

andy potts





Life's code script

Turing machines and cells have much in common, argues Sydney Brenner

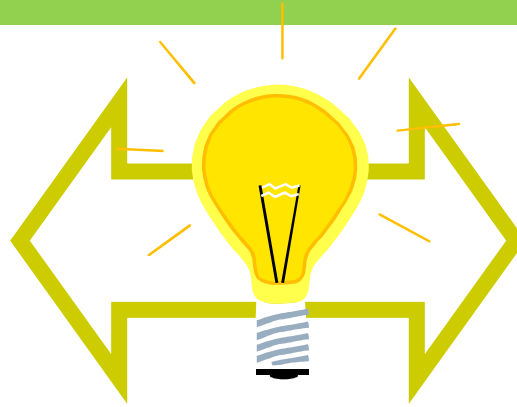
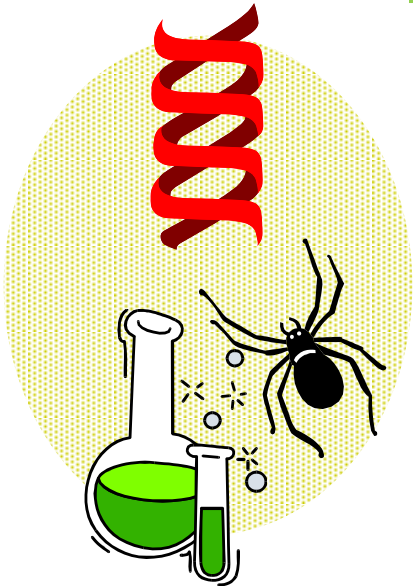
natural computation

dna sorting & networks

understanding nature as a computational process

neural netw & genetic alg

bio inspired computing



bio hardware

this talk

bio-informatics

many facets of ...



Lila Kari, Grzegorz Rozenberg:
The many facets of natural
computing.

CACM 51 (8) 72-83, okt 2008

Turing's Legacy

SNiC – Utrecht

7 maart 2012



Computer in a TestTube

molecular computing

Hendrik Jan Hoogeboom
Computer Science Leiden

Len Adleman

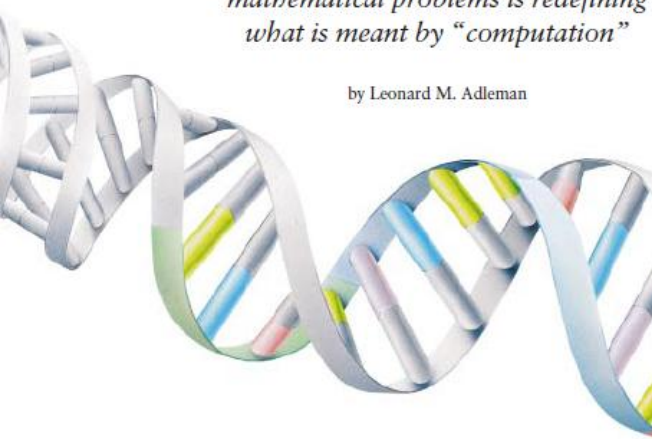
Molecular Computation of Solutions to
Combinatorial Problem,
Science, 266: 1021-1024, (Nov. 11) 1994.



Computing with DNA

The manipulation of DNA to solve mathematical problems is redefining what is meant by “computation”

by Leonard M. Adleman



Scientific American

“DNA polymerase is an amazing little nanomachine, a single molecule that “hops” onto a strand of DNA and slides along it, “reading” each base it passes and “writing” its complement onto a new, growing DNA strand ... I was struck by its similarity to something described in 1936 by Alan M. Turing, the famous British mathematician ...

This realization caused me to sit up in bed and remark to my wife, Lori, ‘Jeez, these things could compute.’ I did not sleep the rest of the night, trying to figure out a way to get DNA to solve problems.”

Leonard M. Adleman - Computing with DNA
Scientific American August 1998

Physicists plunder life's tool chest

If we look inside the cell, we see extraordinary machines that we couldn't make ourselves, says Len Adleman. “It's a great tool chest - and we want to see what can we build with it.”

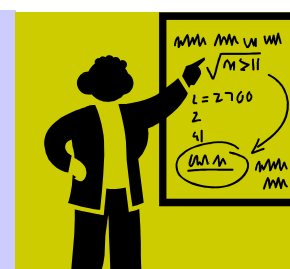
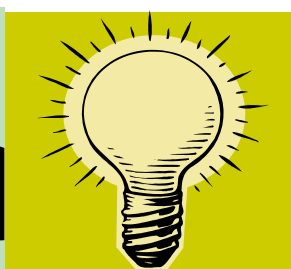
‘travelling salesman’ problem

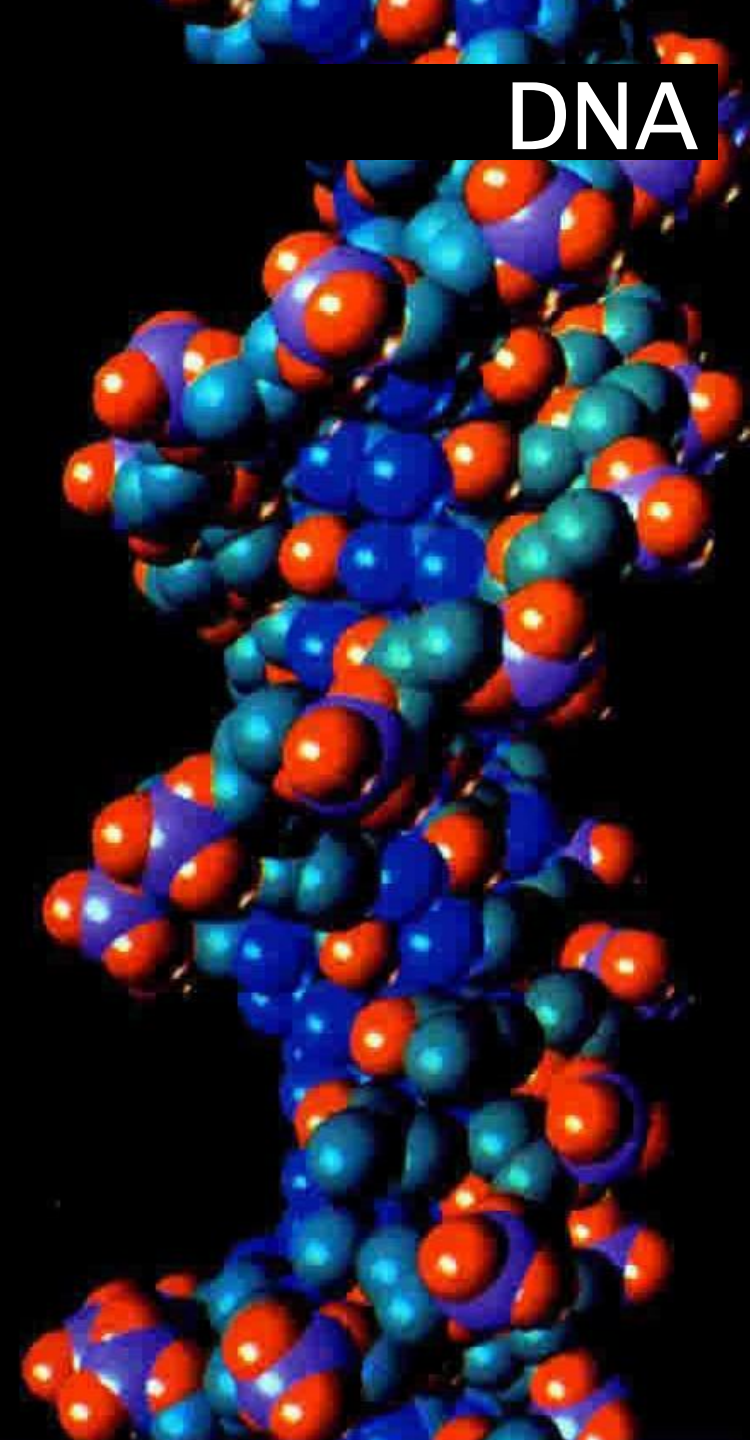
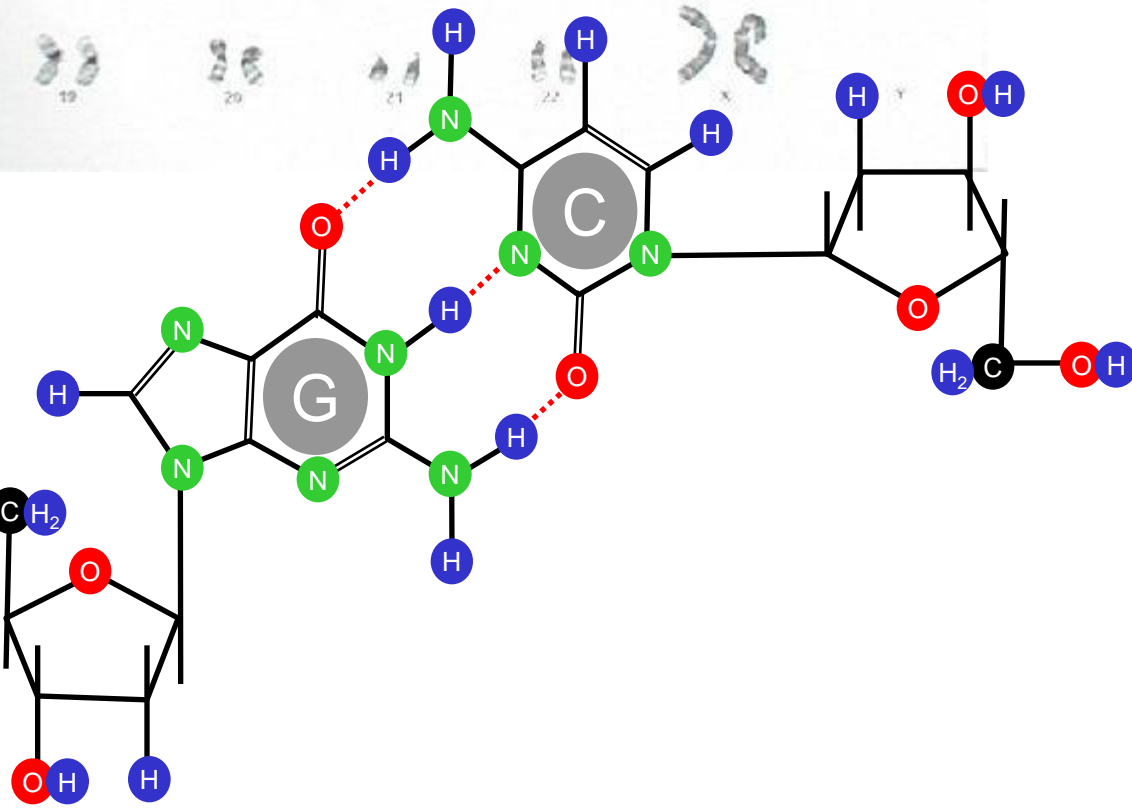
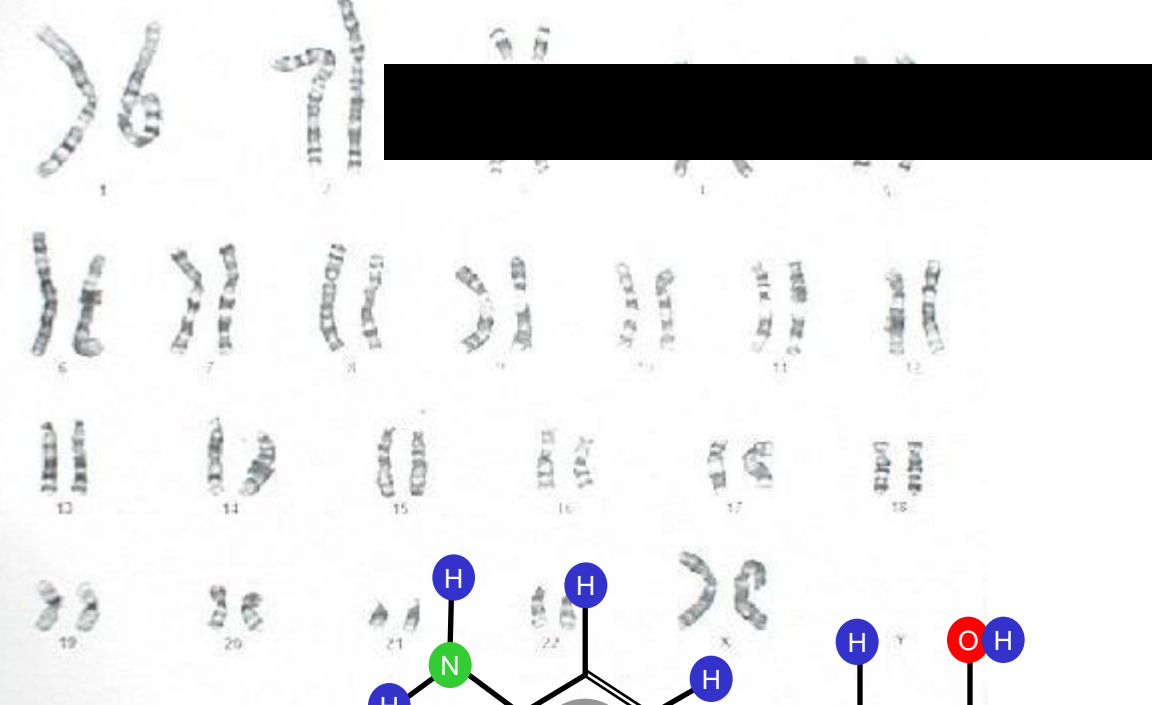
DNA excels at getting an astronomical amount of data into a tiny space. “One gram of DNA can store as much information as a trillion compact discs,” says Adleman. Myriad DNA molecules can examine every possible route at once, rather than one at a time, as in a conventional computer.

massive parallelism

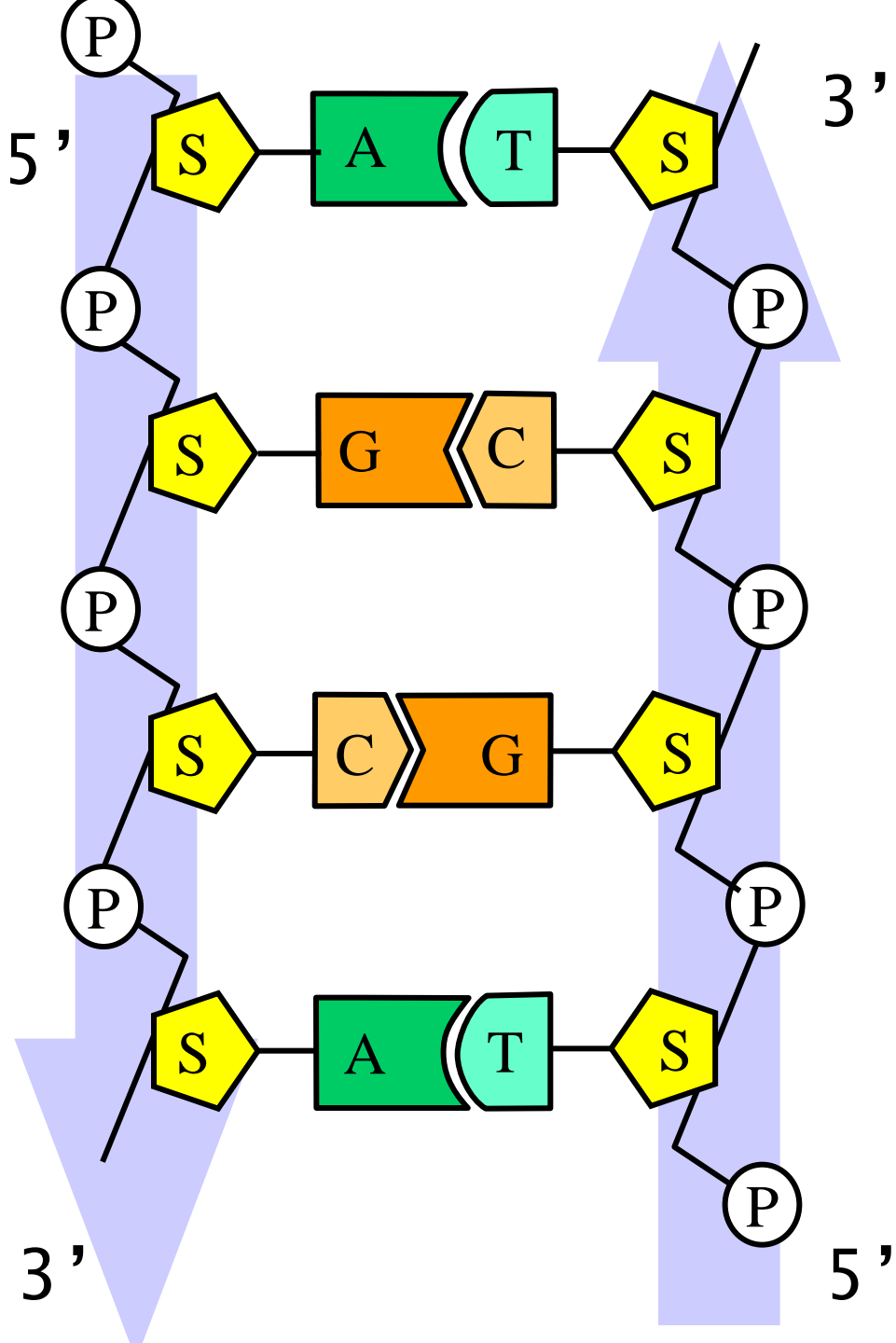


- ❖ DNA ... the **tool chest**
- ❖ Hamilton Path Problem
- ❖ Adleman's algorithm
- ❖ comments
- ❖ theory ... Turing machine
- ❖ recent work + future
- ❖ self assembly





