

Media Technology  
Artificial Intelligence  
for Cocktail Parties



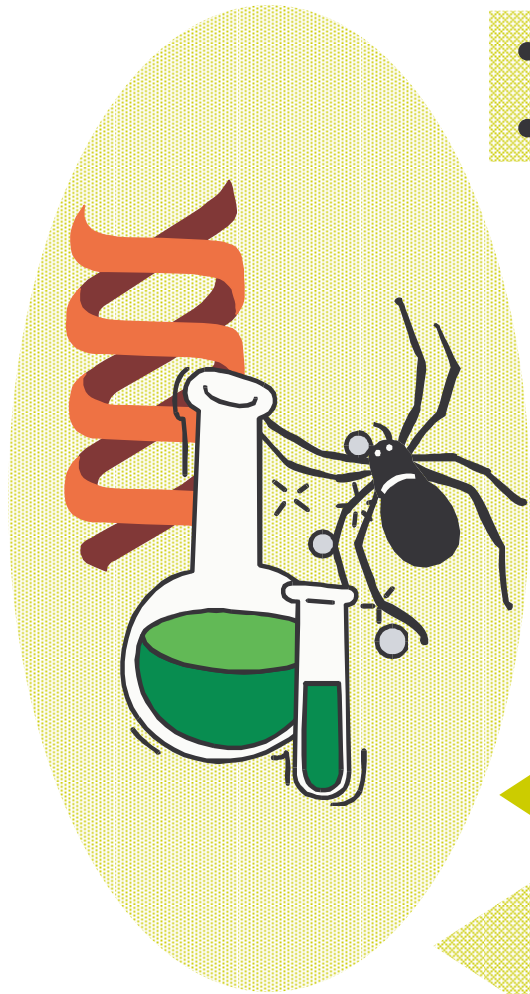
# Computer in a TestTube

DNA computing

Hendrik Jan Hoogeboom  
Computer Science (LIACS)  
14 April 2008

# natural computation

- genetic algorithms
- neural networks



DNA computing

bio-informatics

# Len Adleman

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



<http://www.usc.edu/dept/molecular-science/fm-adleman.htm>

## 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.”**

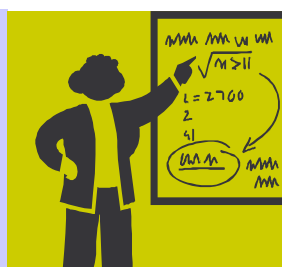
Adleman created the first computer to use DNA to solve a problem. He was struck by the **parallels between DNA**, with its long ribbon of information, and the **theoretical computer** known as the Turing Machine.

Adleman tackled the famous **'travelling salesman'** problem - finding the shortest route between cities. Such problems rapidly become mind-boggling. The only way is **to examine every possible option**. With many cities, this number is astronomical.

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.

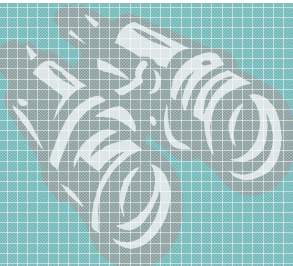
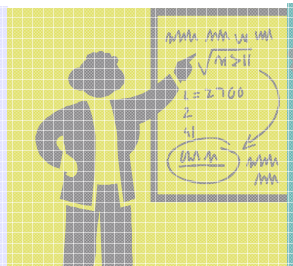
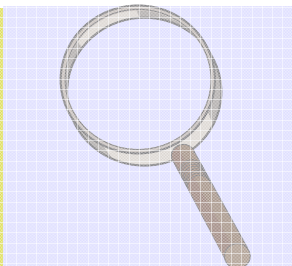
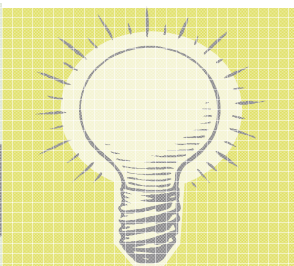
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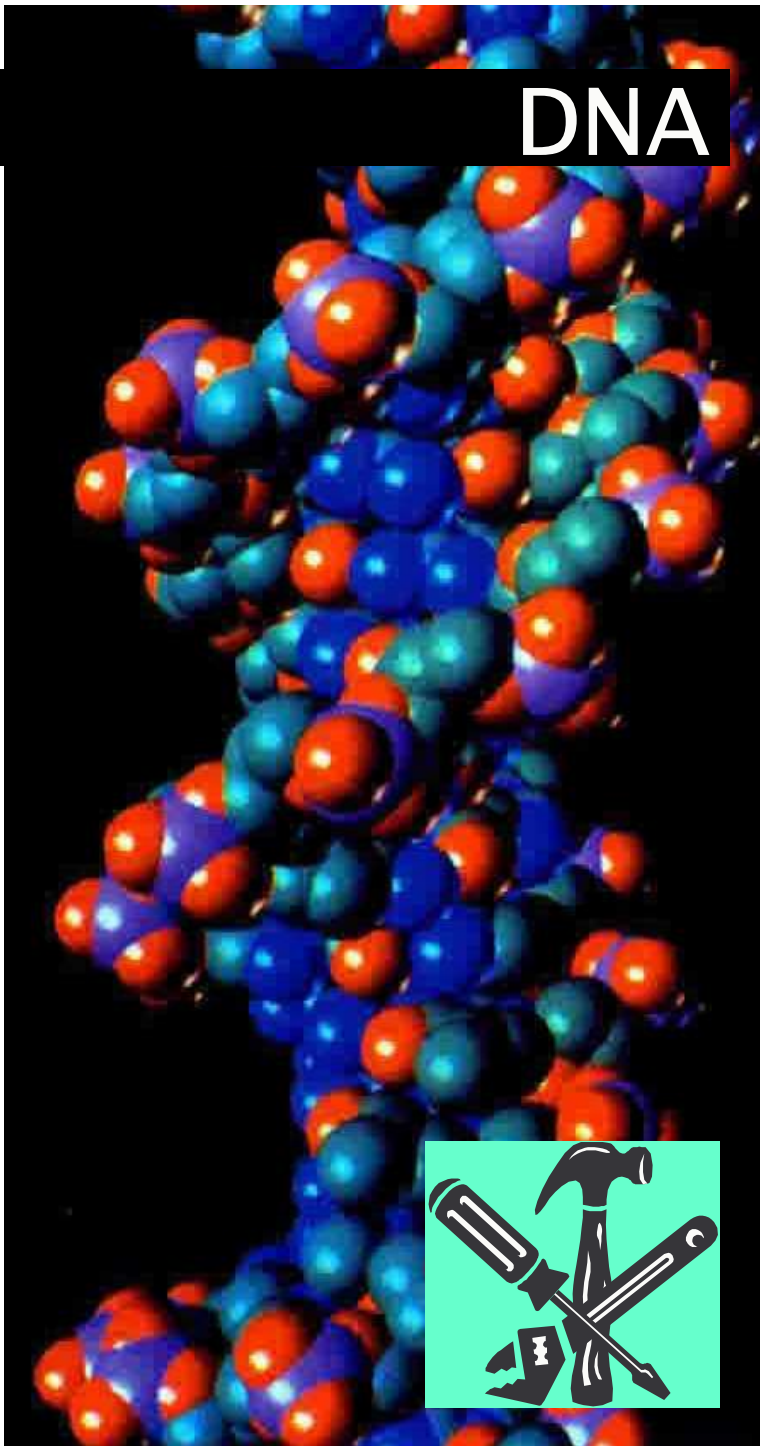
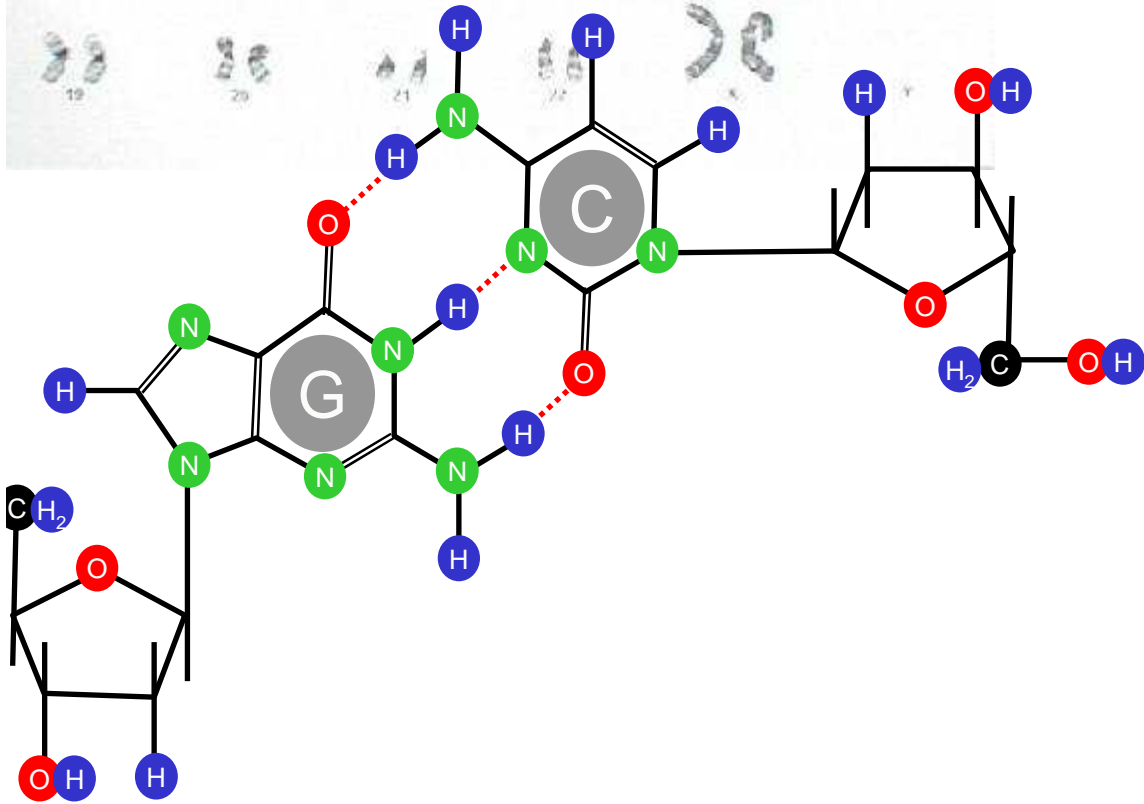
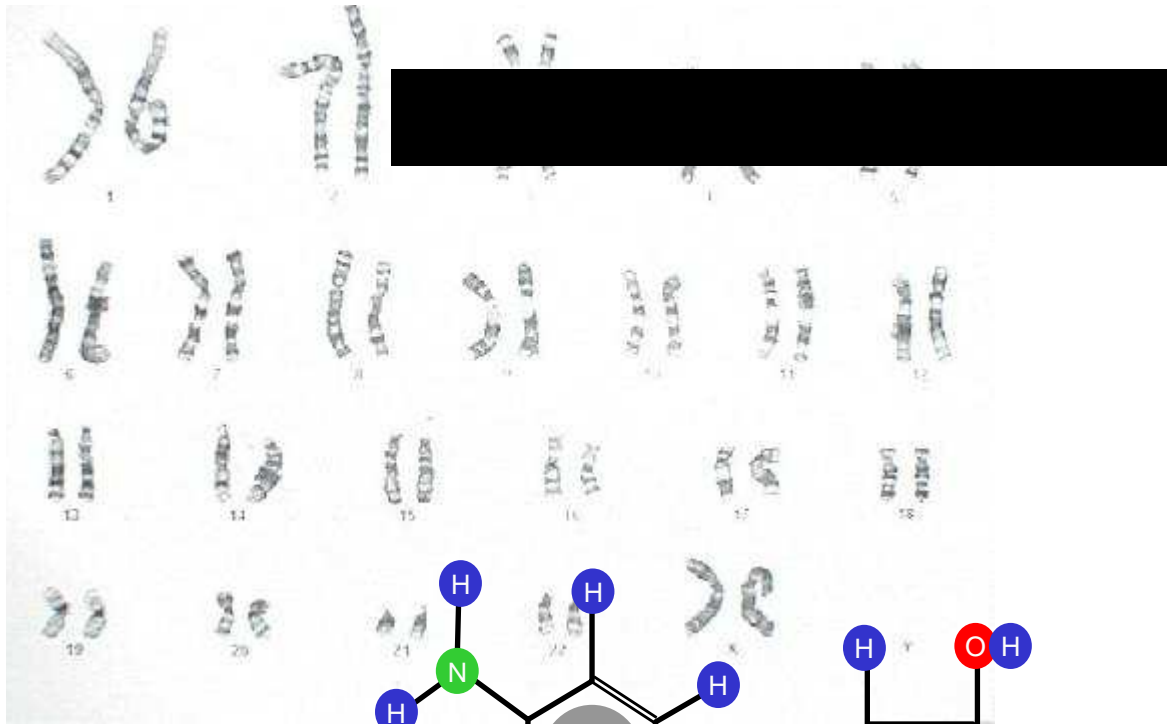
- ❖ DNA ... the tool chest
- ❖ problem complexity ... P & NP  
Hamilton Path Problem
- ❖ Adleman's algorithm
- ❖ comments
- ❖ theory ... Turing machine
- ❖ recent work + future



