Algorithms for predicting DNA assembling into a give shape

Objective: To give a presentation of about 60 minutes at the end of the week covering the key aspects of the principles of design of DNA nanostructures and present achievements.

Manipulating objects at the atomic scale has lead to the recent rise of the field of nanoscience and when biomolecules are involved, bionanoscience. There are different approaches to designing nano-object. One approach is to manipulate small object using larger precision instruments. A different approach is to design molecules that self-assemble into a pre-defined structure. In this context nucleic acids play a special role as the base pairing can be used as a cornerstone in self-assembly. A series of impressive structures have been designed (Rothemund, 2006) and application of this on a wider scale posed algorithmic problems: Ie given a structure, define a set of DNA strings that fold into this structure and not into others. What are the key restrictions to this problem: The proposed structure must be planar and it is natural to view it as graph where base pairing segments are nodes and pairing between these nodes constitutes and edge. There will be physical constraints on the DNA for it to fold into the proposed structure and at the same time be able to physically be place on a plane. This constraint will especially be on the length of the spacers between the pairing segments. Too short and two neighbor segments cannot participate in different pairings and too long it will create string that will not stay in the plane. Since it is not allowed to fold into other configurations the proposed structure should be an energetic minimum and alternative minimae should be negligible. One simplification of this could be that close to optimal structures are energetically unfavourably. But radically distinct structures should also be unlikely. An extension of the above problem is that different DNA strands are added one-by-one and an earlier structure is not allowed to rearrange due to the addition of new DNA strands.

Big Questions:

What is the timeline of bionanoconstruction?
What are the basic principles of bionanoconstruction?
What are the key achievements to date?
Are there fundamental physical limits to bionanoconstruction?
Are there interesting algorithimic problems to be pursued?
Which other molecules than DNA could be used as fundamental building blocks?
What are the similarities and differences between bionanoconstruction and biological self-assembly?

Starting pointers

Andersen ES et al. "Self-assembly of a nanoscale DNA box with a controllable lid" Nature. 2009 May 7;459(7243):73-6.
Busch A, Backofen R. (2006) INFO-RNA – a fast approach to inverse RNA folding. *Bioinf* **22**:1823–1831
Dietz et al. (2009) Folding DNA inteo Twisted and Curved Nanoscal Shapes" Science 325.725-
Douglas et al. (2009) "Self-assembly of DNA into nanoscale three-dimensional shapes" Nature 459.476-
Gothelf KV and TH LaBean (2005) "DNA-programmed assembly of nanostructures" Org.Biomol.Chem. 3.4023-37.
Park, SH et al.(2005) "Programmable DNA Self-Assembliers for Nanoscale Organization of Ligands and Proteins" Nano Letters 5.4.729-33
Rothemund, PWK (2006) "Folding DNA to create nanoscale shapes and patterns" Nature440.297-302
Seeman (2007) "An Overview of Structural DNA Nanotechnology" Mol.Biot. 37,246-357
Simmel (2008) "Three-Dimensional Nanoconstruction with DNA" Angw.Chem. Int.Ed. 47.5884-7
Whitesides et al. (1991) Molecular self-assembly and nanochemistry: a chemical strategy for the synthesis of nanostructures Science 29 November 1991 254: 1312-1319
Zheng, J. et al. (2006) "Two-dimensional Nanoparticle Arrays Show the Organisational Power of Robust DNA Motifs Nano Letters 6.7.1502-4