## CSCI 2570 Introduction to Nanocomputing

DNA Tiling

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## Computing with DNA

- Prepare oligonucleotides ("program them")
- Prepare solution with multiple strings.
- Only complementary substrings $q$ and q combine, e.g. $q=C A G$ and $q=G T C$
- E.g. GCTCAG + GTCTAT $=\begin{gathered}\text { GCTCAG } \\ \text { GTCTAT }\end{gathered}$
- 1D \& 2D crystalline structures self-assemble


## Generating Random Paths Through the Graph

- Edge strings $q_{u}^{\prime} p^{\prime}{ }_{v}$ combine with vertex strings $p_{v} q_{v}$ to form duplexes, shown below.

$$
q_{u}^{\prime} p_{v}^{\prime} \quad q_{v}^{\prime} p_{w}^{\prime}
$$

GTATATCCGAGCTATTCGAG CTTAAAGCTAGGCTAGGTAC


$$
\mathrm{p}_{\mathrm{v}} \mathrm{q}_{\mathrm{v}} \quad \mathrm{p}_{\mathrm{w}} \mathrm{q}_{\mathrm{w}}
$$

- Colored pairs of coupled strings act as a unit.
- Each duplex has two sticky ends that can combine with another duplex or strand.


## 1D Tiling Model

- Modeled by non-rotating tiles with binding sites on E \& W sides.

- All paths in a graph G can be produced with such tiles.
- Minimal bonding strength needed for adhesion


## 2D Tiling Model

- Square tiles with labels on each side.
- Tiles do not rotate.
- A tile "sticks" only if the sum of the strengths of all bonds $\geq \mathrm{t}$, threshold of tiling system.
- Goal: build a pattern from a seed tile.
- Note: This is a random process!


## Emulation of a Binary Counter

- Non-rotating tiles have binding sites on all 4 sides. Tile bounding strength: red $=2$, other $=1$
- Threshold = 2 (arrows where tiles can add).

- Tiling starts at seed tile S .


## Tiles Emulating a Decoder

Can a CPU be self-assembled?


Fig: @ DNA9 2004 p91 Cook et al.
Double edges have strength 2 . Thick edges have strength 0 . Others have strength 1. Threshold $t=2$.


## Addressable Memory Constructed from Tiling System



Fig: @ DNA9 2004 p91 Cook et al.

## Languages and Tiling Systems

- Regular, context-free and recursively enumerable languages correspond to tiling systems with various restrictions
- See "Universal Computation via Self-assembly of DNA: Some Theory and Experiments" by Winfree Yang and Seeman


## Questions About Tile Systems

- Can a tile system fill the plane?
- What's the smallest tile system that generates a pattern?
- How hard is it to determine if a tile system uniquely assembles to a shape?


## Universality of Tile Systems

- The Turing machine (TM) is "universal."

- We show that a tile system can simulate TM by computing TM configurations.


## TM Configurations

- Cell contains $\left(q_{i}, x\right)$ if head over it or $(-, x)$ if not.
- Get next config. from current \& FSM state table
- Shows exist universal cellular automata.



## Tiling Emulation of a TM

Colored tile binds to edge with strength $=2$.
All other edge strengths $=1$.


## Tiling Emulation of TM

- Example illustrates the writing of a new symbol and moving the head.
- Must also handle writing over a blank cell and creating a new one on the right (or left), if necessary.
- What tiles would handle this case?


## Answers to Questions

- Can a tile system fill the plane?
- Yes, if TM doesn't halt.
- How hard is it to determine if this is possible?
- What is smallest tile system that generates a pattern?
- Can the "busy beaver problem" be applied?
- On empty tape, what's longest string written by halting TM?
- Related to the Kolmogorov complexity of the pattern?
- Shortest input string generating given string on universal TM.
- How hard is it to determine if a tile system uniquely assembles to a shape?
- NP-complete


## Self Assembly

- DNA tile systems illustrate self assembly
- Errors occur in practice.
- Tiles adhere where they shouldn't and get locked into place by subsequent attachments
- They can also nucleate without using a seed.
- Methods to control errors:
- Proofreading tile sets
- Zig-zag tile set and control of concentrations


## Sierpinski Triangle

- Double-edge strength $=2$, others $=1, t=2$


Fig: @ DNA9, vol 2943, p.91, Cook et al.

## Error in Self Assembly of Sierpinski Triangle

- A single error will propagate
- Error rates in a DNA tiling experiment were 110\%.
- Spurious nucleation dominated outcomes.

Error
compounded

## How to Control Errors in DNA Self-Assembly?

- Error correction?
- Fault tolerant cellular automata are known.
- But challenging.
- Optimizing conditions for assembly?
- A 10-fold reduction in mismatch rates in standard DNA tiling requires 100 -fold increase in assembly time by cooling down the process.
- Redesigning the tile set to reduce error rate?


## Self Assembly/Disassembly

- Rate of assembly is determined by the concentration of free tiles.
- Rate of disassembly is a function of binding energies and temperature of the environment
- Winfree has modeled this process.


## Proofreading Tile Sets ${ }^{\dagger}$ Reduces Spurious Nucleation

- Each original tile replaced by 4 tiles
${ }^{(1)}$

$$
\begin{aligned}
& (x, y) *(z, z), \\
& \text { ismatch }
\end{aligned}
$$ occurs, there is no way to continue without making an additional error.

$\dagger$ Winfree, Procs. DNA9, 2003

## Simulation with $2 \times 2$ Proofreading Tiles



Fig: @ Procs. DNA9, 2003, p126

## DNA Scaffolds

- DNA tile (a Holliday junction) and selfassembled lattice



Figs: @Nanotechnology, v 15, (2004) p S525

## Prospects for DNA-Based Algorithmic Self Assembly

- Combinatorial problems: at best $10^{12} \mathrm{ops} / \mathrm{sec}$
- Can be done faster on conventional computers.
- Not very promising.


## Patterning \& Templating DNA

- Rothemund ${ }^{+}$has presented a remarkably effective method for generating shapes from DNA which he can decorate with molecules to produce patterns. (See his website.)

+ Folding DNA to Create Nanoscale Shapes and Patterns, Nature, March 2006.


## Rothemund's Approach

a



## Rothemund's Commentary ${ }^{+}$on Self-Assembly of DNA Strands

- The widespread use of scaffolded selfassembly ... of long DNA scaffolds in combination with hundreds of short strands, has been inhibited by several (assumptions):
- Sequences must be optimized to avoid secondary structure or undesired binding interactions,
- Strands must be highly purified, and
- Strand concentrations must be precisely equimolar ...
- All three are ignored in the present method.
+Folding DNA to Create Nanoscale Shapes and Patterns, Nature, March 2006.


## Rothemund's Patterins

- Staples were decorated with molecules visible under an atomic force microcroscope.



## Conclusion

- DNA-based computing offers interesting possibilities
- Most likely to be useful for nano fabrication
- However, high error rates may preclude its use