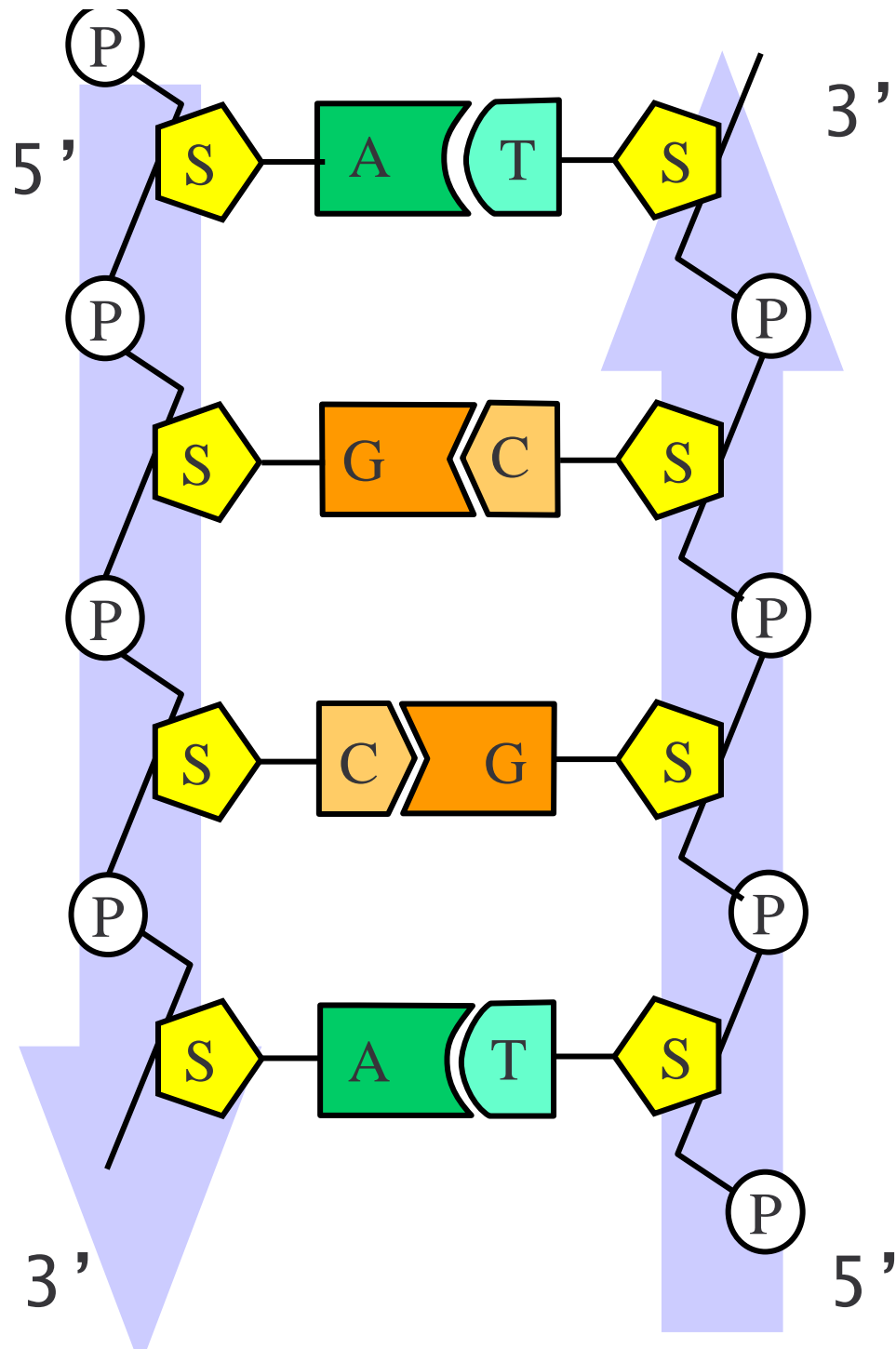
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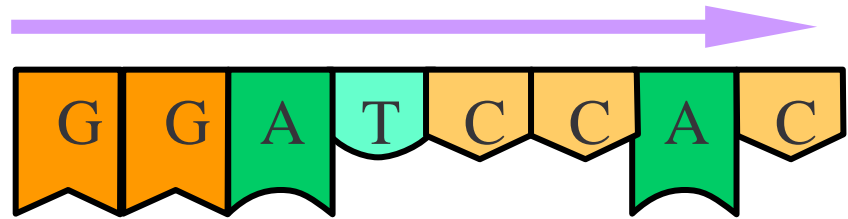
**DNA**

basepairs  
 Watson & Crick  
 [ & Rosalind Franklin ]