DNA



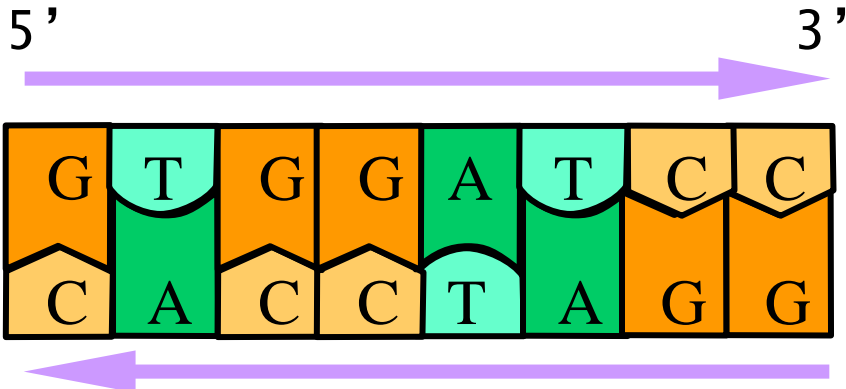
3' **DNA**

Base pairs
 Watson & Crick
 [& Rosalind Franklin]

A=T
 adenine - thymine
 C≡G
 guanine - cytosine

single – double strand

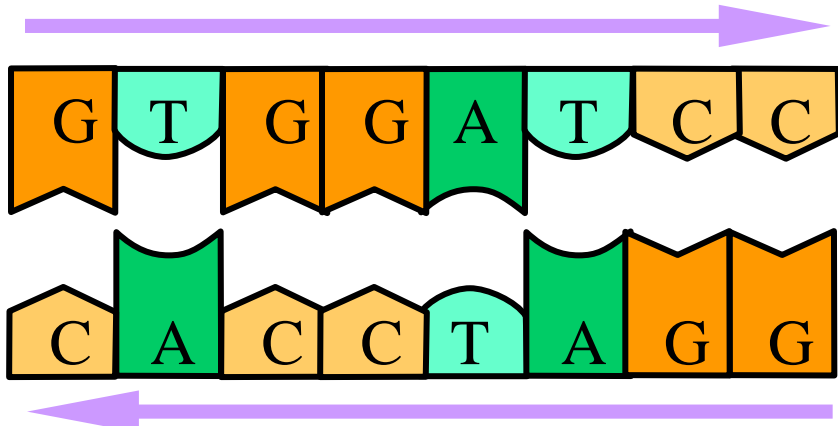
'complementarity'



double strand

annealing

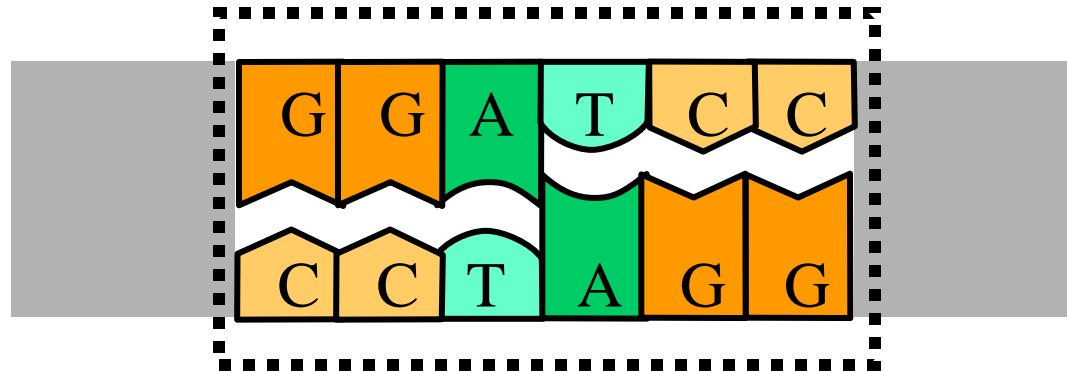
denaturing



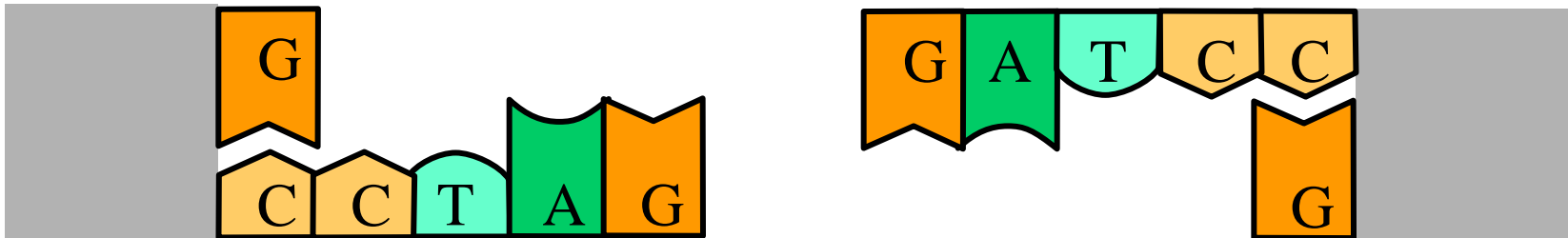
single strands

high temp

restriction enzymes

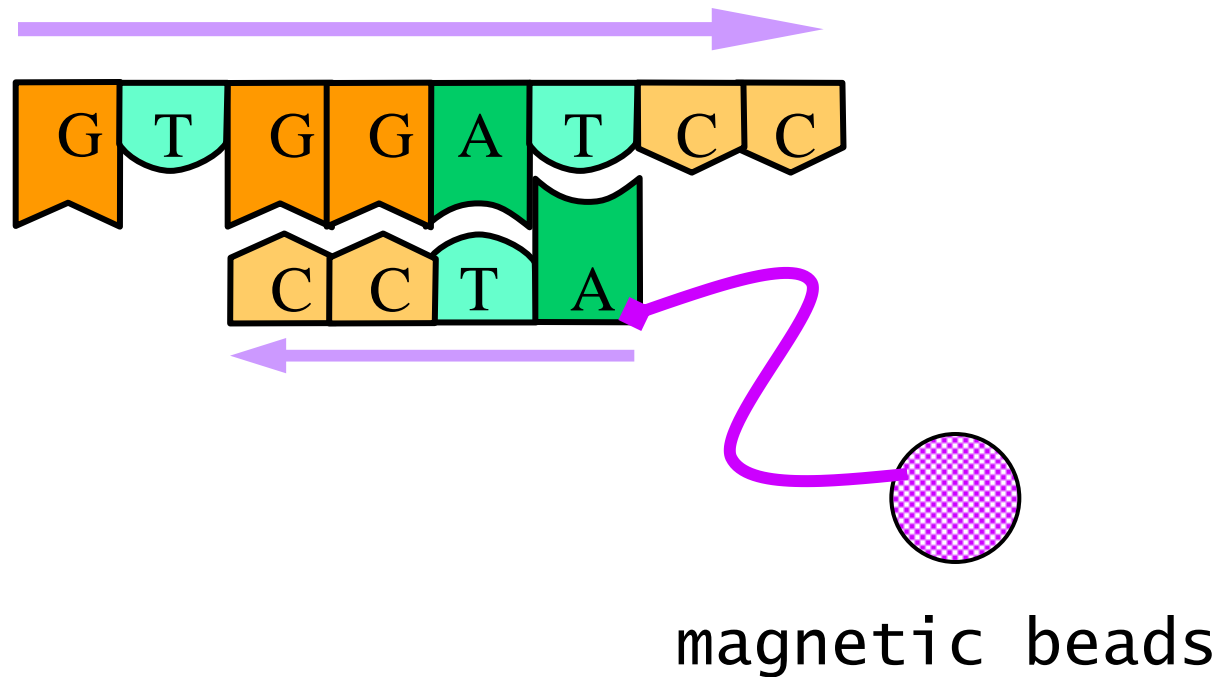


BamHI



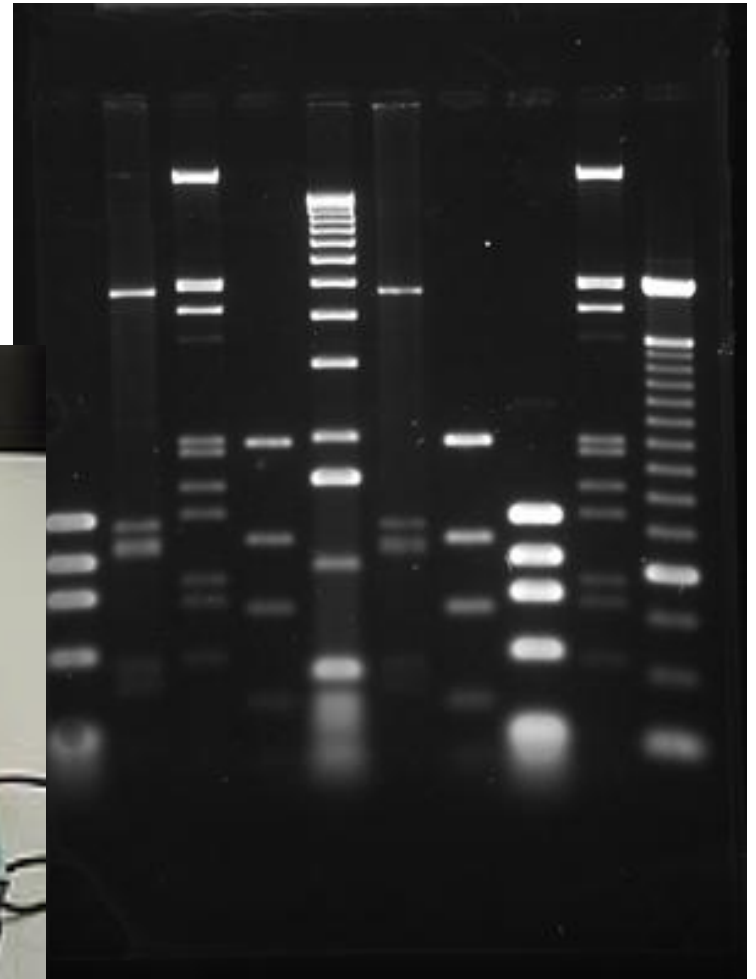
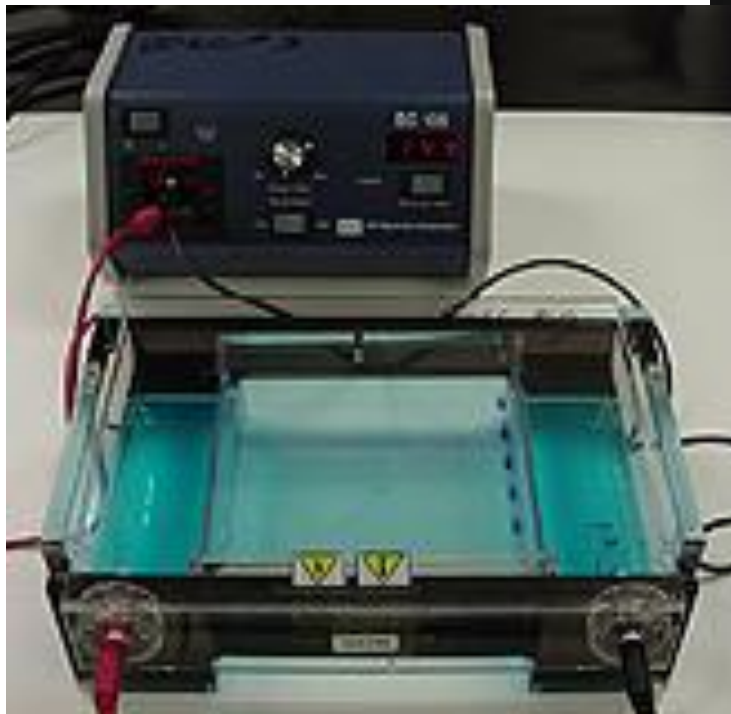
sticky ends

subsequence selection

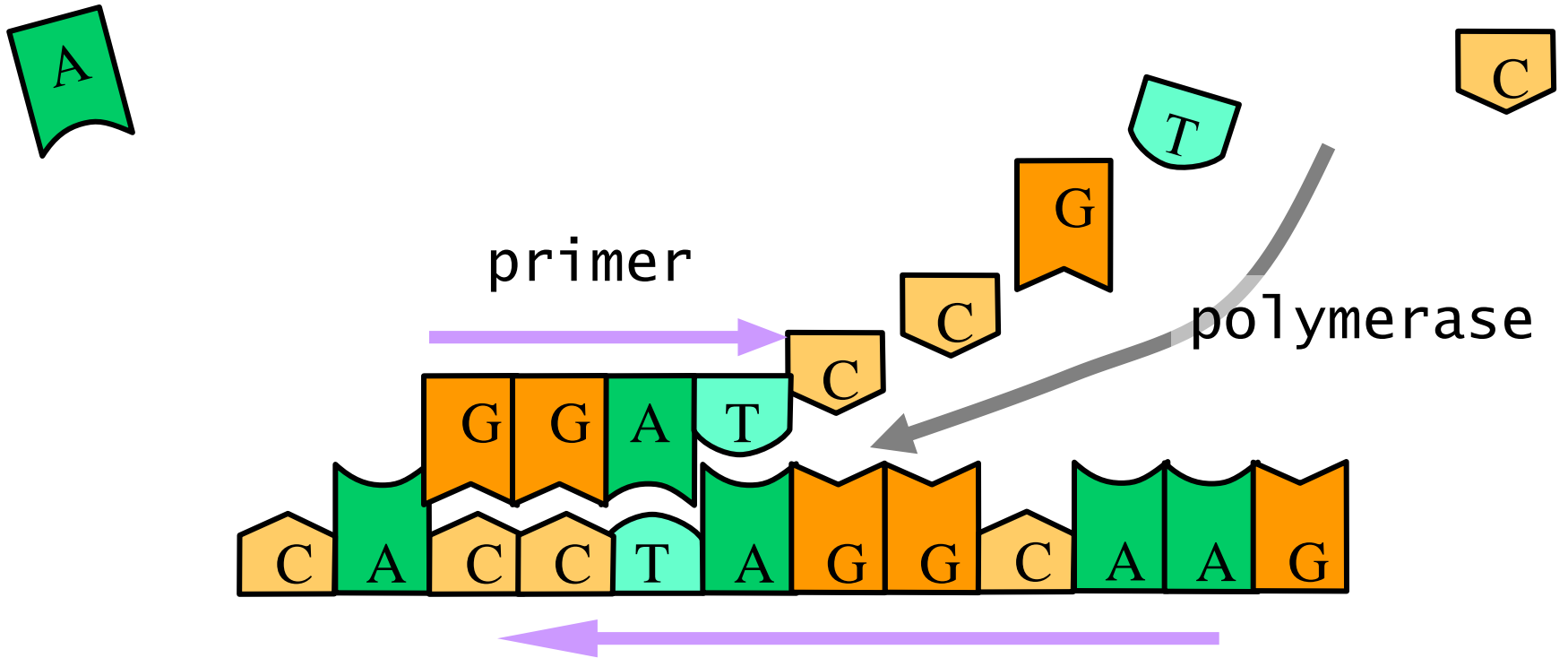


separation on length

DNA gel electrophoresis

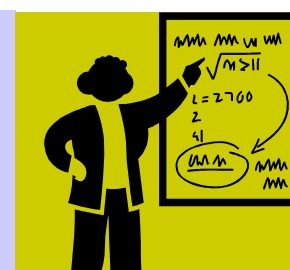
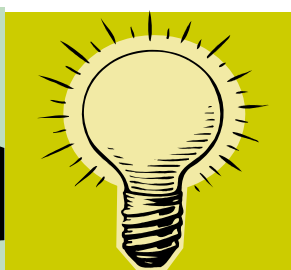


