identifying such configurations relied upon calculations that followed the strained helical paths of DNA. Those methods, however, were computationally expensive, and failed to find many of the possible solutions. I have developed a new approach to identifying Holliday triangles that is computationally faster, and finds well over 95% of the possible solutions.



A and B show two different ways three rods can cross one another to form a triangle. C and D show DNA double helical backbones that are aligned with the rods in A and B respectively. The double helices are placed in such a manner that one helix or the other in each duplex is at the appropriate spot to form a crossover at the locations dictated by the rod geometry. E and F show the composite structures. The number of base pairs between each crossover is shown. In this case, E and F actually have the same 3 edge lengths. Drawn using GIDEON.²

The new approach is based on splitting the problem into two parts. The first part involves figuring out all the different ways that three featureless rods of the appropriate length and diameter can weave over and under one another to form

a triangle. The second part of the computation entails seeing whether double helical DNA backbones can fit into the shape dictated by the rods in such a manner that the strands can cross over from one domain to the other at the appropriate spots. Structures with low strain (that is, good fit between the rods and the helices) on all three edges are recorded as promising for assembly.

I have produced a Mathematica notebook called Holliday Triangle Hunter (HoIT Hunter) that searches for triangles with edge lengths specified by the user. Because such a high percentage of low-strain configurations are successfully identified, almost a million different low-strain triangles were identified in a search of edge lengths of 5 to 64 base pairs (approximately 1% of the structures considered were low-strain). This provides DNA architects with a very large library of low-strain configurations to help select specific crossing angles between DNA double helices connected via Holliday junctions. Such structures can be assembled into regular arrays, combined with each other or with other DNA motifs to form complex compound structures, or can even serve as angle-imposing staples for DNA origami.

HoIT Hunter generates coordinates for drawing models of the triangles and viewing them from convenient angles. A more user-friendly spreadsheet, HoIT Multiplier, has been created, with specific help for drawing the models using GIDEON drawing software.² HoIT Multiplier also helps draw multiple triangles in 1-, 2-, or 3-dimensional arrays and to draw triangles with two or more connected duplex domains on each side.^{2, 3}

The techniques applied here to Holliday triangles can be extended in a straightforward manner to other, more intricate shapes of DNA connected by Holliday junctions (or some other junctions). Future work will attempt to identify other low strain structures, as well as to construct examples of the structures identified.

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References:

1. Liu, D.; Wang, M.; Deng, Z.; Walulu, R.; Mao, C., Tensegrity: Construction of Rigid DNA Triangles with Flexible Four-Arm DNA Junctions. *Journal of the American Chemical Society* **2004**, 126, (8), 2324-2325.
2. Birac, J. J.; Sherman, W. B.; Kopatsch, J.; Constantinou, P. E.; Seeman, N. C., Architecture with GIDEON, a program for design in structural DNA nanotechnology. *Journal of Molecular Graphics & Modelling* **2006**, 25, (4), 470-480.
3. Constantinou, P. E.; Wang, T.; Kopatsch, J.; Israel, L. B.; Zhang, X.; Ding, B.; Sherman, W. B.; Wang, X.; Zheng, J.; Sha, R.; Seeman, N. C., Double cohesion in structural DNA nanotechnology. *Organic & Biomolecular Chemistry* **2006**, 4, (18), 3414-3419.