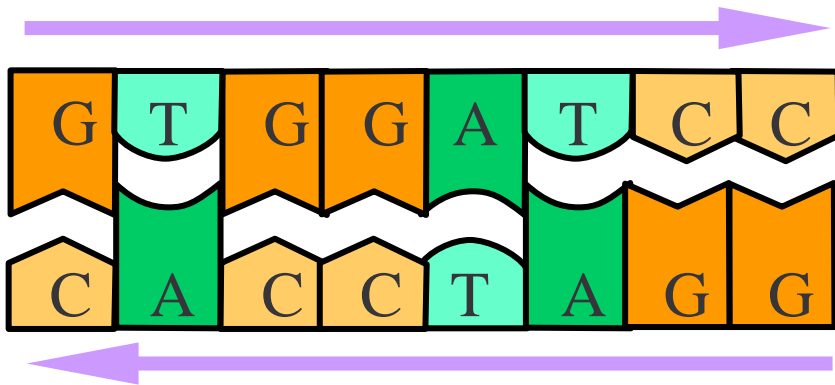
A=T  
 adenine - thymine  
 C≡G  
 guanine - cytosine



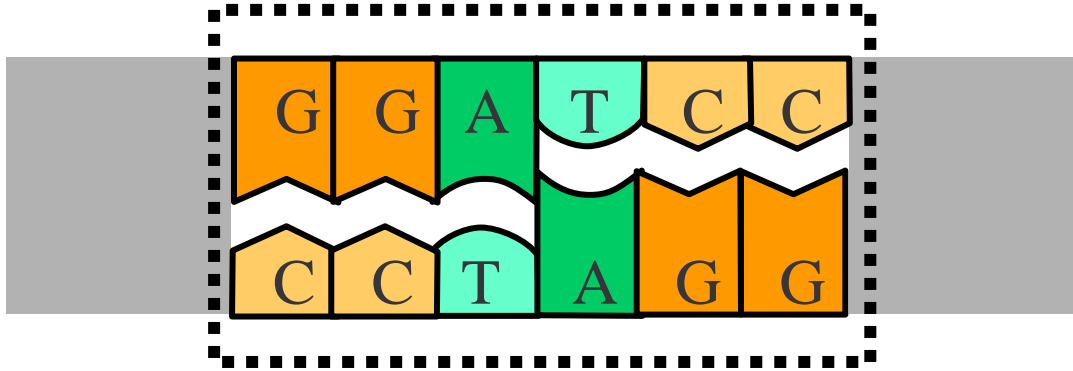
# annealing & denaturing



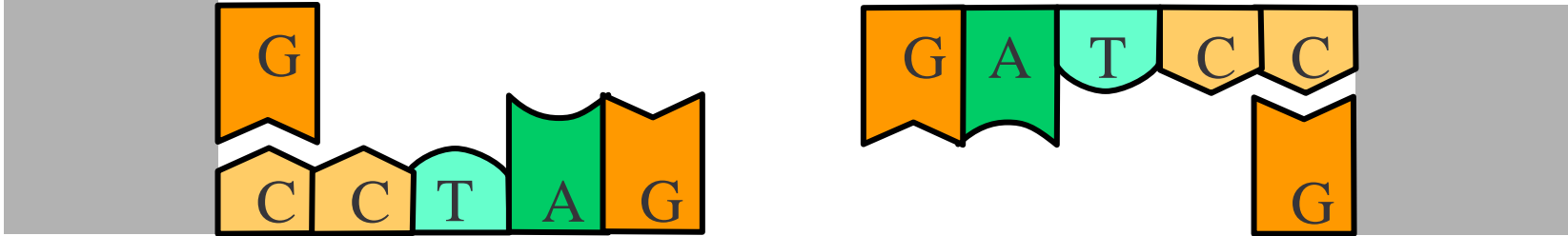
complementary



# restriction enzymes



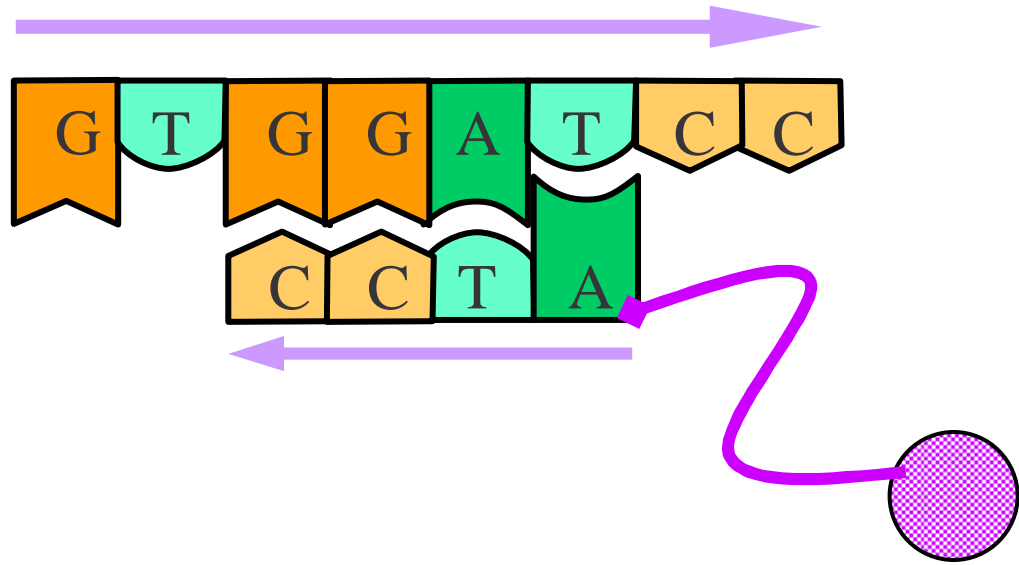
BamHI



*sticky ends*



# selection

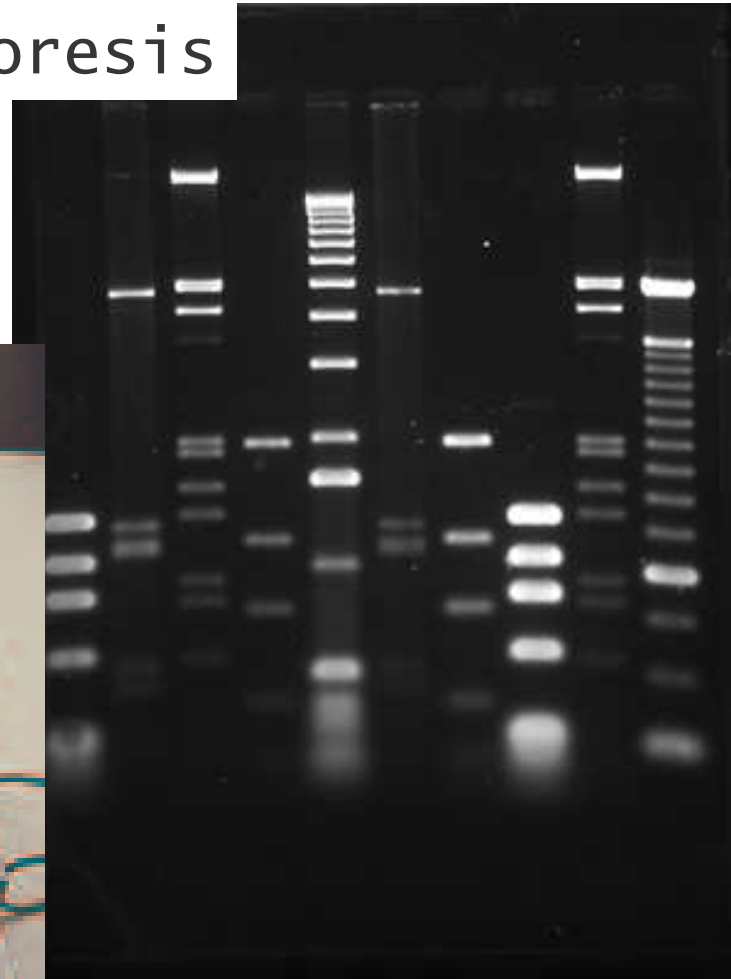


magnetic beads



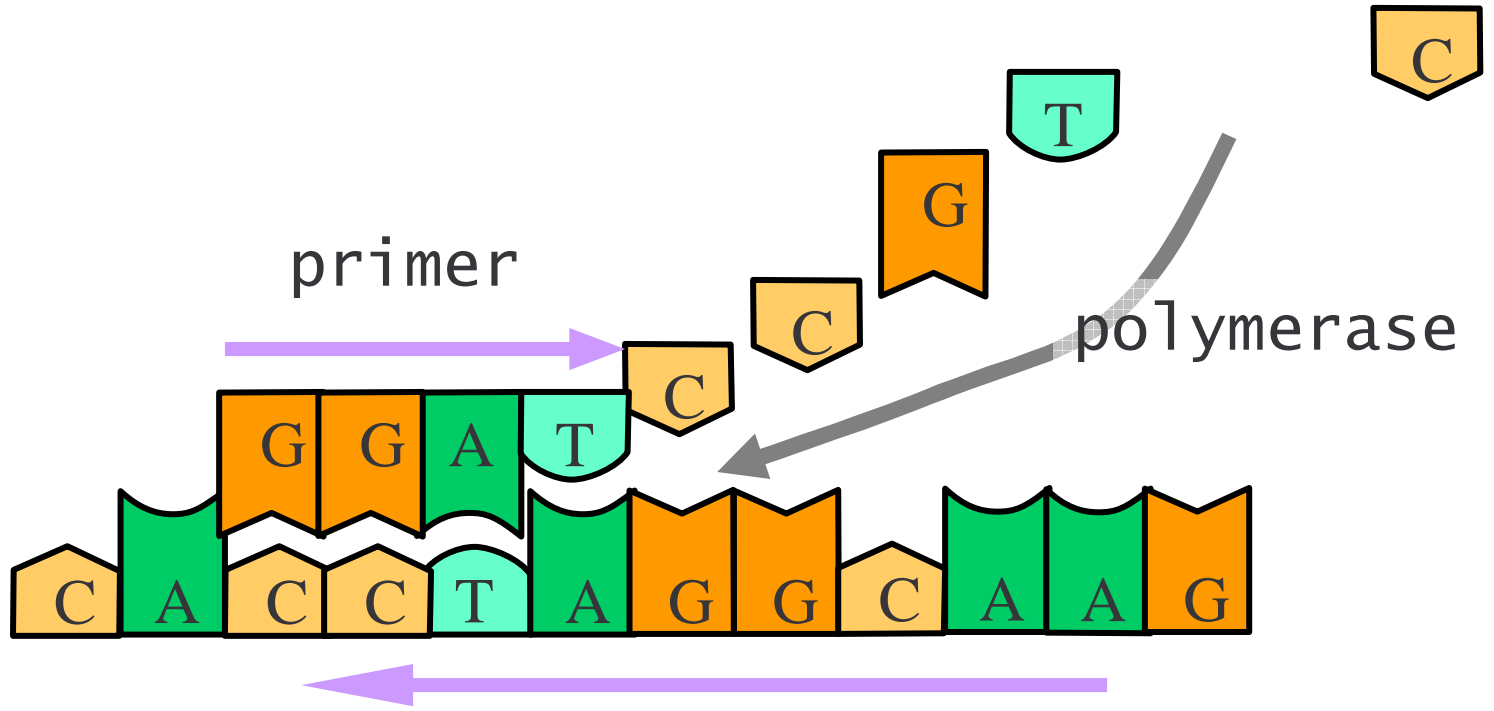
# separation on length

DNA gel electrophoresis



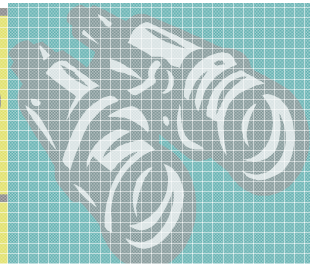
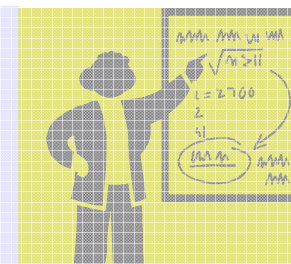
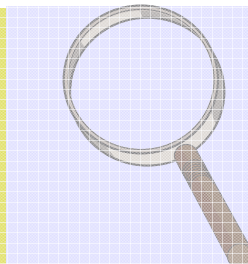
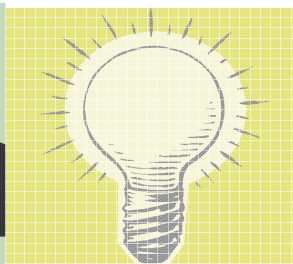
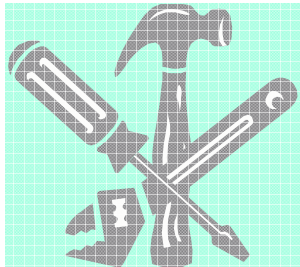
# multiplication / amplification

A