multiplication / amplification

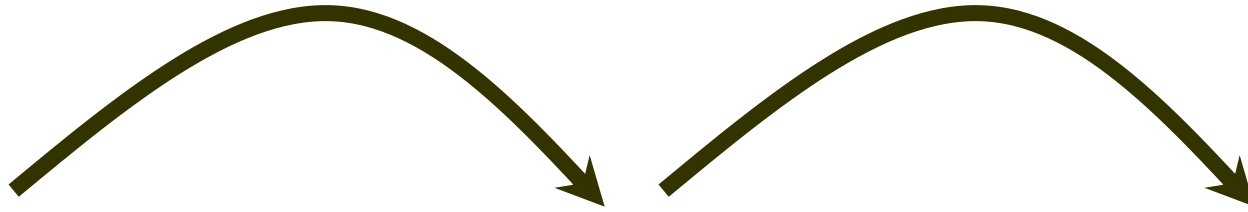


PCR – polymerase chain reaction

- ❖ DNA ... the tool chest
- ❖ Hamilton Path Problem
- ❖ Adleman's algorithm
- ❖ comments
- ❖ theory ... Turing machine
- ❖ recent work + future
- ❖ self assembly



The general idea



custom made
single strands of DNA
(many copies)



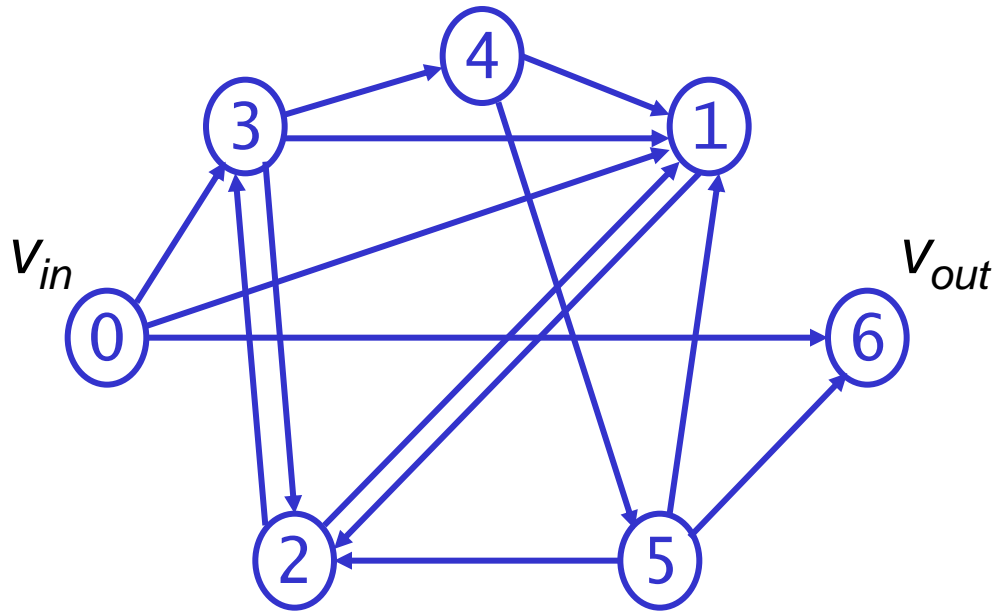
is there a
double strand
with my desired
properties?

properties:

- length,
- subsequence.

if we can do this, then we can solve
certain problems (efficiently)!

HPP: Hamilton Path Problem

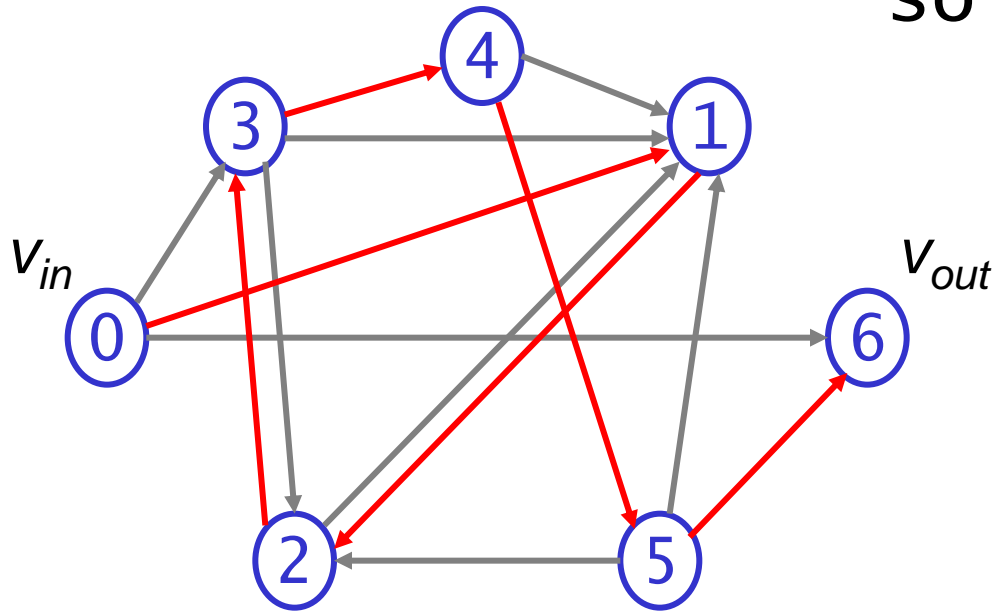


*'travelling
salesman'*

given: directed graph (points & connections)
question: is there a path that visits each
point **exactly once** ?

HPP: Hamilton Path Problem

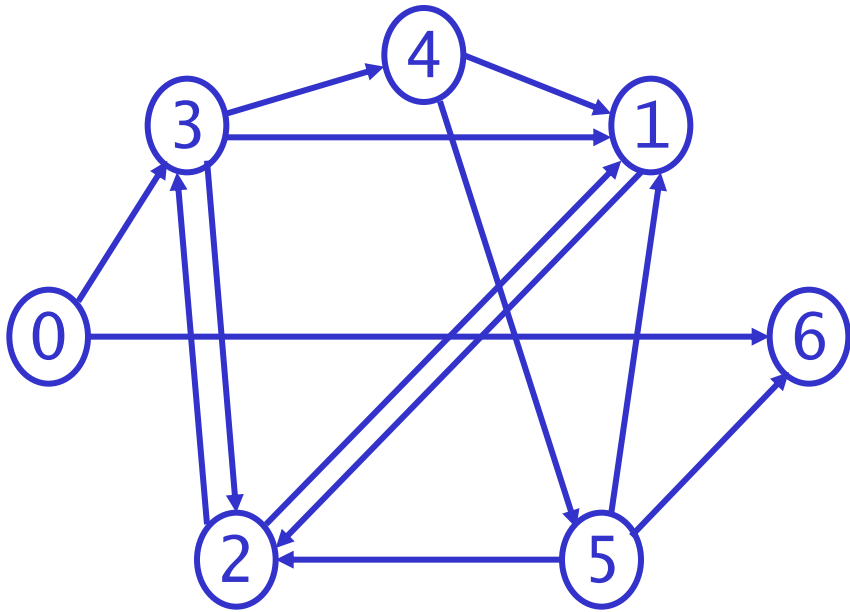
solution



*'travelling
salesman'*

given: directed graph (points & connections)
question: is there a path that visits each
point **exactly once** ?

HPP: Hamilton Path Problem

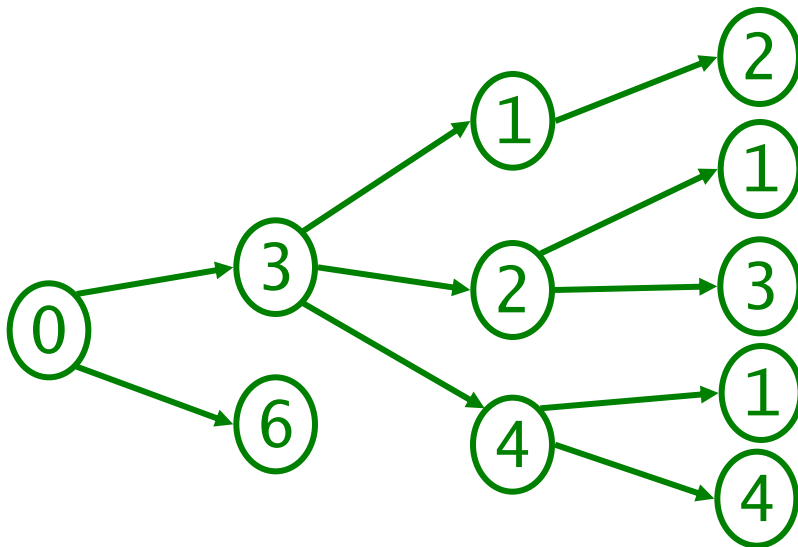


no solution?

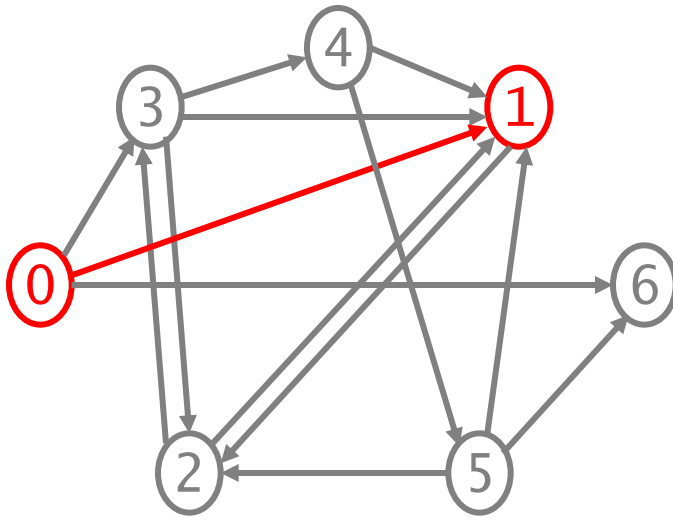
exponential time:
try all possibilities

representative class
'NP complete'

heuristics



Adleman's algorithm



0. coding the graph

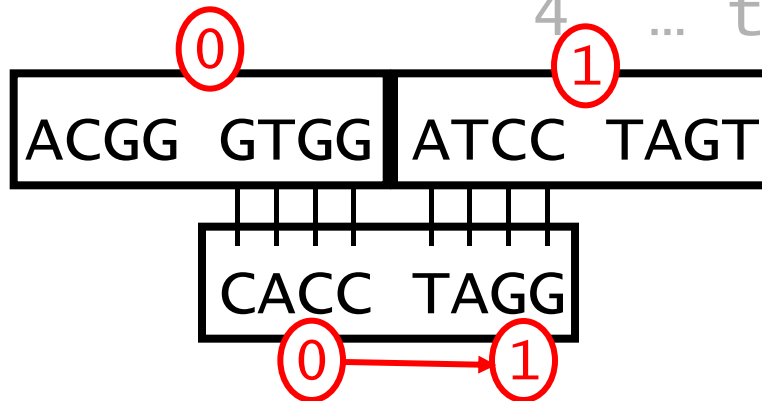
1. generate 'all' paths

keep only paths

2. ... from v_{in} to v_{out}

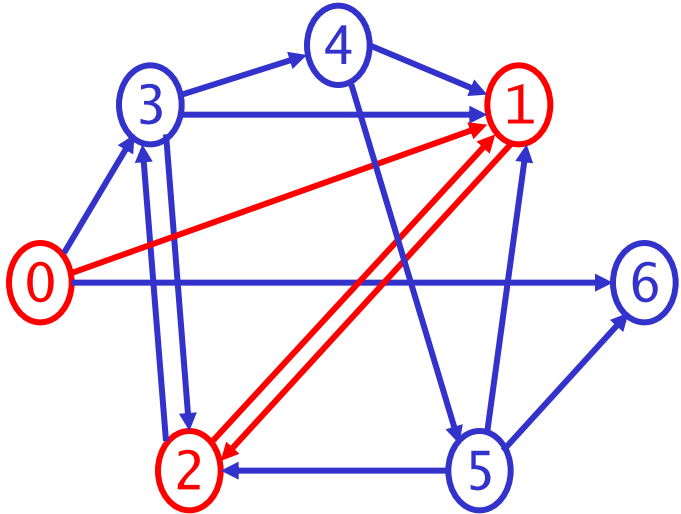
3. ... that enter n vertices

4. ... that enter all vertices



any path remains OK

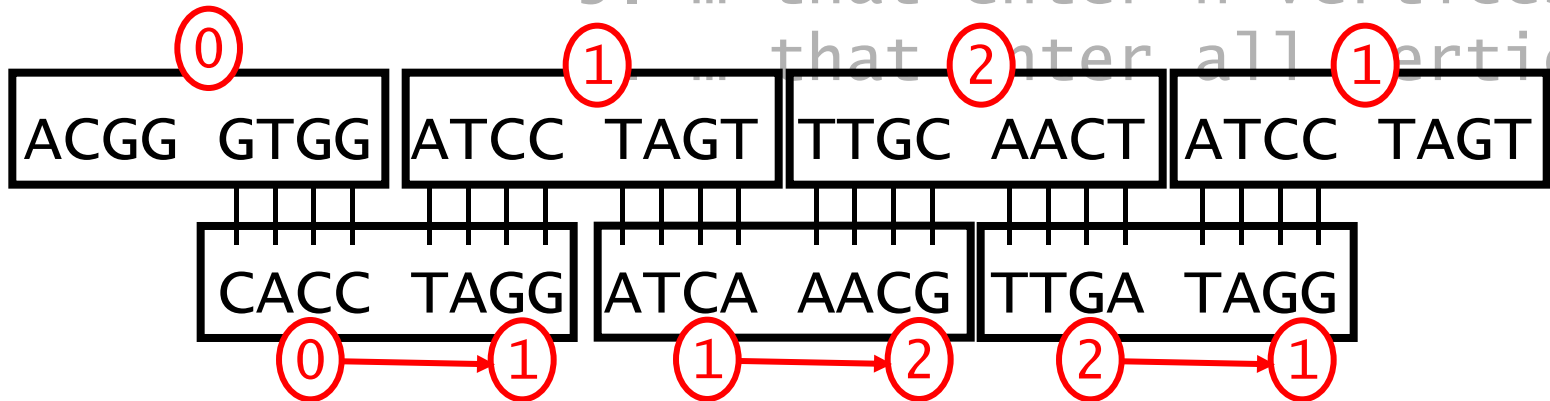
Adleman's algorithm



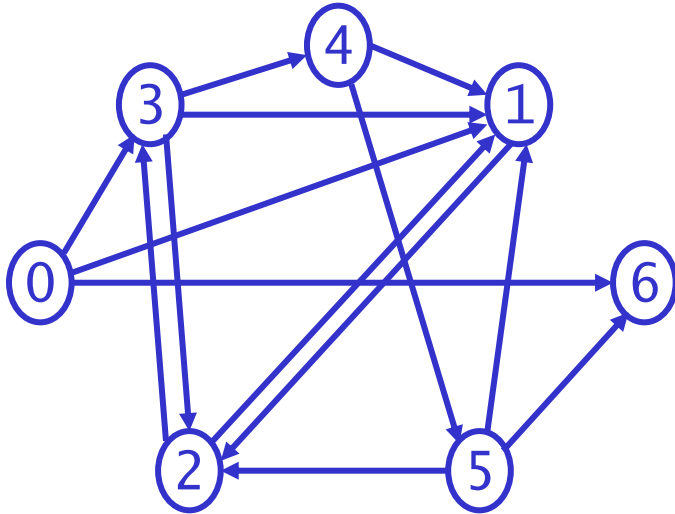
0. coding the graph
- 1. generate 'all' paths**

keep only paths

2. ... from v_{in} to v_{out}
3. ... that enter n vertices
- ... that enter all vertices



