Introduction

slides © 2021, David Doty ECS 232: Theory of Molecular Computation UC Davis

Theory of molecular computation = Theory of computation ∩ nanotechnology

In principle, any nanotechnology... In practice, DNA nanotechnology. Why?

• limitations of my own expertise

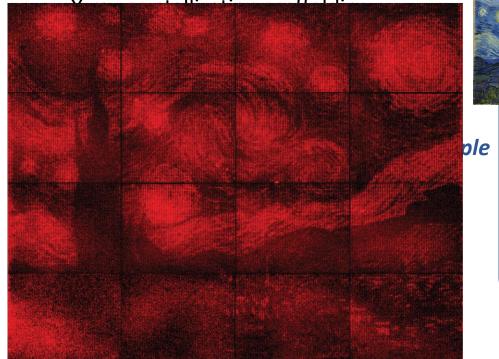


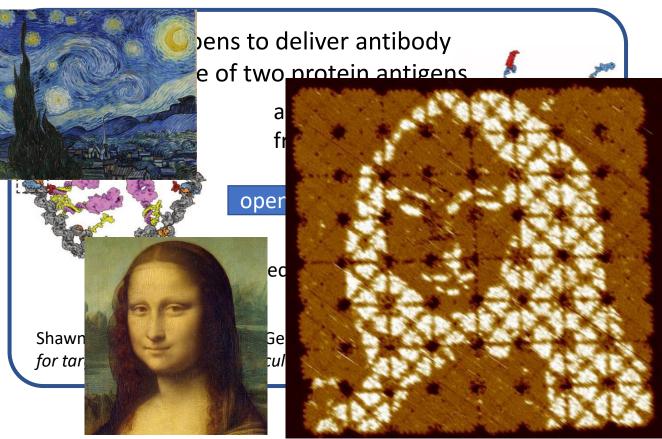
- DNA is naturally information bearing... because of recent technological breakthroughs, also information <u>processing</u>
- More experimentalists in DNA nanotech interested in the idea of "making molecules compute" than in other nanotech fields.

Potential DNA nanotechnology applications

nonbiological:

• antoscale resolution surface placement





Ashwin Gopinath, Evan Miyazono, Andrei Faraon, Paul Rothemund. *Engineering and mapping nanocavity emission via precision placement of DNA origami*, <u>Nature</u> 2016

Grigory Tikhomirov, Philip Petersen, and Lulu Qian. *Fractal assembly of micrometre-scale DNA origami arrays with arbitrary patterns*. <u>Nature</u> 2017.

Theory of computation: Bird's eye view

- <u>Church-Turing thesis</u>: For any physical device that can be built in our universe that can 'reasonably' said to compute a function f: {0,1}*→{0,1}*, f is also computable by a Turing machine.
- Not a mathematical theorem; it is a physical hypothesis.
 - Physicists call such hypotheses "laws of nature" (always the optimists).
 - It's the connection between the <u>physical world</u> of *voltages, transistors,* and *time in seconds,* and the <u>abstract ideas</u> of *digital data, Boolean logic,* and *number of steps in an algorithm*.
- If no Turing machine can solve a computational problem, then no physical device can solve it either.
- Some problems *are* inherently difficult (Boolean satisfiability) or impossible (Halting problem) for computers to solve.
 - Fact about the problem itself, not about a lack of human ingenuity.

Theory of computation: Bird's eye view

- Many models of computation:
 - Turing machine
 - finite state machine
 - polynomial-time Turing machine
 - Boolean circuit
 - distributed network with limited communication between nodes but unlimited computational ability at each node
- None is more or less "correct" as a model of <u>all computing devices</u>.
 - Each is an abstraction useful in some contexts, like Newtonian spherical, frictionless cows.
- Consider: no finite state machine can decide if a binary string has equal 0s and 1s
 - Overly literal interpretation: Your laptop has finite memory, so cannot solve this problem.
 - <u>Better interpretation</u>: If you write an algorithm to solve this problem, then it must, somewhere, use unbounded memory (list, stack, recursion, etc.)

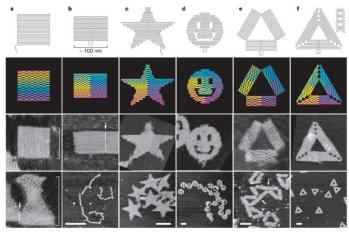
Theory of molecular computation: Bird's eye view

Goal of course: Apply the Theory of Computing "lens" to molecular engineering. Topics we'll cover:

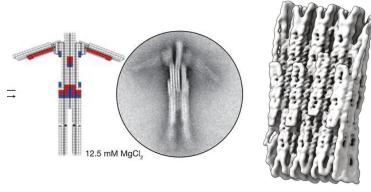
- Basic experimental background
 - structural DNA nanotechnology (building things from molecules)
 - DNA tile self-assembly
 - DNA origami
 - dynamic DNA nanotechnology (reconfiguring molecules)
 - DNA strand displacement
- Algorithmic tile self-assembly
- Chemical reaction networks (and relation to distributed computing)
- Thermodynamic binding networks
- DNA sequence design (classical algorithmic problem helpful in experiments)