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# complexity

	n=10	30	50	60	second minute day year century
n	$10^{-5}s$	$3 \times 10^{-5}s$	$5 \times 10^{-5}s$	$6 \times 10^{-5}s$	
$n^2$	$10^{-4}s$	$9 \times 10^{-4}s$	$2 \times 10^{-3}s$	$4 \times 10^{-3}s$	
$n^5$	$10^{-1}s$	24 s	1.7 m	13 m	
$2^n$	$10^{-3}s$	18 m	13 d	366 c	
$3^n$	$6 \times 10^{-2}s$	6.5 y	3855 c	$10^{13}$ c	

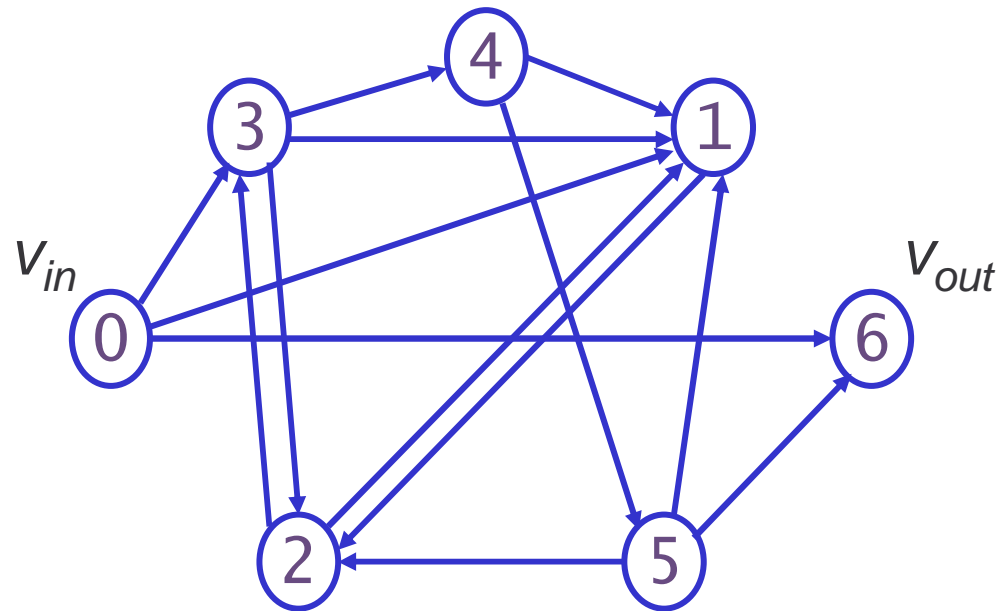
polynomial vs.  
exponential

	now	100x	1000x
n	N	100N	1000N
$n^2$	N	10N	32N
$n^5$	N	2.5N	4N
$2^n$	N	$N+6.6$	$N+10$
$3^n$	N	$N+4.2$	$N+6.3$





# HPP: Hamilton Path Problem



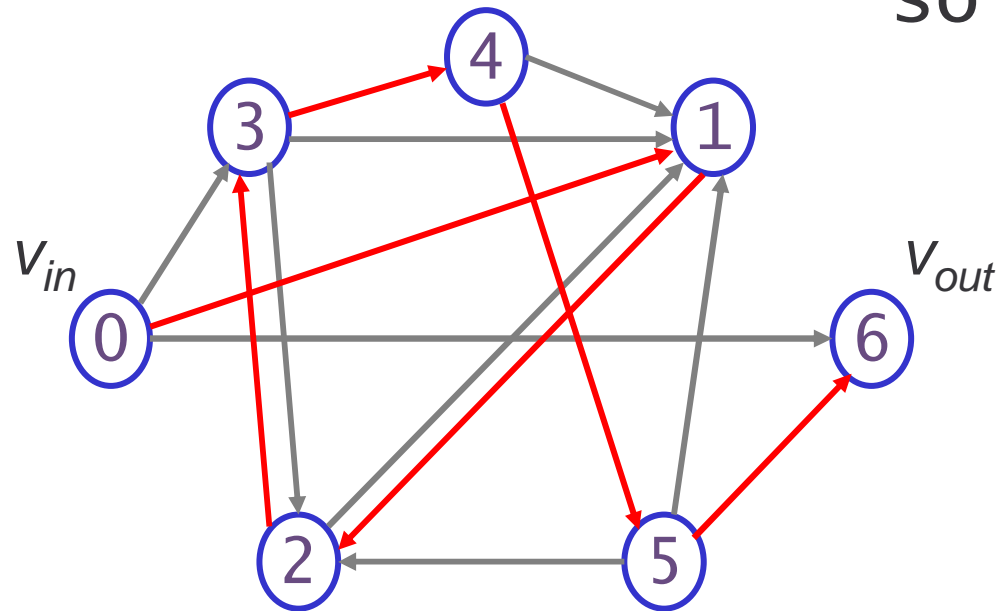
*'travelling  
salesman'*

given: points and connections  
question: is there a path that visits  
each point **exactly once** ?