Adleman's algorithm



0. coding the graph
1. generate 'all' paths

keep only paths

2. ... from v_{in} to v_{out}
3. ... that enter n vertices
4. ... that enter all vertices
5. if any path remains OK

- PCR with v_{in} and v_{out} primers
- gel: separate on length, amplify & purify
- magnetic beads: select strands
- PCR amplification & gel

- “clear that the methods could be scaled up to ... larger graphs”
 - + bath tub of DNA ?
 - + suitable algorithms
- approximately 7 days of lab work
 - + automation
 - + alternative molecular algorithms
- possibility of errors
 - + pseudopaths: accidental ligation
 - + PCR, separation procedures
 - + hairpin loops
 - + stability when scaled



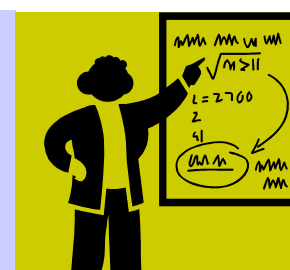
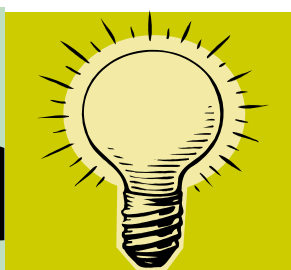
- “power of this method of computation”
 - 10^{14} operations 10^{20} plausible
 - exceed supercomputers by thousandfold

:)

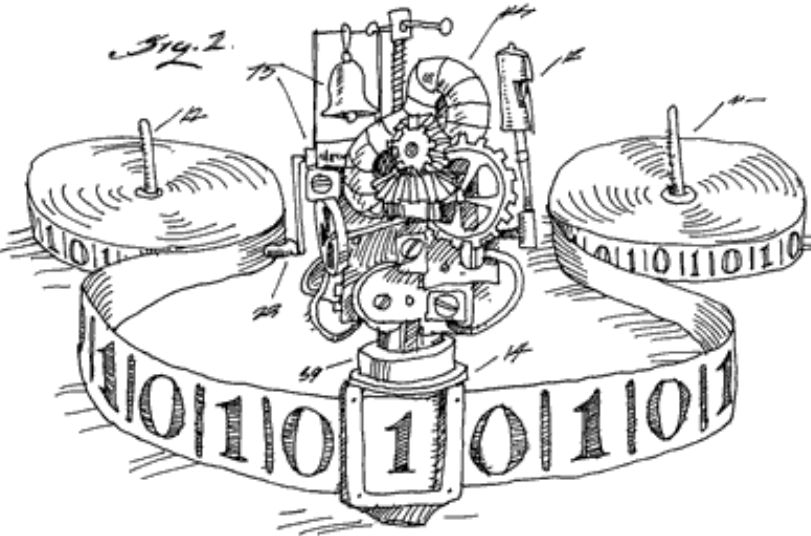
- “not clear whether ... used to solve real computational problems”
 - . multiplying 100 digit numbers
- potential: massively parallel searches



- ❖ DNA ... the tool chest
- ❖ Hamilton Path Problem
- ❖ Adleman's algorithm
- ❖ comments
- ❖ **theory ... Turing machine**
- ❖ recent work + future
- ❖ self assembly



Turing machine



GGATGnnnnnnnnnn
CCTACnnnnnnnnnn

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FokI



| Catalog # | Size | Concentration | Price | Q |
|-----------|-------------|----------------|----------|---|
| R0109L | 5,000 units | 4,000 units/ml | \$244.00 | 1 |
| R0109S | 1,000 units | 4,000 units/ml | \$61.00 | 1 |

Prices are in US dollars and valid only for US orders.

[Download: MSDS PDF](#)

Recognition Site:

5'... GGATG(N)₉▼... 3'
3'... CCTAC(N)₁₃▲... 5'

[isoschizomers](#) | [compatible ends](#) | [single letter code](#)

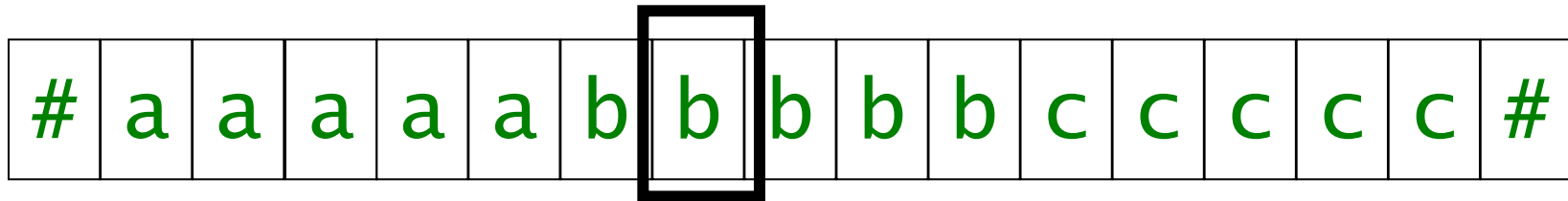
Source:

A *E. coli* strain that carries the FokI gene from *Flavobacterium okeanokoites*

Reagents Supplied:

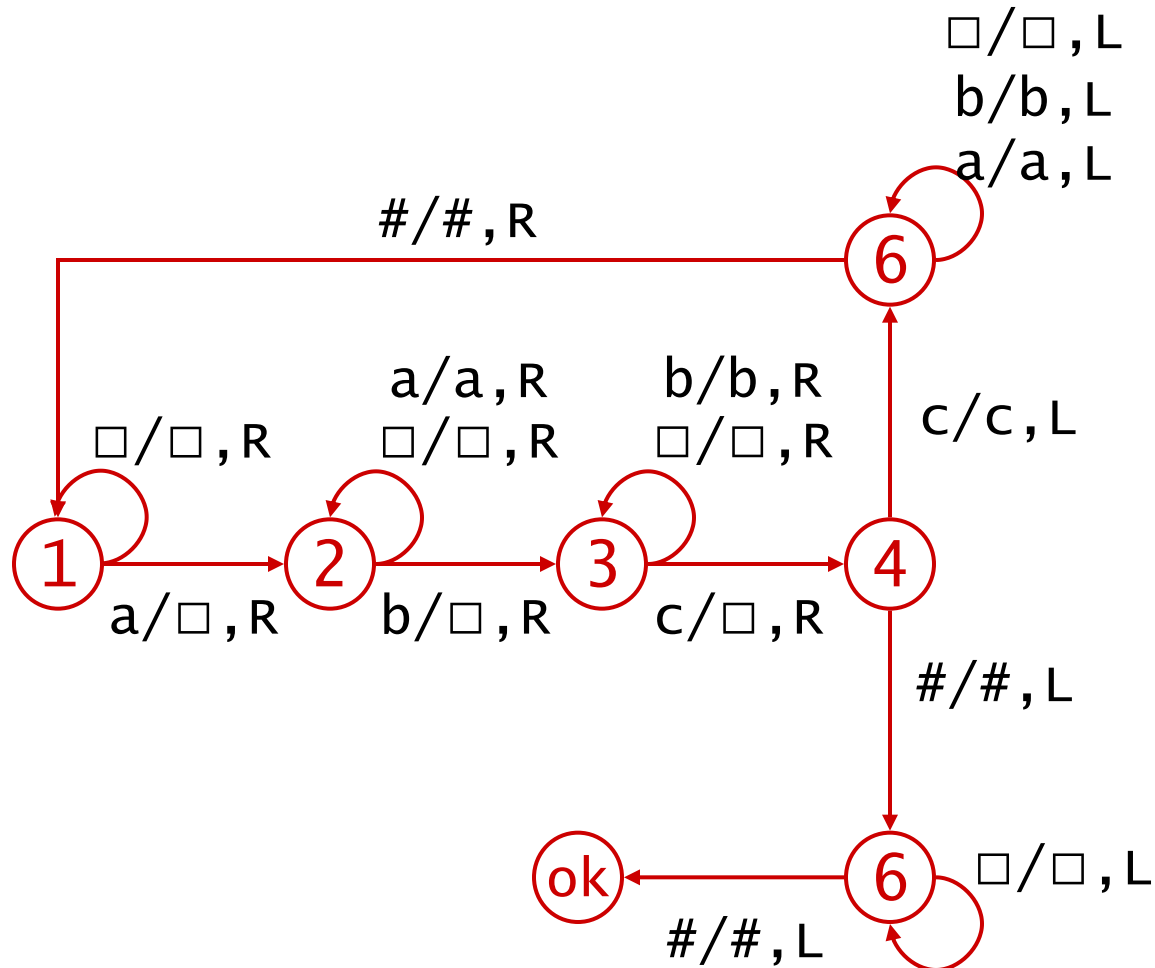
NEBuffer 4

Turing machine



tape

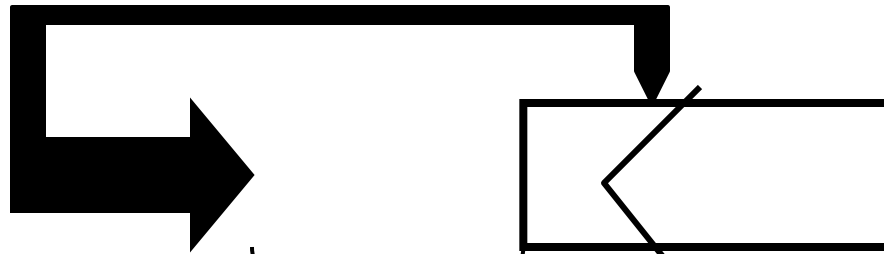
1. mark a
2. move to b's
mark b
3. move to c's
mark c
4. if another c
5. then back to a's
goto 1.
6. else back to a's
6. check marks
stop



'universal' Turing machine

GGATGnnnnnnnnnn
CCTACnnnnnnnnnnnnnnnn

Rothemund
FokI
circular DNA



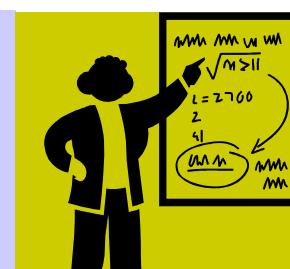
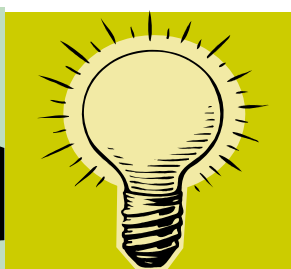
spacing

symbol

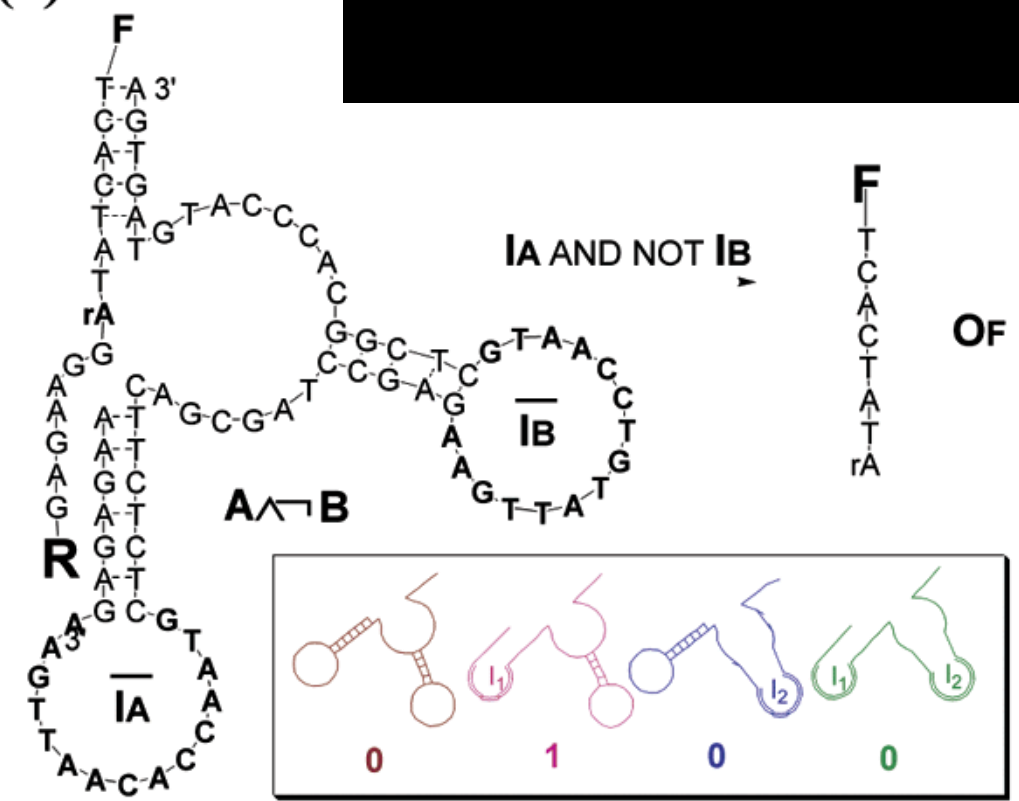
state = position of cut

- cut states with restriction enzyme
- mix 'instructions' with 'tape'
- 'activate' instructions (cut protected end)
- ligate to form circles
- cut old symbol
- recircularize