Basic experimental background: Structural DNA nanotechnology

DNA origami

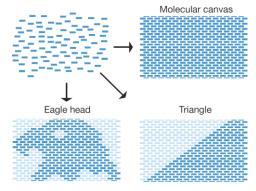


https://www.nature.com/articles/nature04586

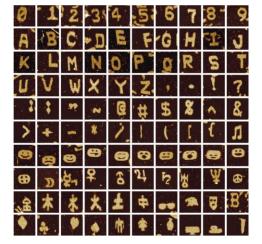


https://science.sciencemag.org/content/347/6229/1446.full https://www.nature.com/articles/s41467-020-20020-7

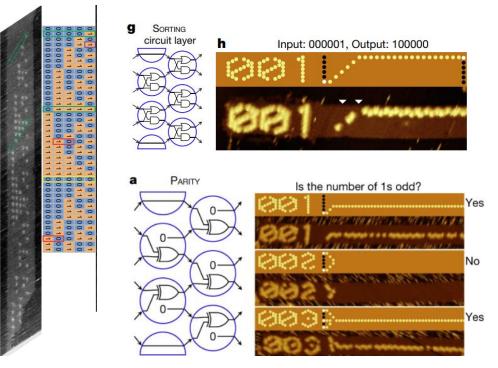
DNA tile self-assembly



https://www.nature.com/articles/nature11075



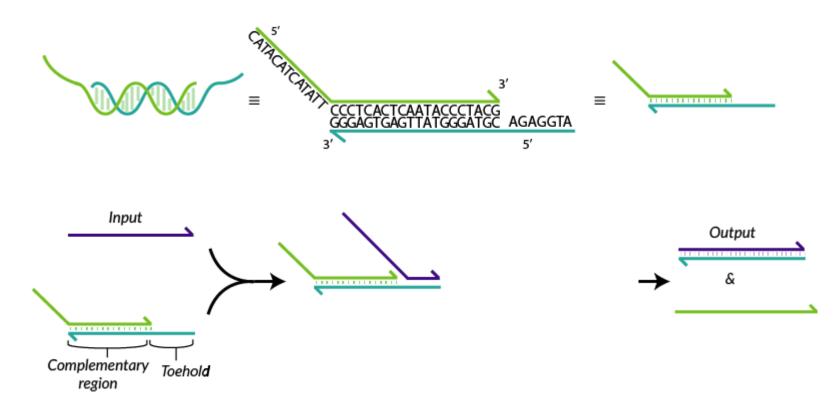
<u>algorithmic</u> DNA tile self-assembly



https://www.dna.caltech.edu/Papers/cge-thesis2014.pdf https://www.nature.com/articles/s41586-019-1014-9