# HPP: Hamilton Path Problem

solution

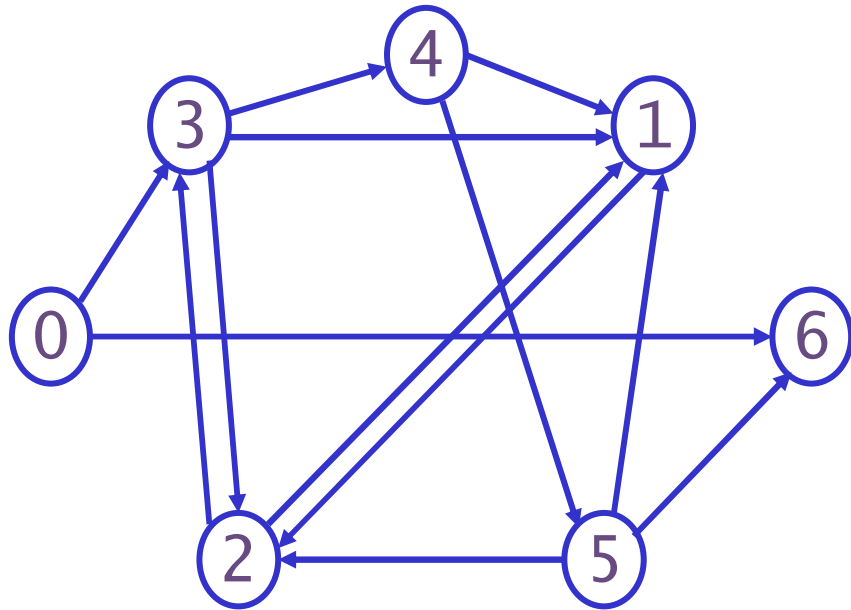


*'travelling salesman'*

given: points and connections  
question: is there a path that visits  
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# HPP: Hamilton Path Problem

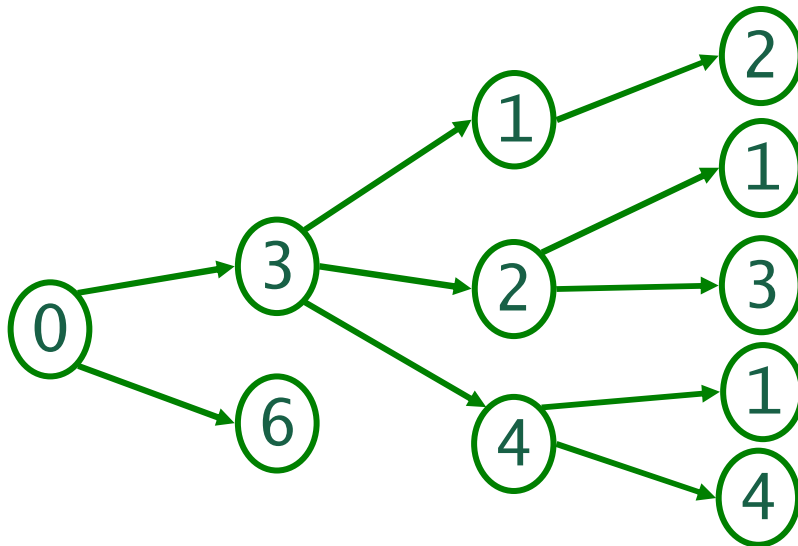


no solution?

exponential time:  
try all possibilities

representative  
'NP complete'

heuristics



# complexity (theory) - P vs. NP

P

polynomial algorithm  
to **find** a solution

NP

polynomial algorithm  
to **verify** a solution

NP-complete

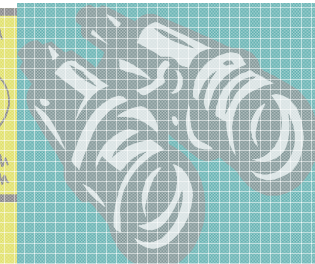
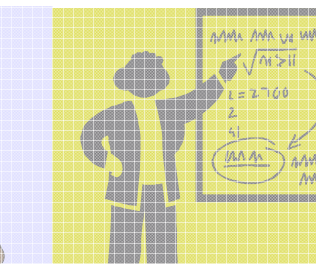
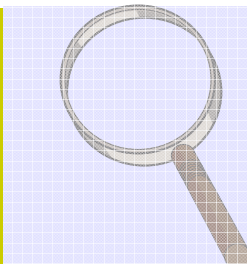
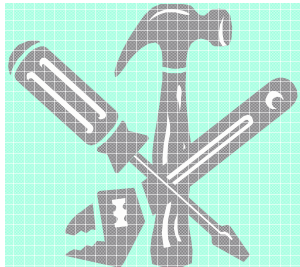
millenium prize problem  $P \stackrel{?}{=} NP$

[www.claymath.org/Millennium\\_Prize\\_Problems/](http://www.claymath.org/Millennium_Prize_Problems/)