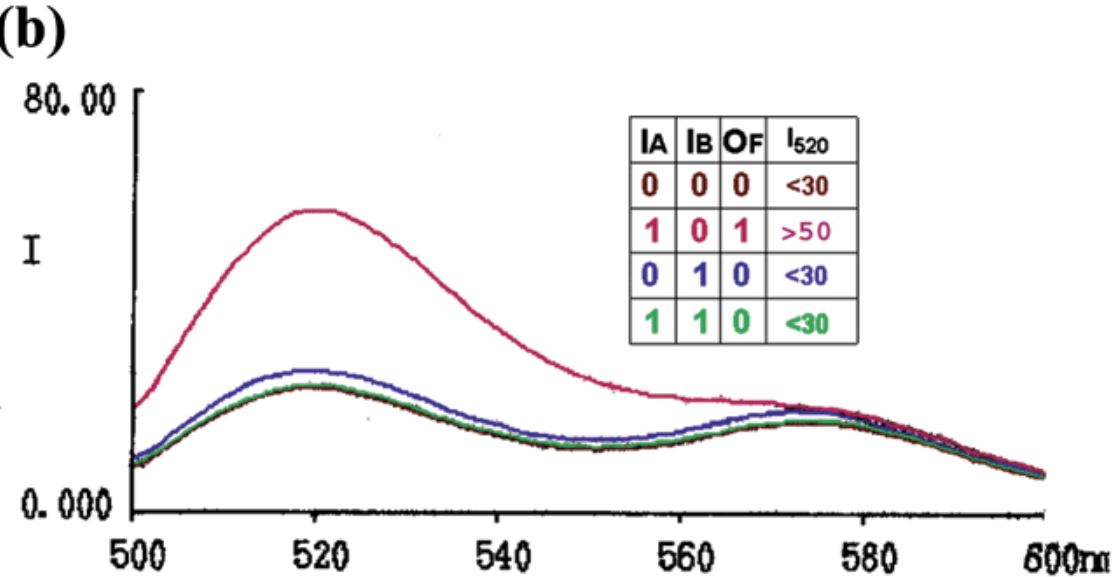
- ❖ DNA ... the tool chest
- ❖ Hamilton Path Problem
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- ❖ comments
- ❖ theory ... Turing machine
- ❖ recent work + future
- ❖ self assembly



tic-tac-toe

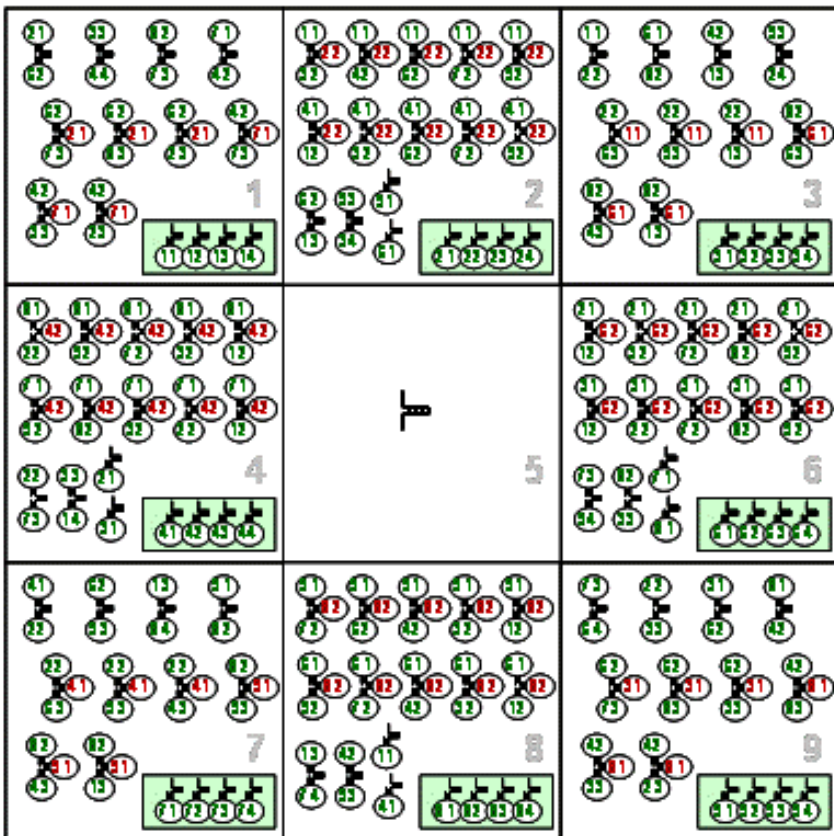


Logic gates
fluorescence



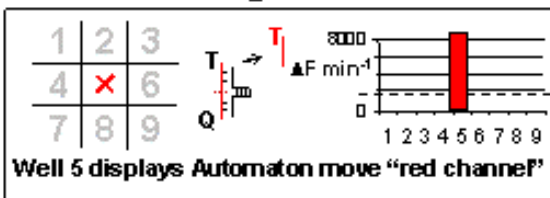
Stojanovic & Stefanovic, **Deoxyribozyme-Based Molecular Automaton**. *Nature Biotechnol.* 2003. **Deoxyribozyme-Based Logic Gates** *J. Am. Chem. Soc.* 2002. **Medium Scale Integration of Molecular Logic Gates in an Automaton** *Nano Letters* 2006.

A. MAYA-II gate distribution



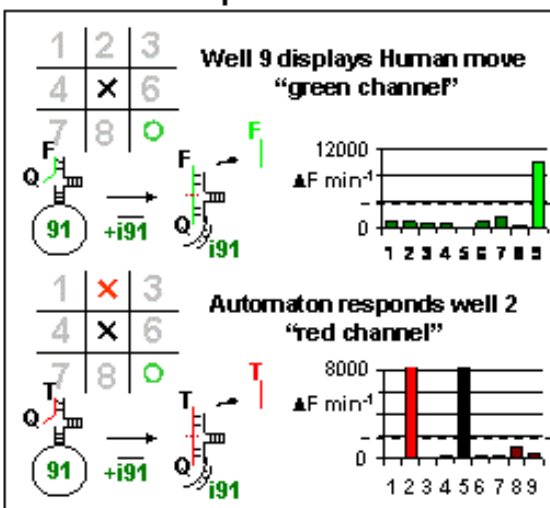
B. Example game:

0. Automaton goes first - well 5

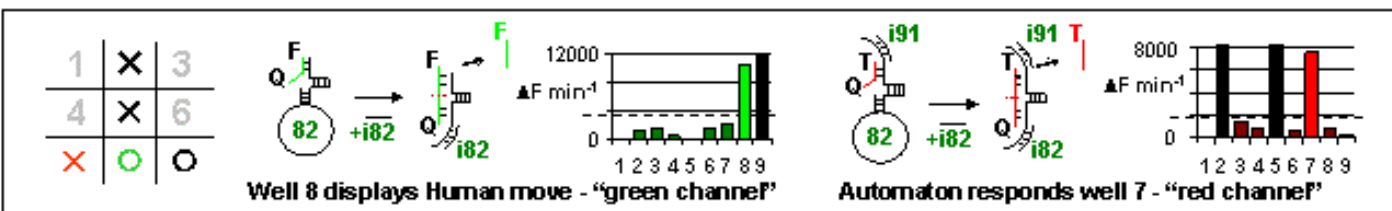


1. Human chooses well 9

- Adds input i91 to all wells



2. Human chooses well 8 – adds i82

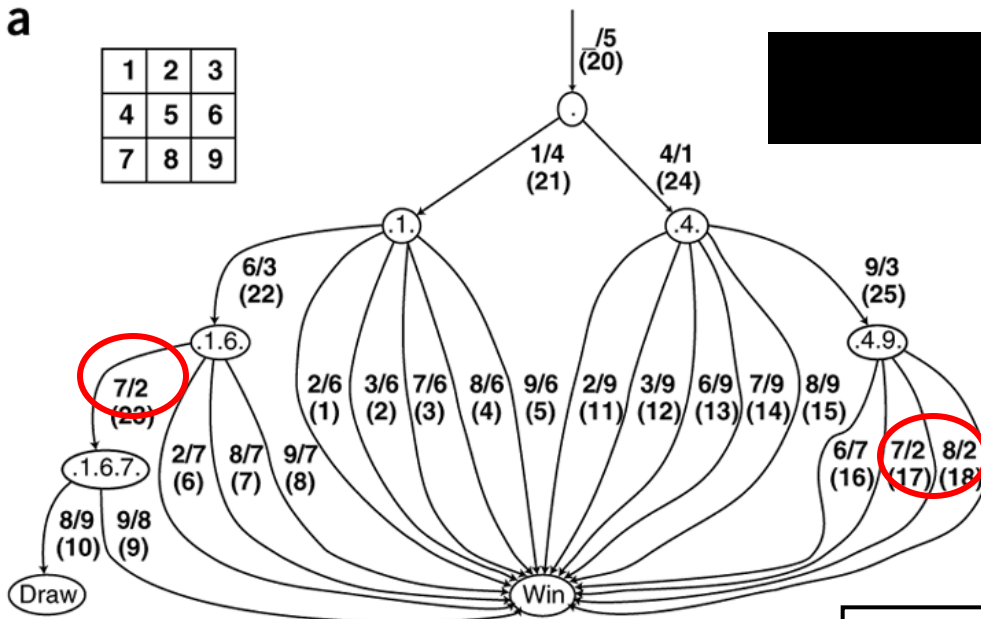


3. Human first "medium-scale integrated molecular circuit", integrating 128 deoxyribozyme-based logic gates, 32 input DNA molecules, and 8 two-channel fluorescent outputs across 8 wells

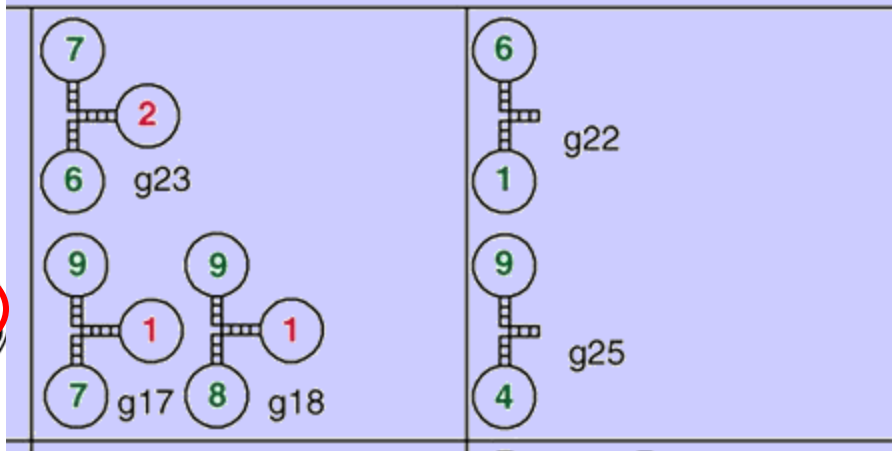
MAYA-II

a

| | | |
|---|---|---|
| 1 | 2 | 3 |
| 4 | 5 | 6 |
| 7 | 8 | 9 |



tic-tac-toe



$$O_2 = (i_6 \wedge i_7 \wedge \neg i_2) \vee (i_7 \wedge i_9 \wedge \neg i_1) \vee (i_8 \wedge i_9 \wedge \neg i_1)$$

b

$$o_1 = \underbrace{i_4}_{\text{edge (24)}}$$

$$o_2 = \underbrace{(i_6 \wedge i_7 \wedge \neg i_2)}_{\text{edge (23)}} \vee \underbrace{(i_7 \wedge i_9 \wedge \neg i_1)}_{\text{edge (17)}} \vee \underbrace{(i_8 \wedge i_9 \wedge \neg i_1)}_{\text{edge (18)}}$$

$$o_3 = \underbrace{(i_1 \wedge i_6)}_{\text{edge (22)}} \vee \underbrace{(i_4 \wedge i_9)}_{\text{edge (25)}}$$

$$o_4 = \underbrace{i_1}_{\text{edge (21)}}$$

$$o_5 = \underbrace{1}_{\text{edge (20)}}$$

$$o_6 = \underbrace{(i_1 \wedge i_2 \wedge \neg i_6)}_{\text{edge (1)}} \vee \underbrace{(i_1 \wedge i_3 \wedge \neg i_6)}_{\text{edge (2)}} \vee \underbrace{(i_1 \wedge i_7 \wedge \neg i_6)}_{\text{edge (3)}} \vee \underbrace{(i_1 \wedge i_8 \wedge \neg i_6)}_{\text{edge (4)}} \vee \underbrace{(i_1 \wedge i_9 \wedge \neg i_6)}_{\text{edge (5)}}$$

$$o_7 = \underbrace{(i_2 \wedge i_6 \wedge \neg i_7)}_{\text{edge (6)}} \vee \underbrace{(i_6 \wedge i_8 \wedge \neg i_7)}_{\text{edge (7)}} \vee \underbrace{(i_6 \wedge i_9 \wedge \neg i_7)}_{\text{edges (8) and (16)}} \vee \underbrace{(i_9 \wedge i_2 \wedge \neg i_1)}_{\text{edge (19)}}$$

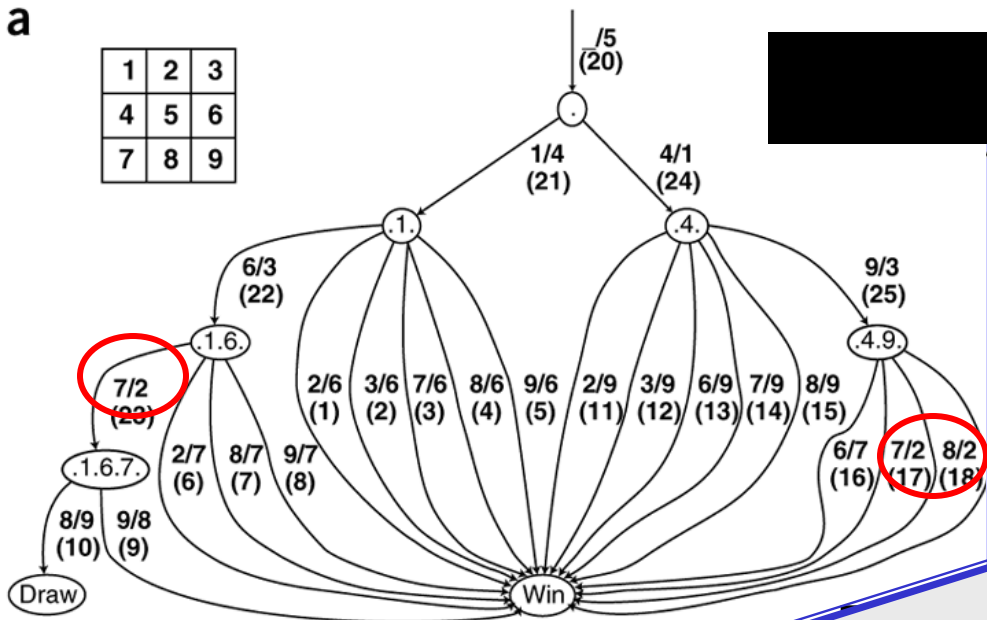
$$o_8 = \underbrace{i_9 \wedge i_7 \wedge \neg i_4}_{\text{edge (9)}}$$

$$o_9 = \underbrace{(i_7 \wedge i_8 \wedge \neg i_4)}_{\text{edge (10)}} \vee \underbrace{(i_4 \wedge i_2 \wedge \neg i_9)}_{\text{edge (11)}} \vee \underbrace{(i_4 \wedge i_3 \wedge \neg i_9)}_{\text{edge (12)}} \vee \underbrace{(i_4 \wedge i_6 \wedge \neg i_9)}_{\text{edge (13)}} \vee \underbrace{(i_4 \wedge i_7 \wedge \neg i_9)}_{\text{edge (14)}} \vee \underbrace{(i_4 \wedge i_8 \wedge \neg i_9)}_{\text{edge (15)}}$$