Basic experimental background: Dynamic DNA nanotechnology

DNA strand displacement: DNA reconfiguring itself without enzymes

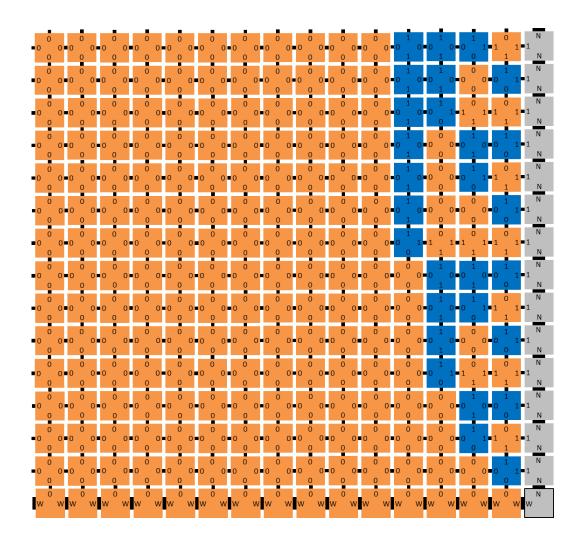


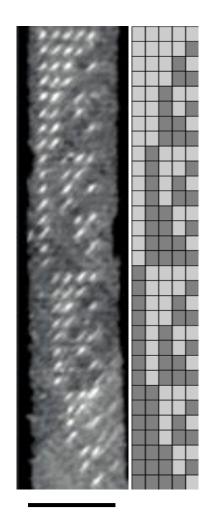
DNA strand displacement

https://www.microsoft.com/en-us/research/video/dna-strand-displacement/



Algorithmic tile self-assembly



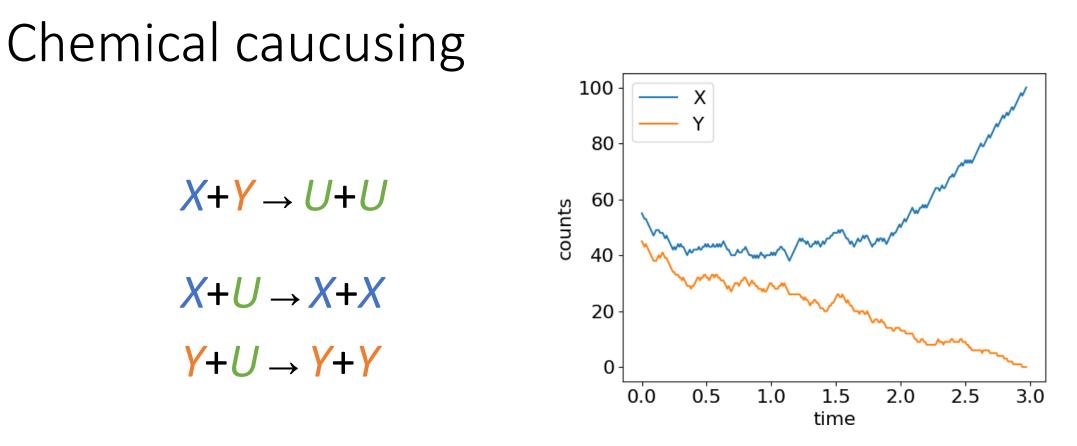


80 nm

Chemical reaction networks

reactant(s)
$$R \rightarrow P_1 + P_2$$
product(s)monomers $M_1 + M_2 \rightarrow D$ dimercatalyst $C + X \rightarrow C + Y$

Traditionally a descriptive modeling language... Let's instead use it as a prescriptive programming language



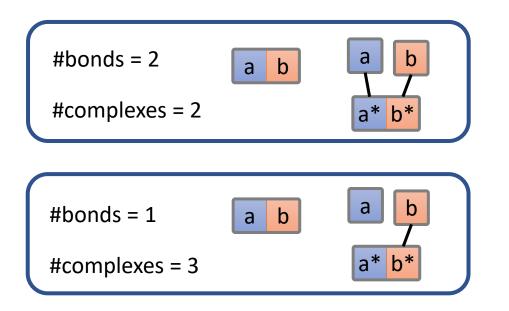
distributed algorithm for *"approximate majority"*: initial majority (*X* or *Y*) quickly overtakes whole population

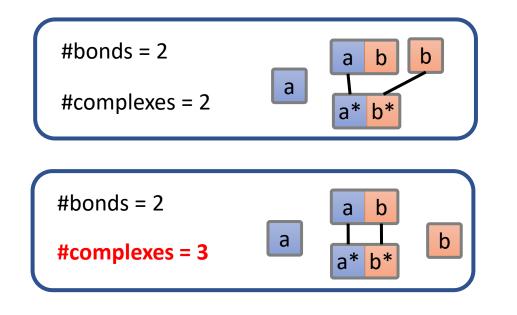
[Angluin, Aspnes, Eisenstat, A simple population protocol for fast robust approximate majority, DISC 2007]

Thermodynamic binding networks

<u>Goal of model</u>: abstract away geometry of DNA to understand effect of two contributions to energetics:

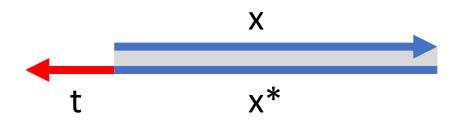
- 1. number of bonds formed ("enthalpy")
- 2. number of separate complexes ("entropy")





DNA sequence design

Goal: given strands with abstract "binding domains"

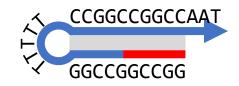


assign to domains concrete DNA sequences:

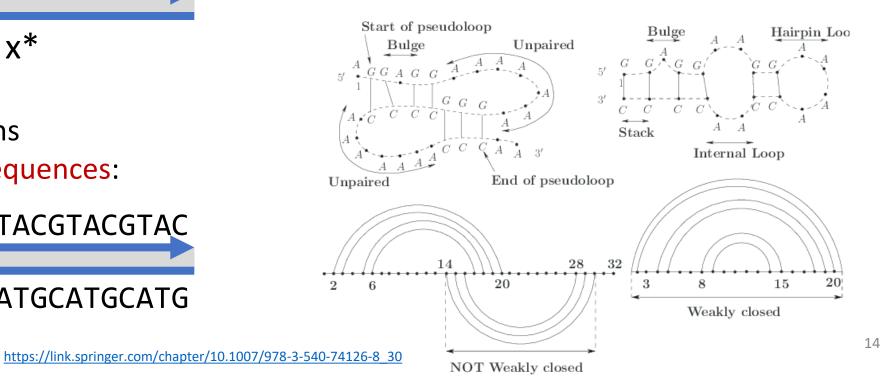
ACGTACGTACGTACGTAC



while preventing unwanted interactions (e.g., strand folds up on itself)



using combinatorial predictive models of DNA energy:



Logistics

Grading

- 60% homework
- 30% final project
- 10% in-class participation

Prerequisites

- Undergraduate theory of computation (ECS 120)
 - experience with proofs, formal definitions, discrete math (*sets, sequences, finite strings, graphs, big-O notation*)
 - finite automata, Turing machines, computability (*halting problem, decidable versus computably enumerable languages*) and complexity theory (*polynomial-time, NP-completeness*)
- Probability
 - events
 - random variables
 - expected value