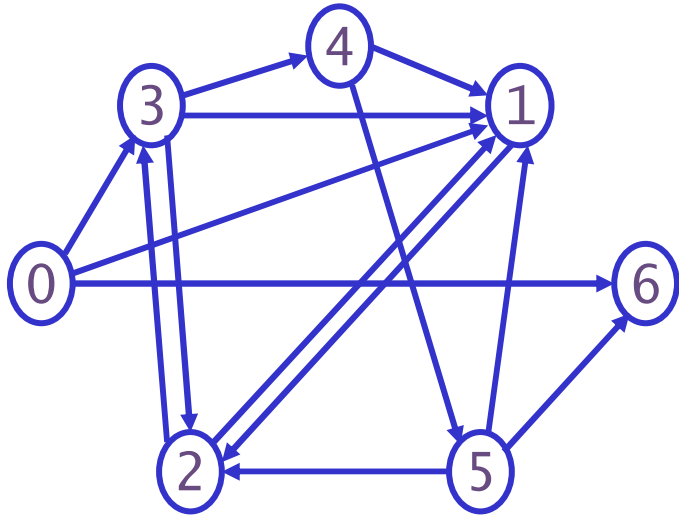


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# Adleman's algorithm



1. generate 'all' paths

keep only paths

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

3. ... that enter  $n$  vertices

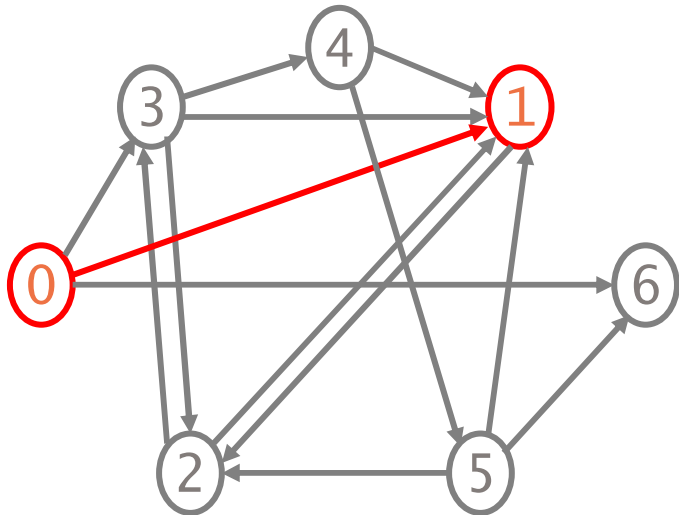
4. ... that enter all vertices

5. if any path remains OK

*'massive parallelism'*



# Adleman's algorithm



0. coding the graph

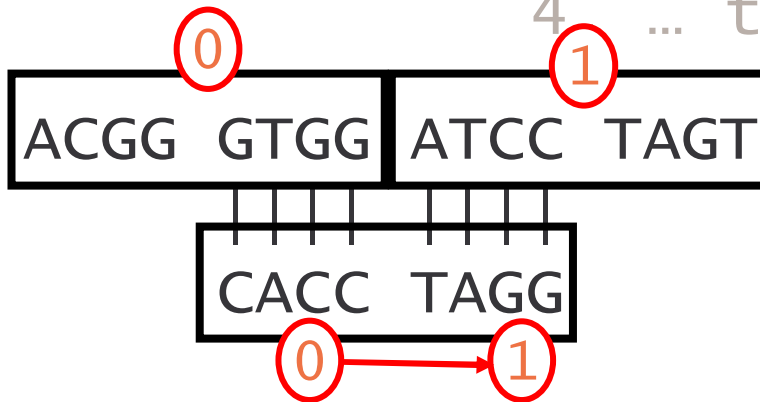
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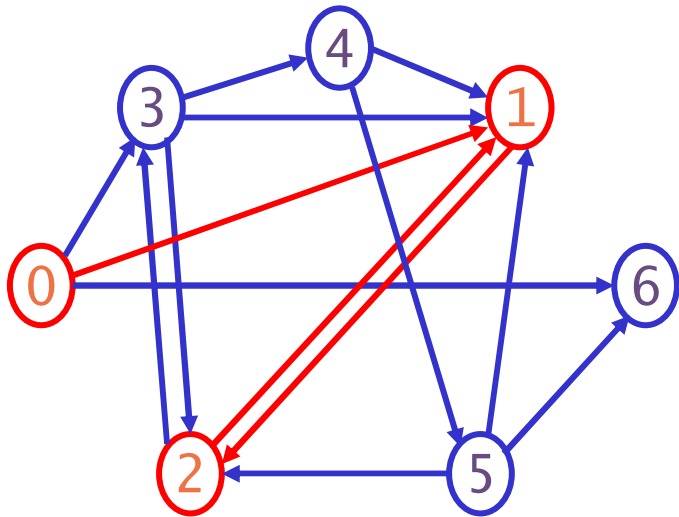
4. ... that enter all vertices



any path remains OK



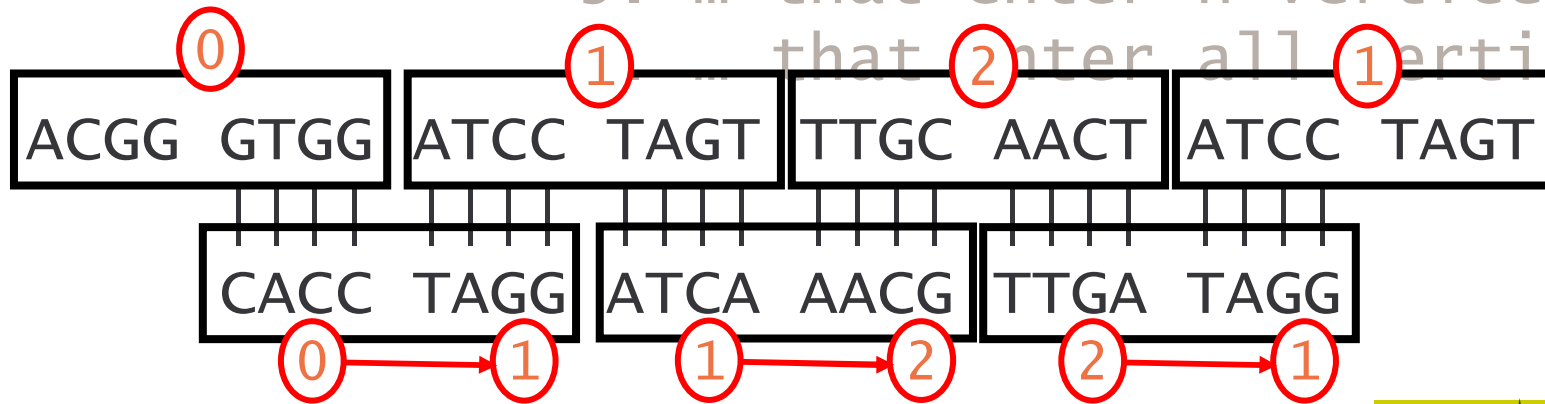
# Adleman's algorithm



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

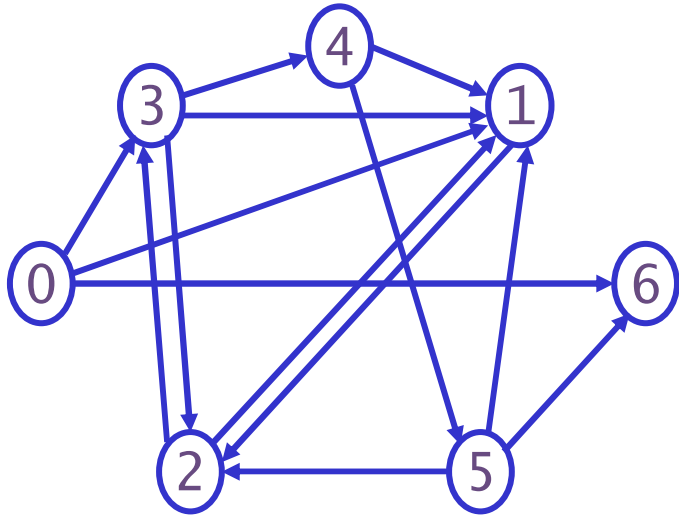
keep only paths

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





# Adleman's algorithm



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

keep only paths

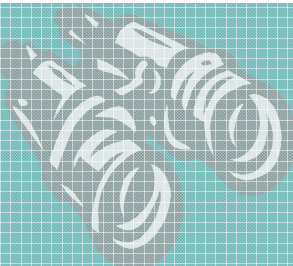
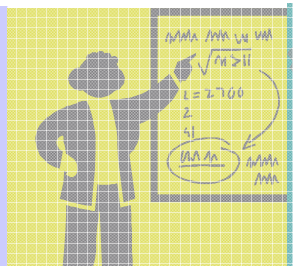
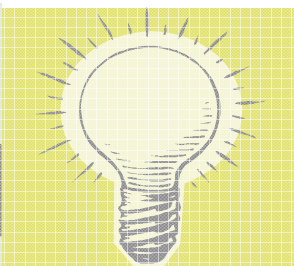
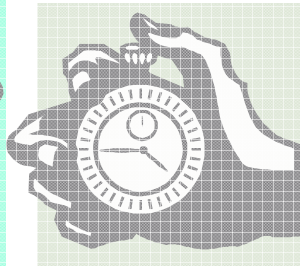
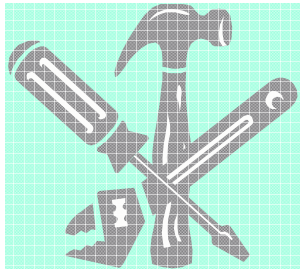
2. ... from  $v_{in}$  to  $v_{out}$
3. ... that enter  $n$  vertices
4. ... that enter all vertices
5. if any path remains OK

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



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- “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

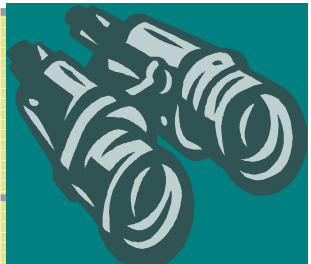
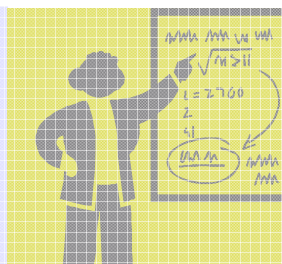
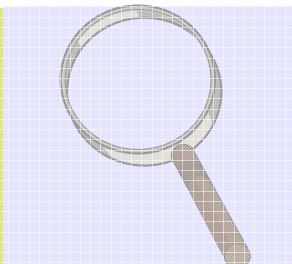
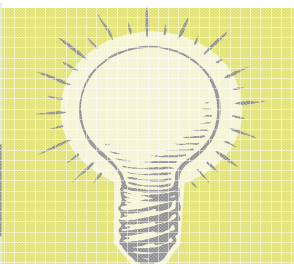
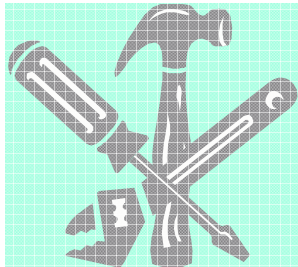
:)