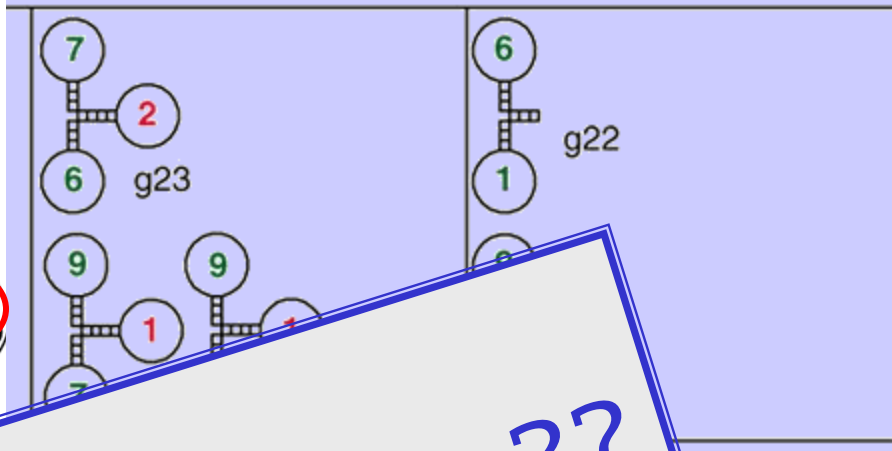
| | | | | | | | |
|-------|-----|-----|-----|-----|-----|-----|---|
| i_1 | TCT | GCG | TCT | ATA | AAT | | |
| i_2 | ATC | GTA | TGT | TGT | TCA | | |
| i_3 | GTA | TAG | TCT | GTT | TGT | | |
| i_4 | G | TAA | GTG | CTC | AAA | TGT | C |
| i_5 | G | TCT | AAT | TCT | CAC | GGT | C |

a

| | | |
|---|---|---|
| 1 | 2 | 3 |
| 4 | 5 | 6 |
| 7 | 8 | 9 |



tic-tac-toe



b

$$o_1 = \underbrace{i_4}_{\text{edge (24)}}$$

$$o_2 = \underbrace{(i_6 \wedge i_7 \wedge \neg i_2)}_{\text{edge (23)}}$$

$$o_3 = \underbrace{(i_1 \wedge i_6)}_{\text{edge (22)}} \vee \underbrace{(i_4 \wedge i_9)}_{\text{edge (25)}}$$

$$o_4 = \underbrace{i_1}_{\text{edge (21)}}$$

$$o_5 = \underbrace{1}_{\text{edge (20)}}$$

$$o_6 = \underbrace{(i_1 \wedge i_2 \wedge \neg i_6)}_{\text{edge (1)}} \vee \underbrace{(i_1 \wedge i_3 \wedge \neg i_6)}_{\text{edge (2)}} \vee \underbrace{(i_1 \wedge i_7 \wedge \neg i_6)}_{\text{edge (3)}} \vee \underbrace{(i_1 \wedge i_8 \wedge \neg i_6)}_{\text{edge (4)}} \vee \underbrace{(i_1 \wedge i_9 \wedge \neg i_6)}_{\text{edge (5)}}$$

$$o_7 = \underbrace{(i_2 \wedge i_6 \wedge \neg i_7)}_{\text{edge (6)}} \vee \underbrace{(i_6 \wedge i_8 \wedge \neg i_7)}_{\text{edge (7)}} \vee \underbrace{(i_6 \wedge i_9 \wedge \neg i_7)}_{\text{edges (8) and (16)}} \vee \underbrace{(i_9 \wedge i_2 \wedge \neg i_1)}_{\text{edge (19)}}$$

$$o_8 = \underbrace{i_9 \wedge i_7 \wedge \neg i_4}_{\text{edge (9)}}$$

$$o_9 = \underbrace{(i_7 \wedge i_8 \wedge \neg i_4)}_{\text{edge (10)}} \vee \underbrace{(i_4 \wedge i_2 \wedge \neg i_9)}_{\text{edge (11)}} \vee \underbrace{(i_4 \wedge i_3 \wedge \neg i_9)}_{\text{edge (12)}} \vee \underbrace{(i_4 \wedge i_6 \wedge \neg i_9)}_{\text{edge (13)}} \vee \underbrace{(i_4 \wedge i_7 \wedge \neg i_9)}_{\text{edge (14)}} \vee \underbrace{(i_4 \wedge i_8 \wedge \neg i_9)}_{\text{edge (15)}}$$

eeuh ...
is this a computer ??

| | | | | | | | |
|-------|-----|-----|-----|-----|-----|-----|---|
| i_1 | TCT | GCG | TCT | ATA | AAT | | |
| i_2 | ATC | GTA | TGT | TGT | TCA | | |
| i_3 | GTA | TAG | TCT | GTT | TGT | | |
| i_4 | G | TAA | GTG | CTC | AAA | TGT | C |
| i_5 | G | TCT | AAT | TCT | CAC | GGT | C |

Future directions in computing: DNA Computing, *BBC News*,
13 Nov 2007

<http://news.bbc.co.uk/2/hi/technology/7085154.stm>

"This soup of DNA and enzymes implements a well known mathematical model of computation known as **finite automaton**," he explained.

"This finite automaton knows how to do very simple computation such as recognising whether a list of zeros and ones has an even number of ones."

In the case of his 2004 computer this method of computation was used to analyze ratios of specific molecules **related to prostate cancer** and a specific type of lung cancer.

The "computer" consisted of a chain of **three segments of DNA and an enzyme** which could cut the strands.

Tom's Links

DNA computer 'answers questions', *BBC News*, 05-Aug-2009
<http://news.bbc.co.uk/2/hi/technology/8184033.stm>

... they tried the system with **simple "if.. then..." propositions**. One of these went as follows: "All men are mortal. Socrates is a man. Therefore, Socrates is mortal."



The answer was encoded in a **flash of green light**. Some of the DNA strands were equipped with a naturally glowing fluorescent molecule bound to a second molecule which keeps the light covered.

The system can take in facts and rules as a computer file of simple text. The **robotic "compiler"** can then turn those facts and rules into the DNA starting products of a logical query.

In other words, **computers that go to work inside a cell**.

Tom's Links

DNA computer 'answers questions', *BBC News*, 05-Aug-2009

<http://news.bbc.co.uk/2/hi/technology/8184033.stm>



DNA logic gates herald injectable computers, *New Scientist*,
02 June 2010

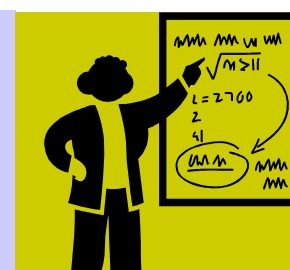
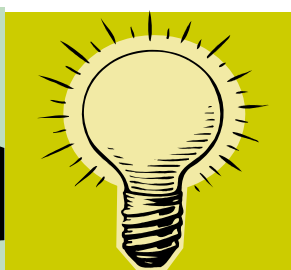
<http://www.newscientist.com/article/dn18989-dna-logic-gates-herald-injectable-computers.html>

"The biocomputer would sense biomarkers and immediately react by **releasing counter-agents for the disease**," says Itamar Willner, who led the work.

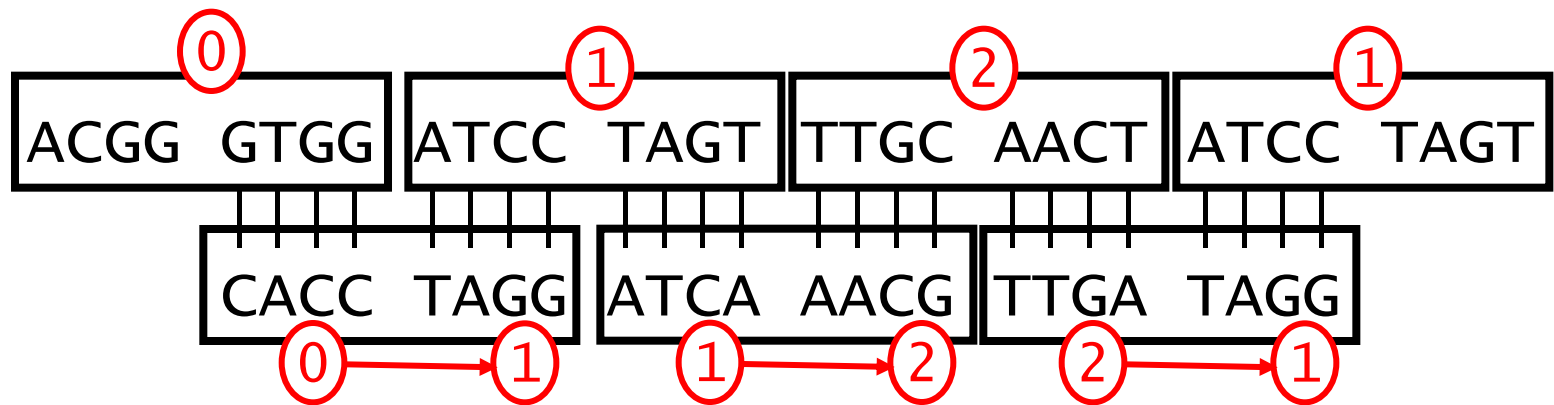
The new logic gates are formed from short strands of DNA and their complementary strands, ... Two strands act as the input: each represents a 1 when present or a 0 when absent. ... Take the "**exclusive OR**" or XOR logic gate. It produces an output when either of the two inputs is present but not when both are present or both are absent.

Willner and his team added molecules to both the complementary strands that **caused them to fluoresce** when each was present in isolation, representing a logical 1 as the output. But when both were present, the complementary strands combined and **quenched** the fluorescence, representing a 0 output.

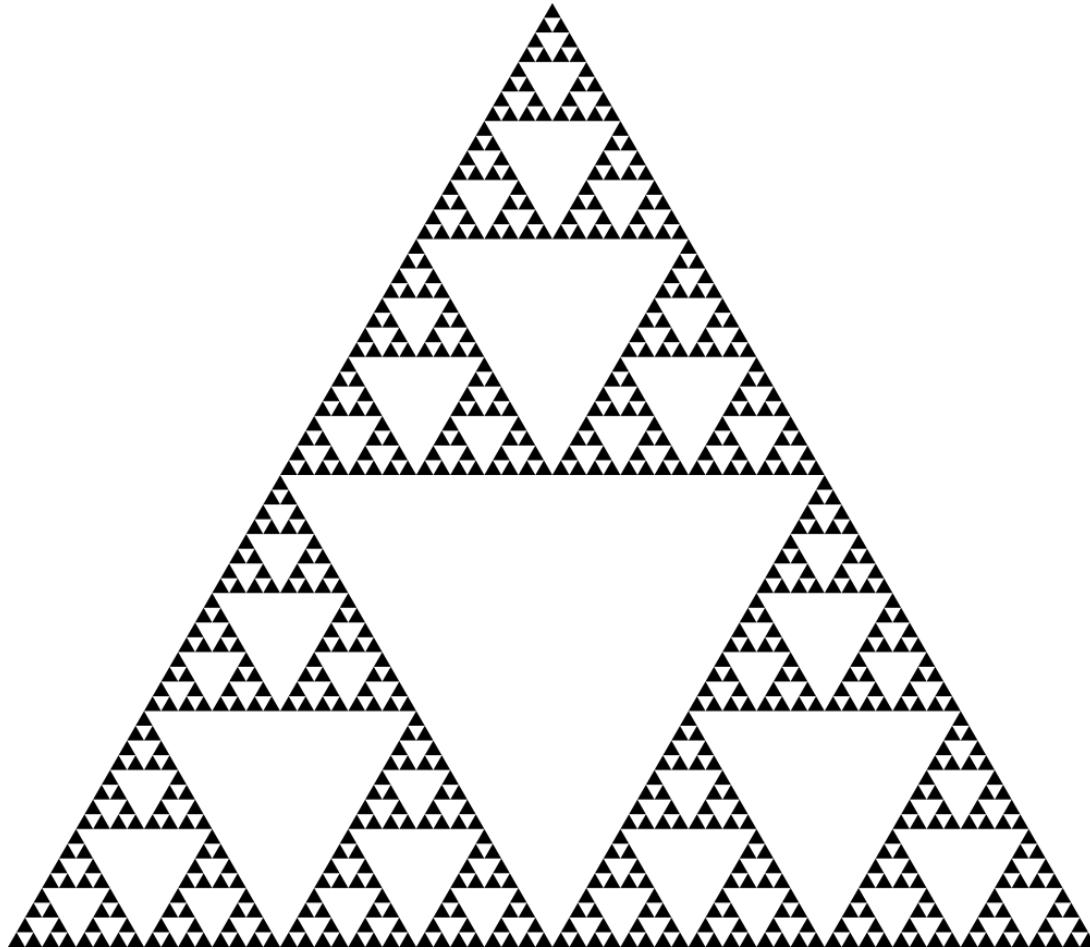
- ❖ DNA ... the tool chest
- ❖ Hamilton Path Problem
- ❖ Adleman's algorithm
- ❖ comments
- ❖ theory ... Turing machine
- ❖ recent work + future
- ❖ **self assembly**



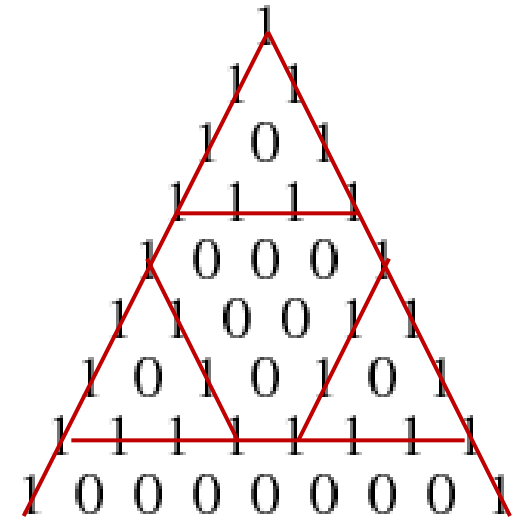
self assembly



Sierpinski triangle



‘fractal’

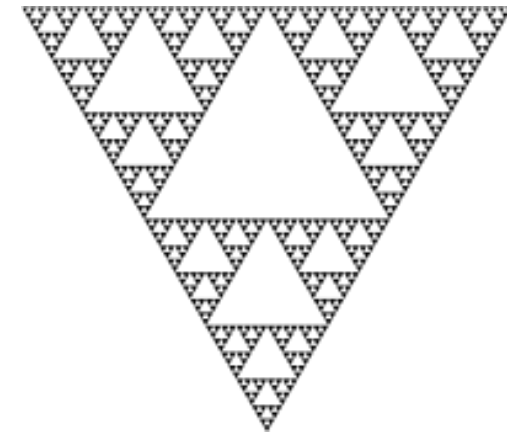
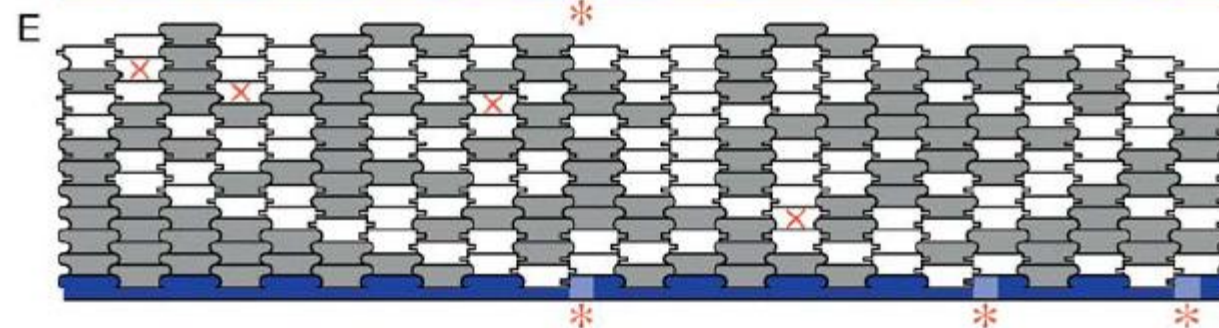
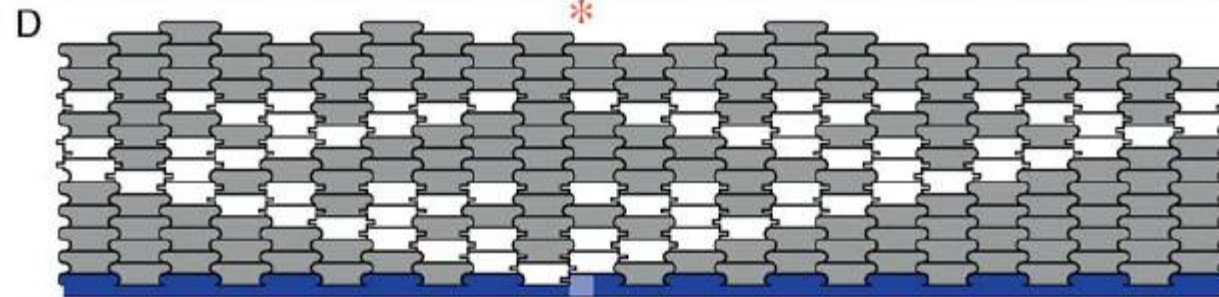
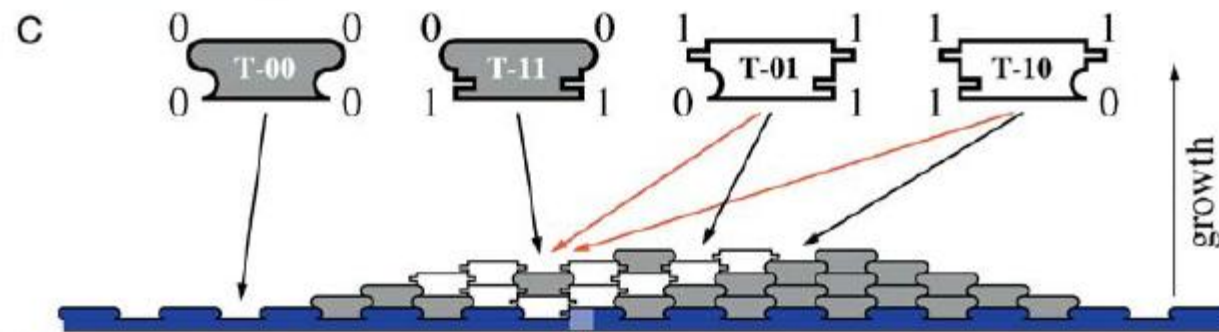
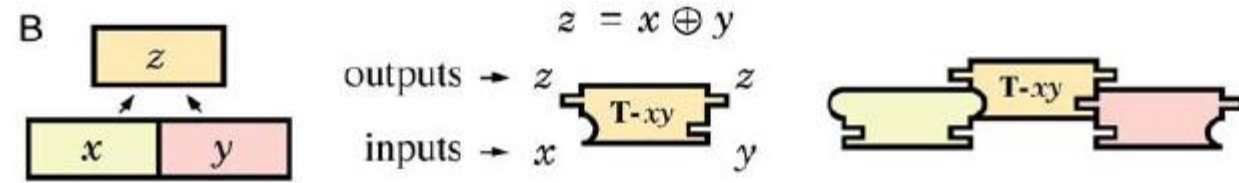


