How to build with DNA

Biophysicists at the University of Oxford are using DNA to build complex, self-assembling structures - and many of them may have exciting applications.

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Since Watson and Crick discovered DNA in 1953, most of us have become well aware of its role as a fundamental building block of life. But for Prof. Andrew Turberfield in the University of Oxford's Department of Physics, DNA can be used to build in rather different ways.

The secret lies in DNA's structure. Its four bases, adenine, cytosine, guanine and thymine, bind more or less strongly to one another depending on how they are paired up along the length of a DNA double helix. By creating strands of DNA with carefully controlled base sequences, that binding can be specifically tailored - and different, customized strands can be combined to bind with each other to construct exotic structures.

Initially, each geometric structure is modelled computationally, in order to create appropriate designs for each of the DNA strands. Once a solution has been identified for a particular structure, the appropriate DNA is synthesised. When combined in solution, the DNA can form structures without intervention: the interactions between strands are controlled by their base sequences, and sequence design is sufficient to program self-assembly.

A particularly elegant example is the DNA tetrahedron. Samples of four different DNA strands are combined in equal quantities at 96ºC and, as they are gently cooled to room temperature, the strands bind together to form tetrahedra with 7 nanometre edges. They look impressive when imaged using electron microscopy, but they are

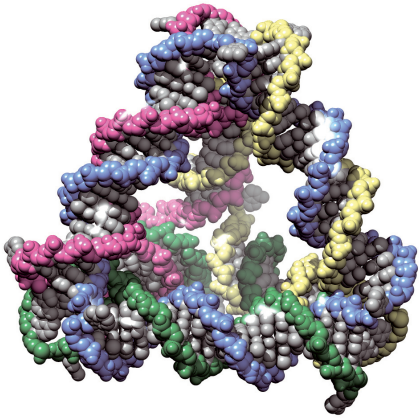

Image: A. Tuberfield

also useful: they may be used to provide targeted drug delivery, as the nature of the tetrahedron allows proteins to be locked inside the structure, to be deployed to an area where treatment is required.

A similar strategy of DNA encoding has made it possible to build large, two-dimensional lattices out of DNA, onto which proteins can be pinned. The result is a two-dimensional sheet of regularly spaced proteins that can be used to analyse protein structure more easily than conventional methods allow. In fact, this technique has drawn such commercial interest that a patent has been taken out on the technology, and is currently being developed by ISIS Innovation.

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