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

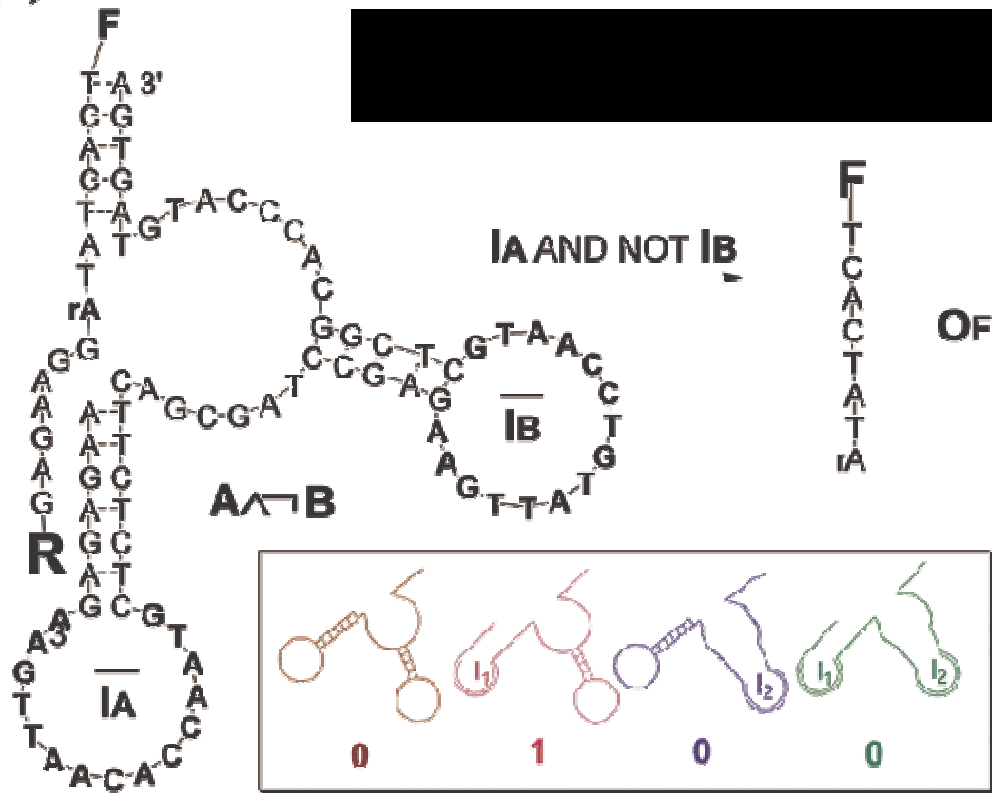


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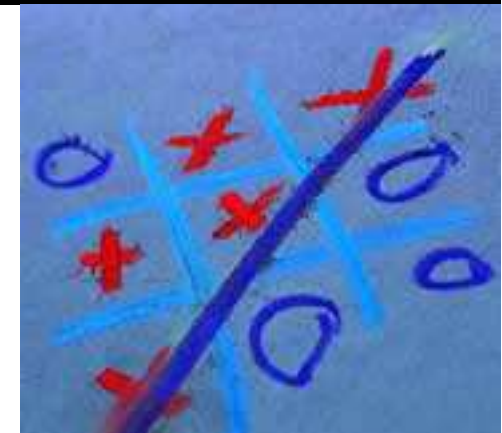
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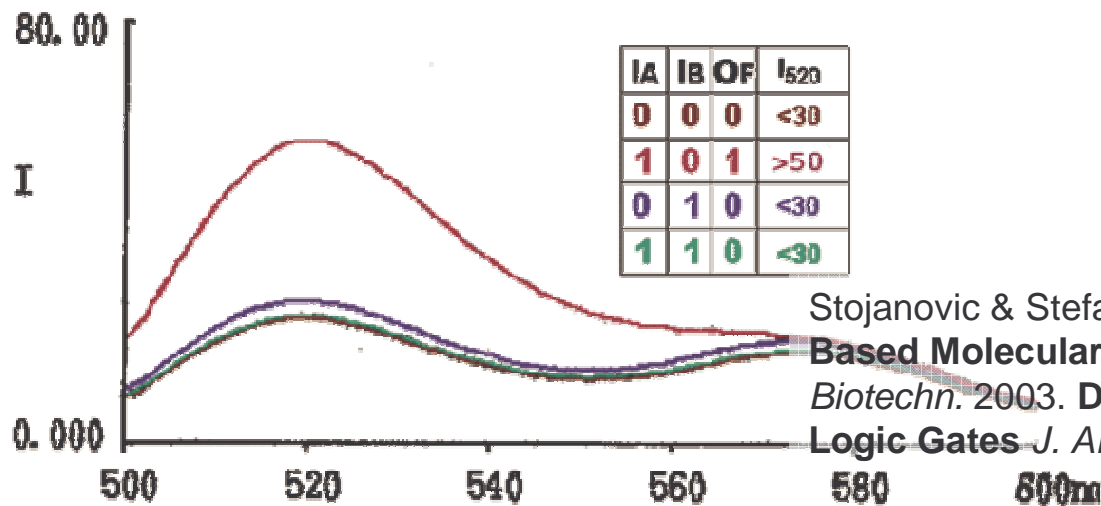
(a)



in Nature

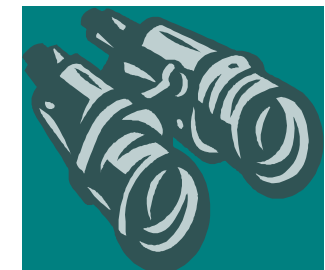


(b)



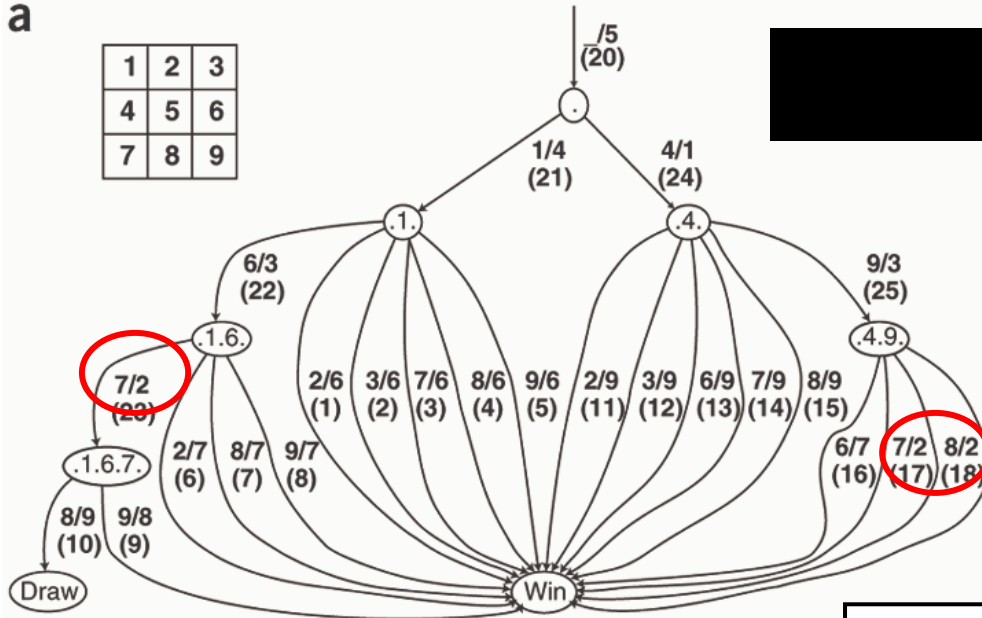
Logic gates  
fluorescence

Stojanovic & Stefanovic, **Deoxyribozyme-Based Molecular Automaton**. *Nature Biotechnol.* 2003. **Deoxyribozyme-Based Logic Gates** *J. Am. Chem. Soc.* 2002

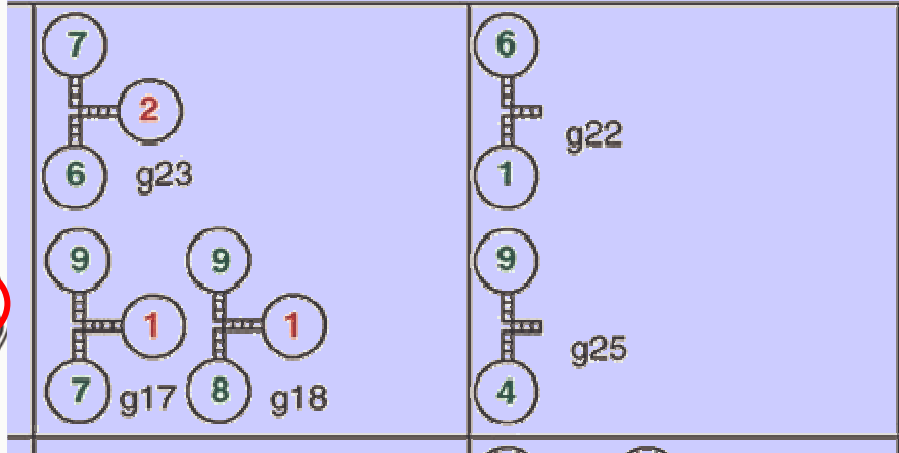


a

1	2	3
4	5	6
7	8	9



in Nature



b

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

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

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

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

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

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

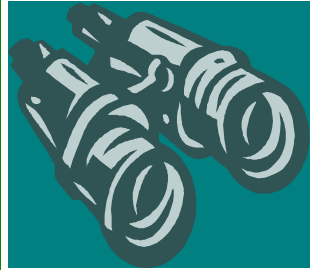
$$o_7 = \underbrace{(i_2 \wedge i_6 \wedge \neg i_7)}_{\text{edge (6)}} \vee \underbrace{(i_6 \wedge i_8 \wedge \neg i_7)}_{\text{edge (7)}} \vee \underbrace{(i_6 \wedge i_9 \wedge \neg i_7)}_{\text{edges (8) and (16)}} \vee \underbrace{(i_9 \wedge i_2 \wedge \neg i_1)}_{\text{edge (19)}}$$