Sierpinski
triangle

\oplus XOR

even / odd

self assembly: sierpinski

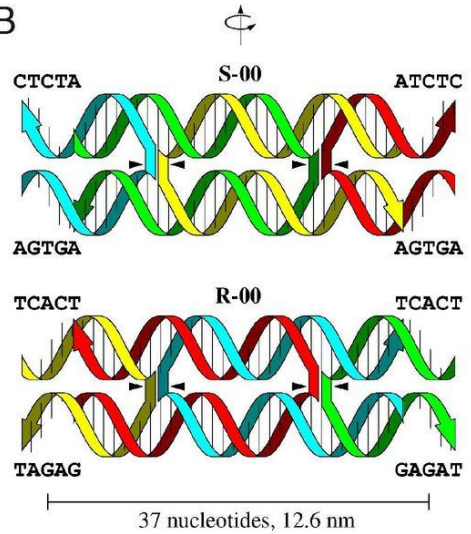


Sierpinski

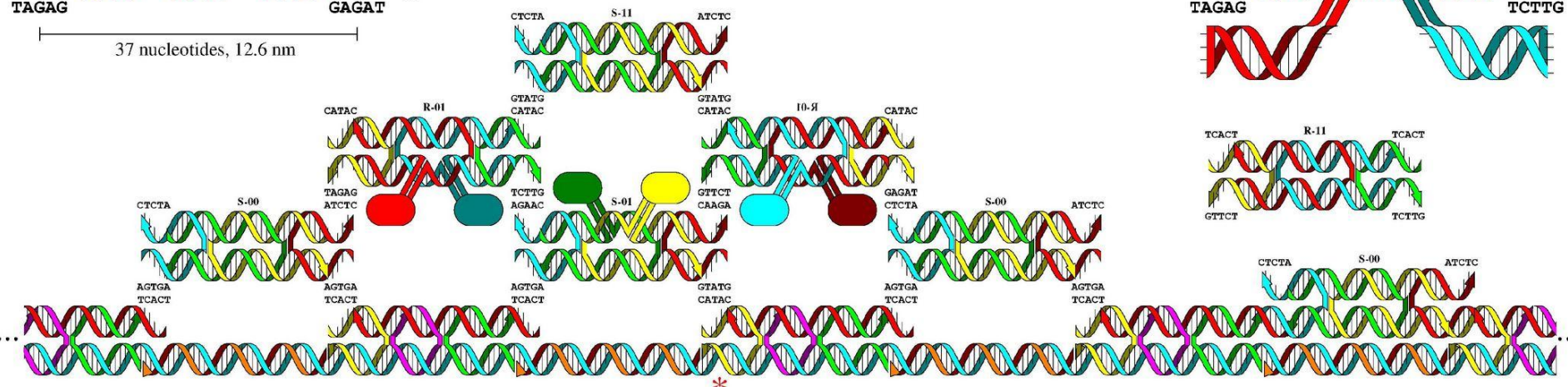
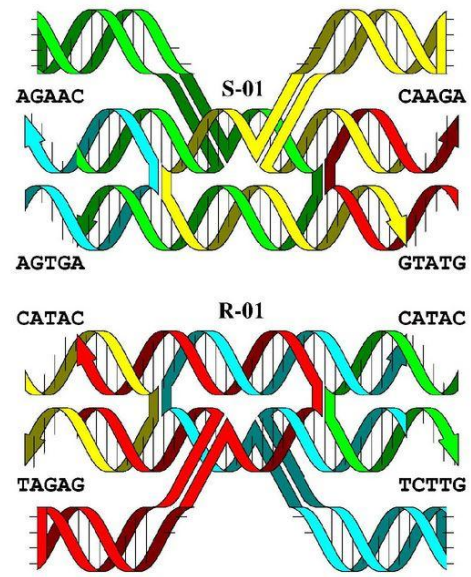
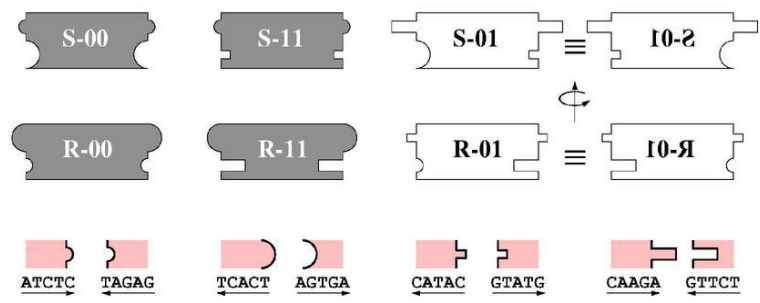
*Algorithmic Self-Assembly
of DNA Sierpinski
Triangles*, Rothmund,
Papadakis, Winfree; PLOS
Biology (2004)

self assembly

B



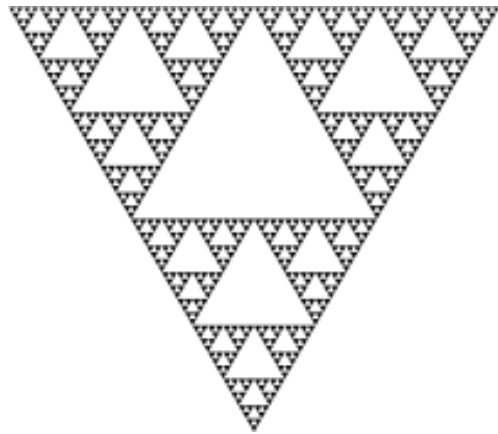
DAO-E



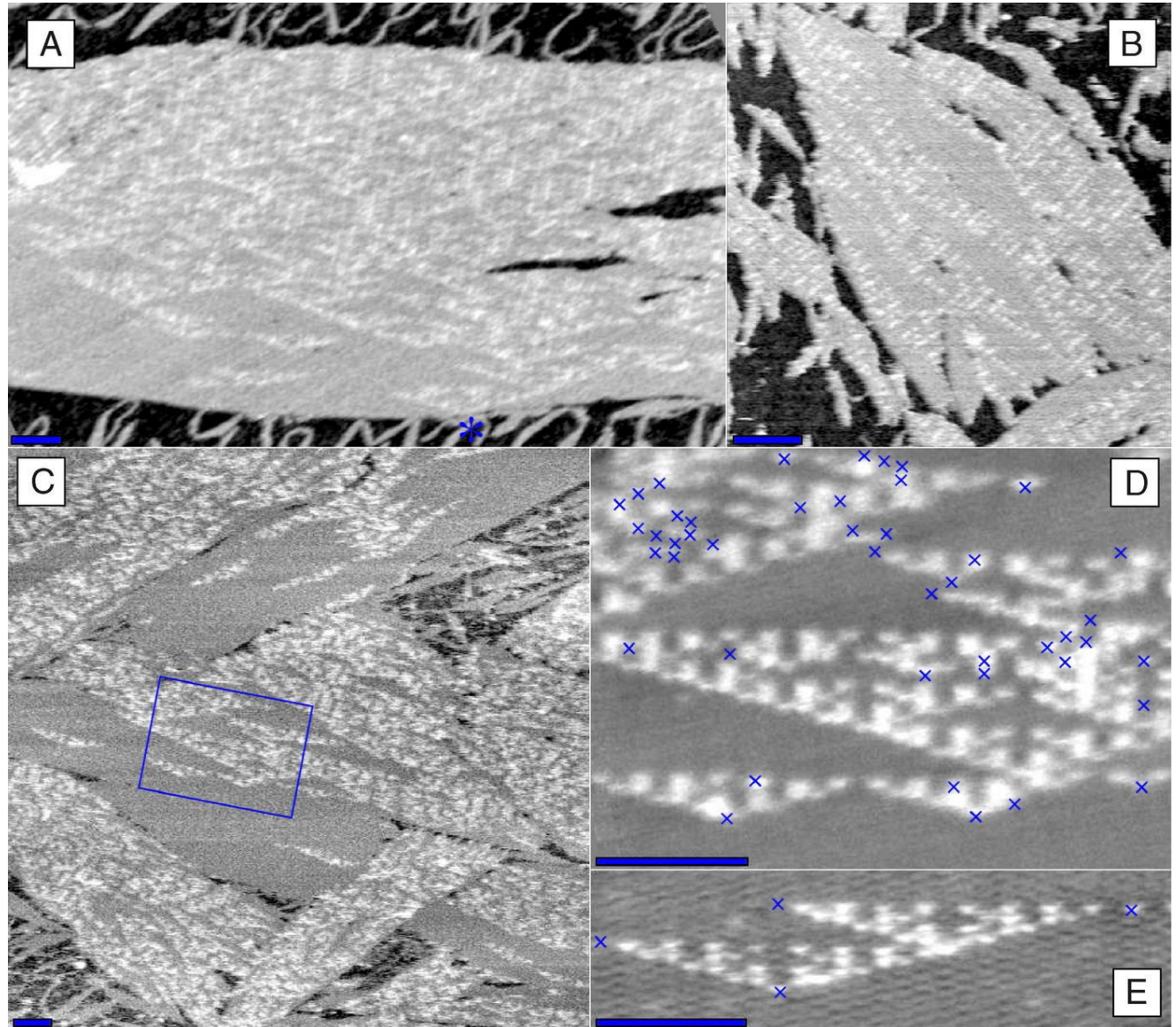
<http://dx.doi.org/10.1371/journal.pbio.0020424>

Algorithmic Self-Assembly of DNA Sierpinski Triangles
Rothenmund, Papadakis, Winfree; PLOS Biology (2004)

