Self-assembly pathways for DNA origami

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Abstract:

DNA origami is a robust method to create DNA nanostructures to nearly any size and shape. Although widely applied, quantitative understanding of the self-assembly process remains elusive. The yield of well-formed structures is sensitive to crossover placement and especially layered structures may require secondary adjustments to optimize yield. Frequent prototyping could be avoided altogether if the assembly process and kinetics were fully understood. To this end, we introduce an unique origami tile that self-assembles into different shapes. We model the self-assembly process of DNA origami at the domain level and apply our model to the polymorphic tile. The model indicates that the early formation of stable bonds between distant sites strongly correlates with the eventual shape of the tile. We find that that small changes to the design significantly affect the folding pathway and the observed distribution of shapes. The model and experiment show that assembly is cooperative, sensitive to domain and crossover design, and we find that reversible bond formation is important to recover from temporary misfolds.

Dunn, Dannenberg et al. Nature 525, 82–86
Dannenberg et al. J. Chem. Phys, in press

Friday, October 16th, 2015, 10:00

Room: ZNN Ground Floor, Seminarraum

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BIOMATERIALS

Forces in Biomolecular Systems SFB 863

Predicting the dynamic behaviour of DNA computers

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Abstract:

Synthetic DNA computers are a promising approach to interface with biological material, with potential applications in disease detection and genetic screening. Predicting the dynamic behaviour of such DNA systems, prior to experimental realization, is an important part of the design process. However, estimating the kinetic parameters that determine this dynamic behaviour is a major challenge. Here I present a method for predicting the kinetic parameters of a DNA device based on existing models of thermodynamic stability, which I apply to a distributed consensus network. The method is accurate while significantly reducing the number of kinetic parameters that need to be measured experimentally. I have implemented this method within the Visual DNA Strand Displacement software developed by Microsoft Research, enabling predictions for a broad range of DNA devices.

Joint work with the biological computational group at Microsoft Research

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