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Synthesizing small and reliable tile sets for patterned DNA self-assembly. (English)

Zbl 1347.68140

Cardelli, Luca (ed.) et al., DNA computing and molecular programming. 17th international conference, DNA 17, Pasadena, CA, USA, September 19–23, 2011. Proceedings. Berlin: Springer (ISBN 978-3-642-23637-2/pbk). Lecture Notes in Computer Science 6937, 145-159 (2011).

Summary: We consider the problem of finding, for a given 2D pattern of colored tiles, a minimal set of tile types self-assembling to this pattern in the abstract Tile Assembly Model of Winfree (1998). This Patterned self-Assembly Tile set Synthesis (PATS) problem was first introduced by Ma and Lombardi (2008), and subsequently studied by Göös and Orponen (2011), who presented an exhaustive partition-search branch-and-bound algorithm (briefly PS-BB) for it. However, finding the true minimal tile sets is very time consuming, and PS-BB is not well-suited for finding small but not necessarily minimal solutions. In this paper, we modify the basic partition-search framework by using a heuristic to optimize the order in which the algorithm traverses its search space. We find that by running several parallel instances of the modified algorithm PS-H, the search time for small tile sets can be shortened considerably. We also introduce a method for computing the reliability of a tile set, i.e. the probability of its error-free self-assembly to the target tiling, based on Winfree's analysis of the kinetic Tile Assembly Model (1998). We present data on the reliability of tile sets found by the algorithms and find that also here PS-H constitutes a significant improvement over PS-BB.

For the entire collection see [Zbl 1222.68005].

MSC:

68Q05	Models of computation (Turing machines, etc.) (MSC2010)
68Q10	Modes of computation (nondeterministic, parallel, interactive, probabilistic, etc.)
92D20	Protein sequences, DNA sequences

Software:

Smodels

Full Text: DOI

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