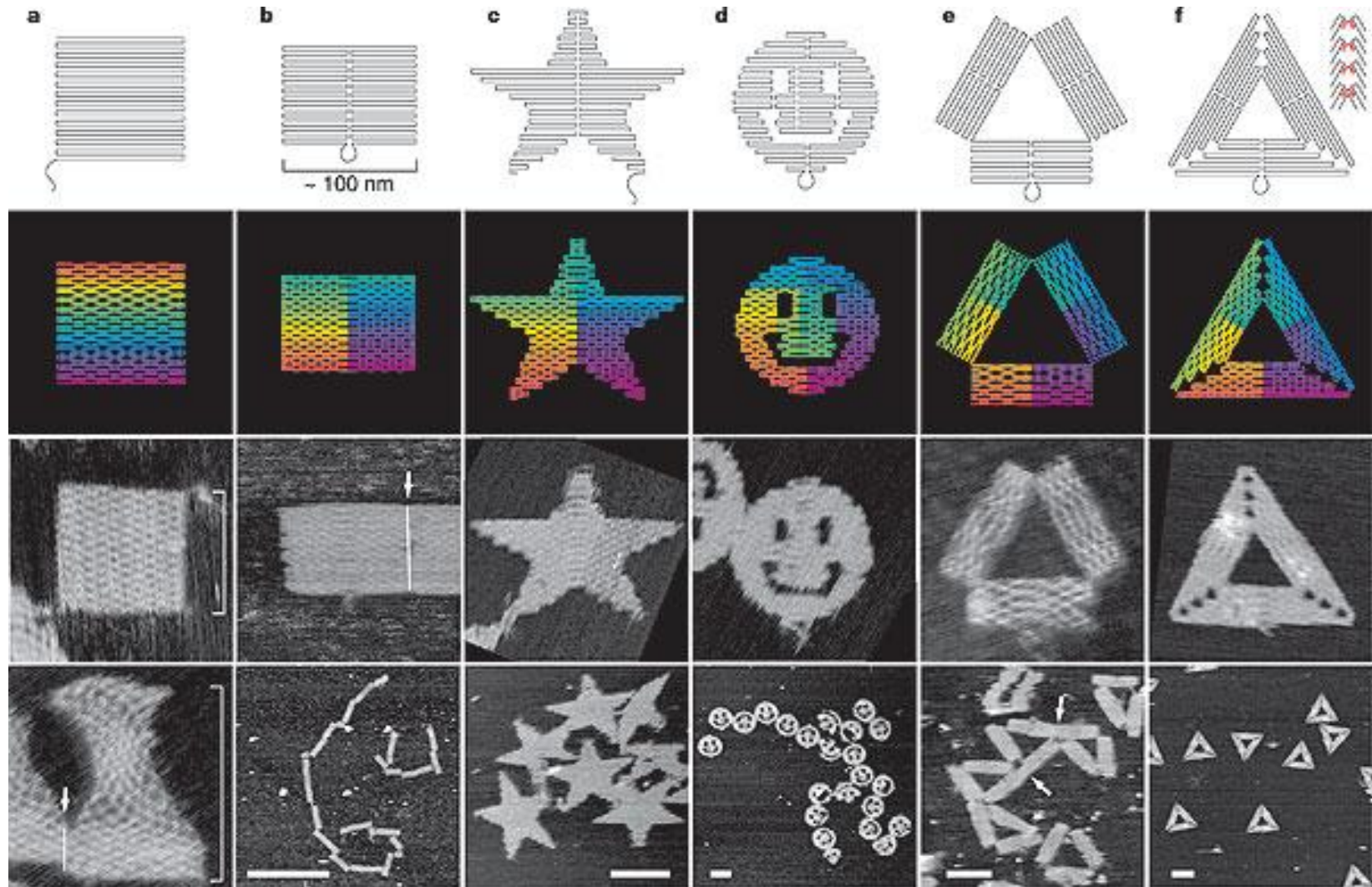
self assembly



Sierpinski

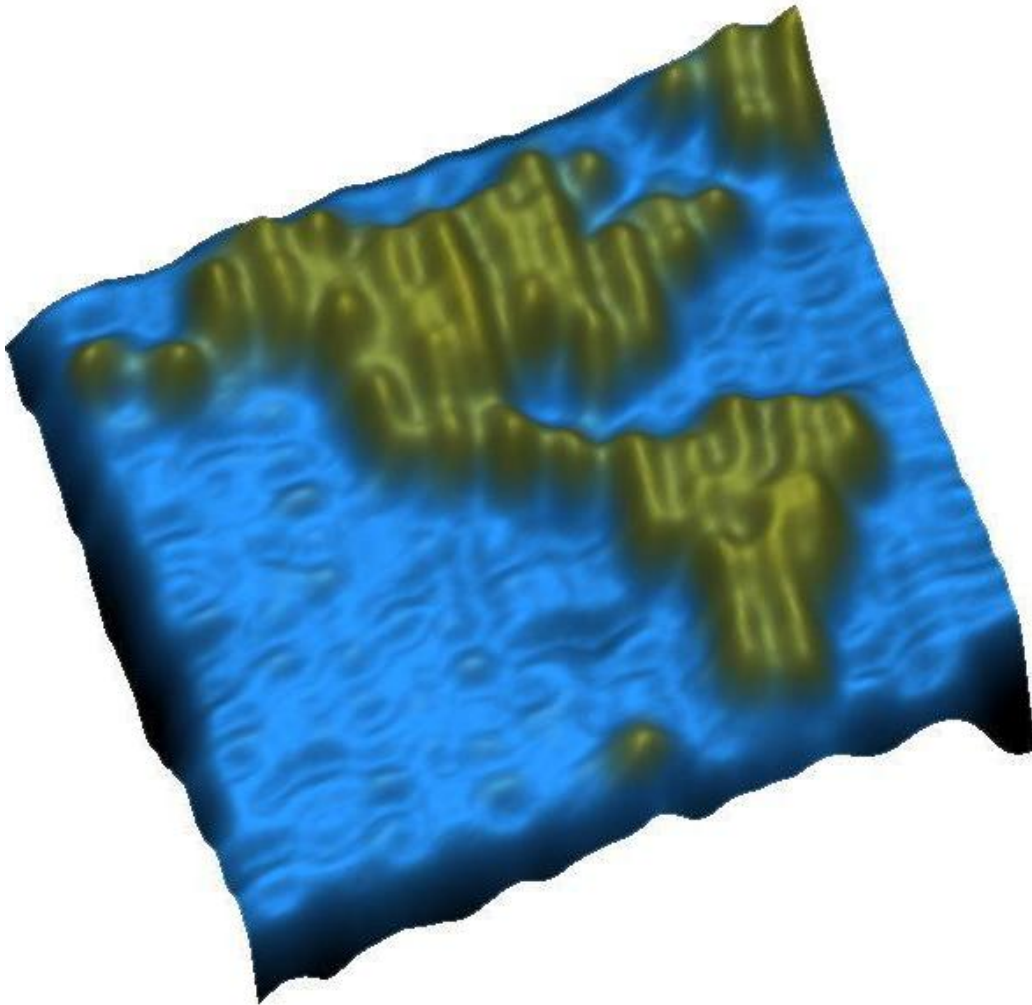


self assembly: DNA origami



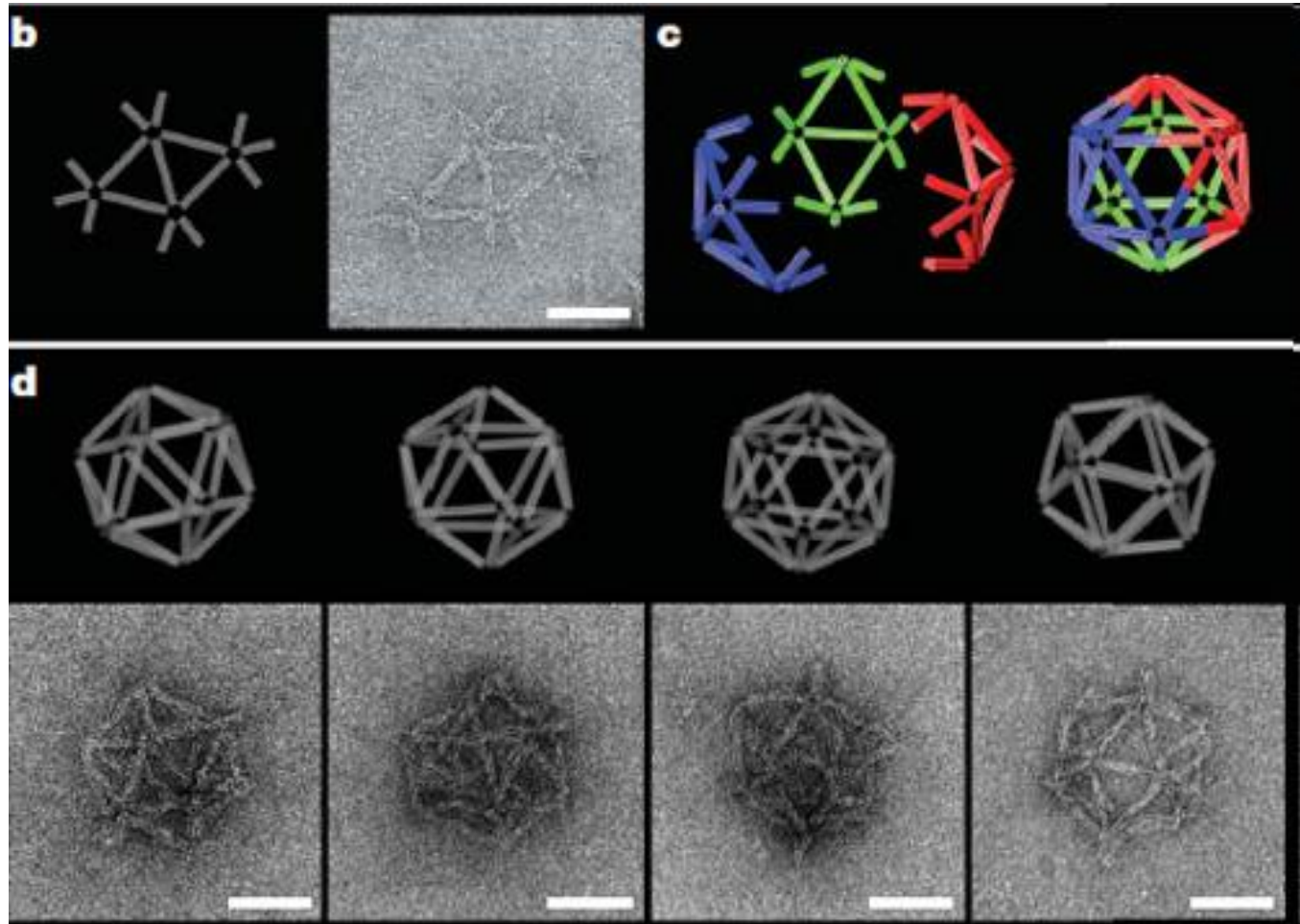
Folding DNA to create nanoscale shapes and patterns
Paul W. K. Rothemund, *Nature* 440, 297-302 (16 March 2006)

Self Assembly: DNA origami



Paul W. K. Rothemund, <http://www.dna.caltech.edu/~pwkr/>

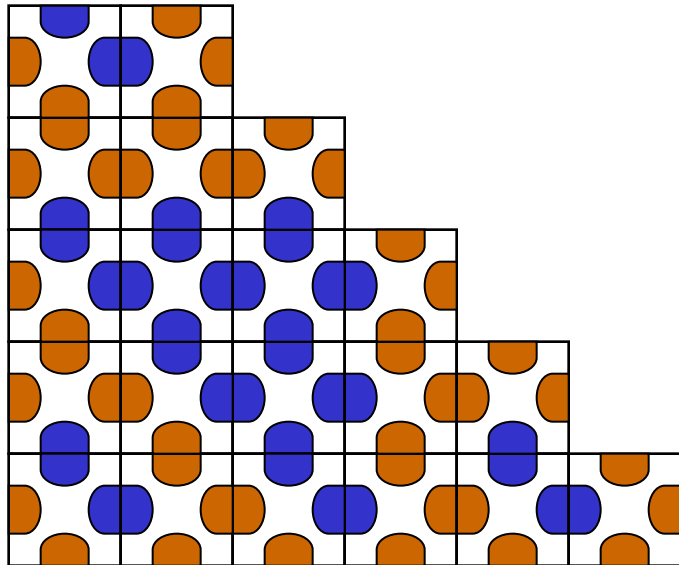
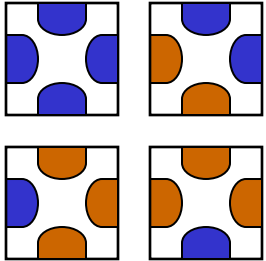
3D DNA origami



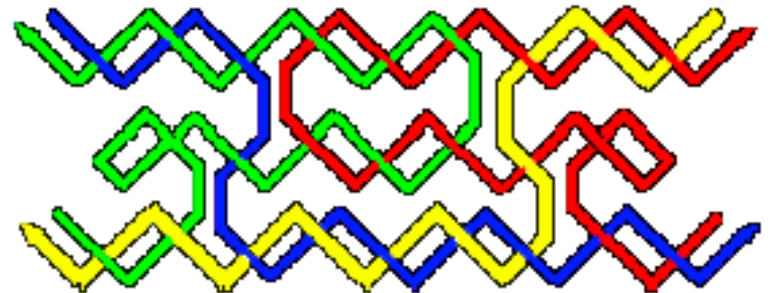
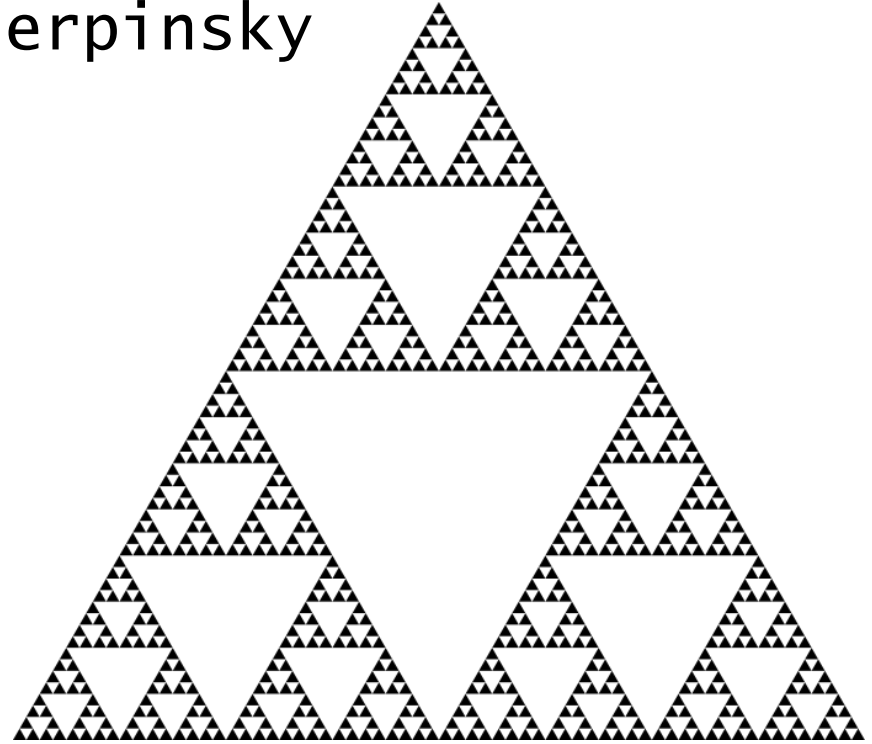
Self-assembly of DNA into nanoscale three-dimensional shapes
S.M. Douglas, H. Dietz, T. Liedl, B. Hogberg, F. Graf, W.M. Shih,
Nature 459, 414-418 (21 May 2009)

self assembly (theory)

wang tiles

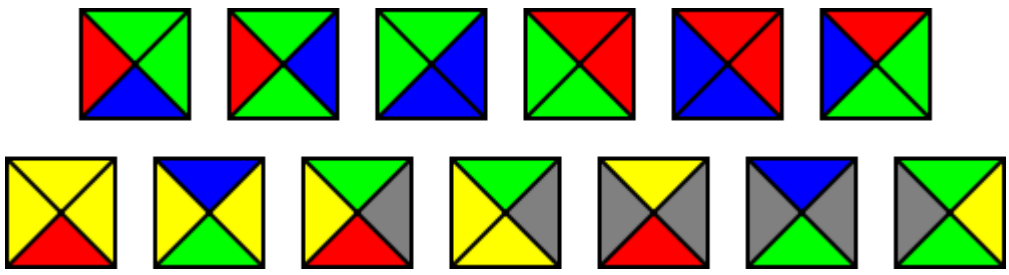
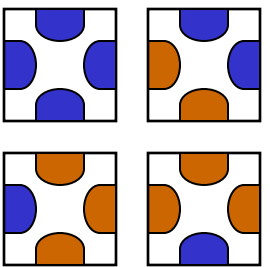


sierpinsky



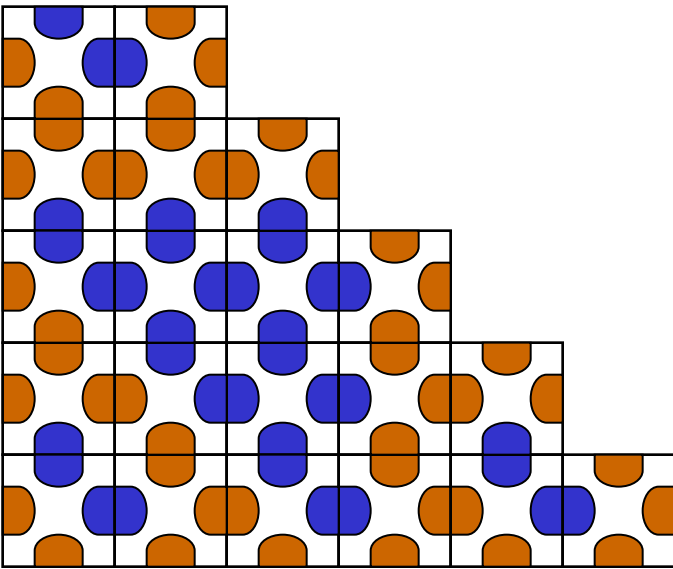
self assembly

wang tiles

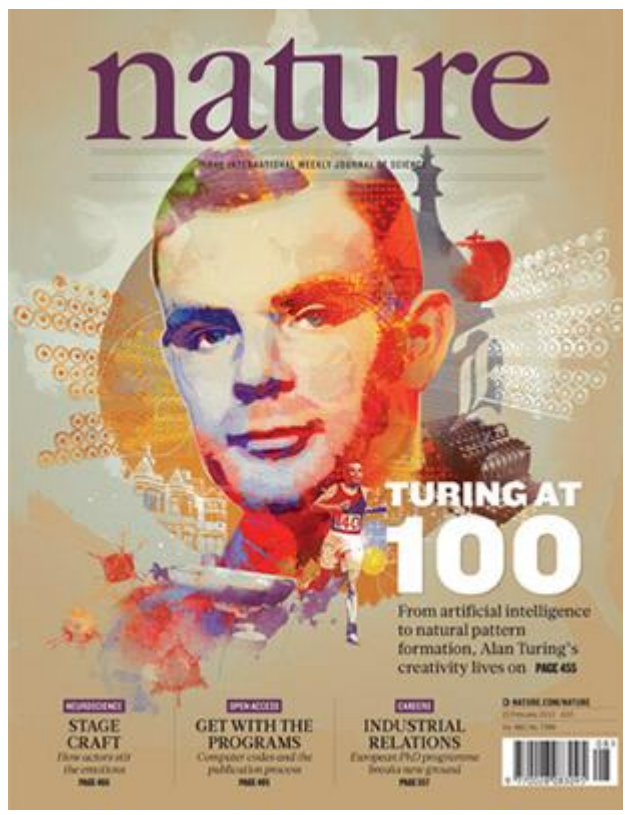
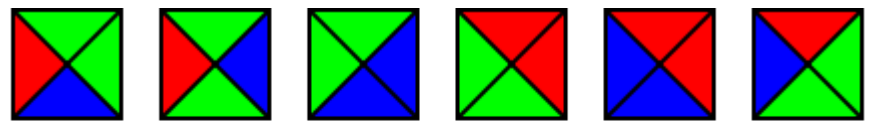


can we tile
the plane?

undecidable



self assembly



can we tile
the plane?

undecidable

rectangle

NP-complete

strip

PSPACE-comp1

conclusion

take home message

DNA can be used for applications it was not “intended” for

computing
a very interesting
proof of concept

find niche