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

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

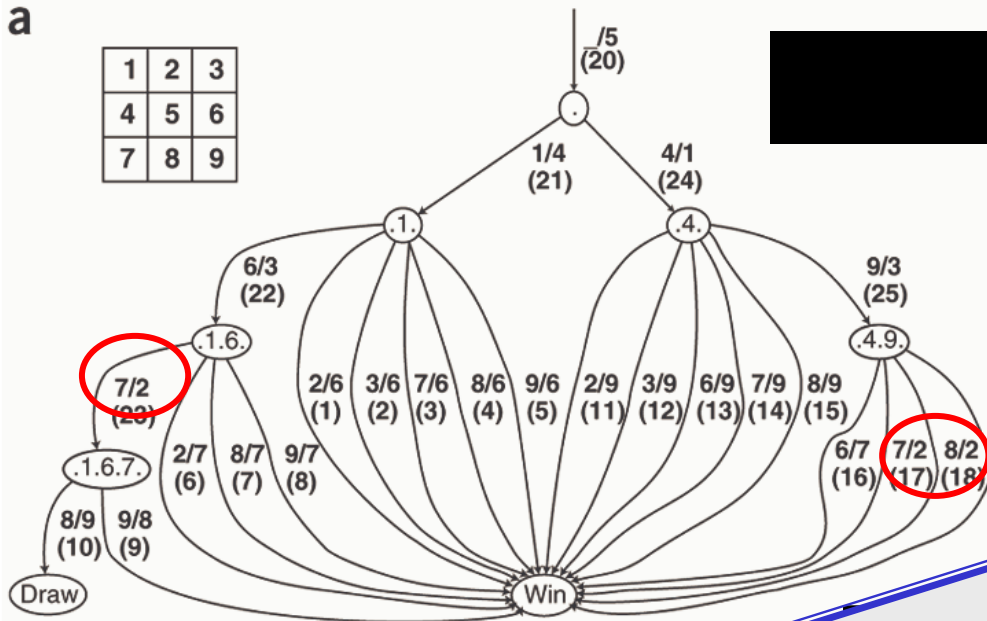
$$O_2 = (i_6 \wedge i_7 \wedge \neg i_2) \vee (i_7 \wedge i_9 \wedge \neg i_1) \vee (i_8 \wedge i_9 \wedge \neg i_1)$$

$i_1$	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

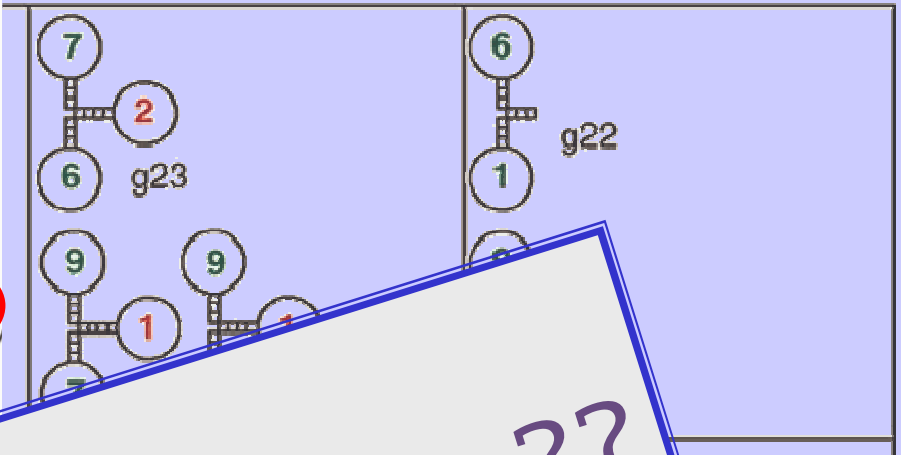


a

1	2	3
4	5	6
7	8	9



in Nature



b

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

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

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

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

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

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

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

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

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

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





## DNA computing today

“There are many practical hurdles. Even with the best techniques of today, **DNA still lags behind silicon computers,**” says Ehud Shapiro. Instead, he advocates creating DNA devices that can do things, and **go to places,** that silicon can't - such as **inside our cells,** to make and control drugs.

...

Ultimately, Seeman hopes to build **DNA scaffolding for electrical circuits,** or for other molecular machines.

...

Yurke is focusing on **DNA machines with moving parts.** In 2000, he and his colleagues devised a set of DNA tweezers

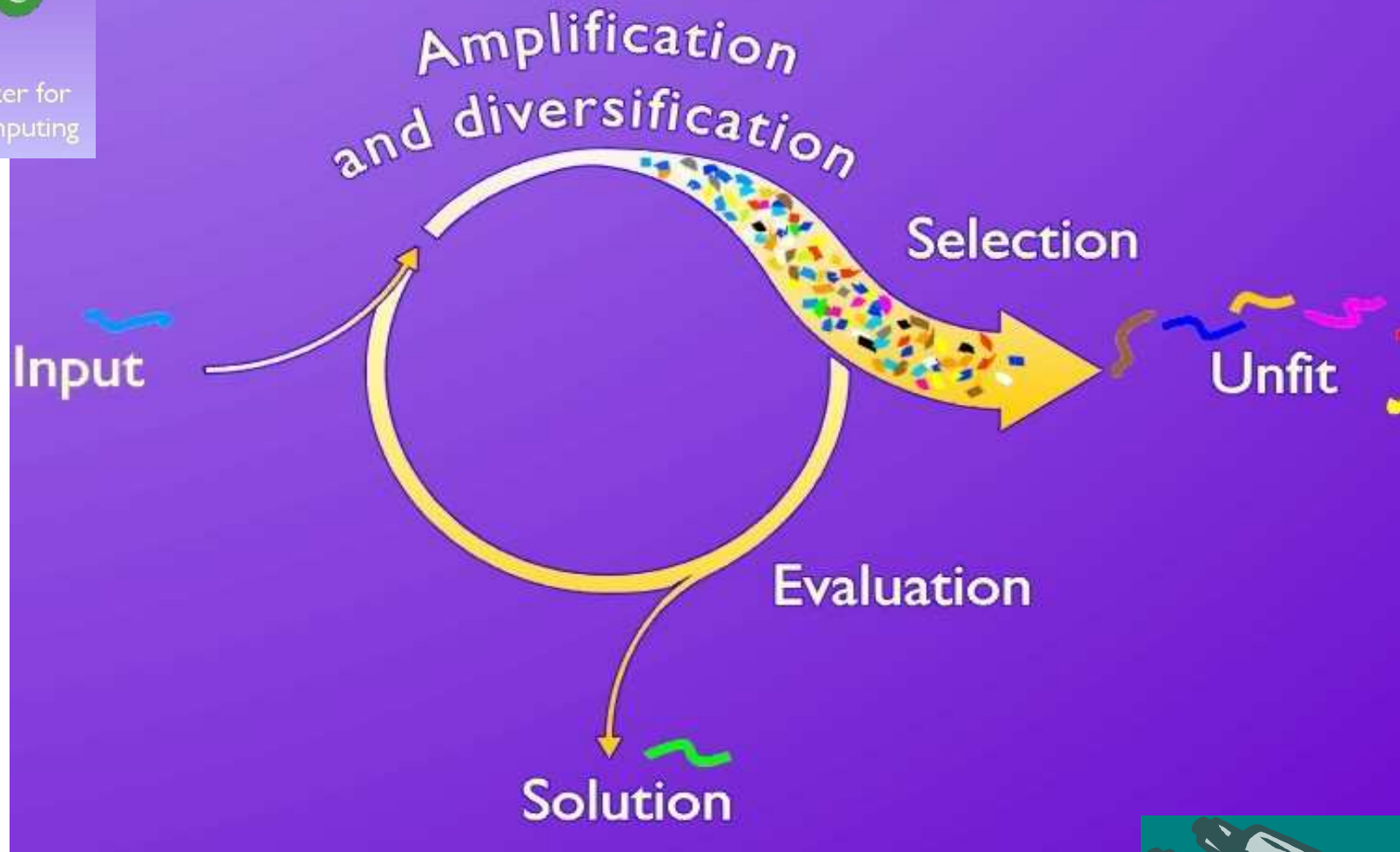
....





Leiden Center for  
Natural Computing

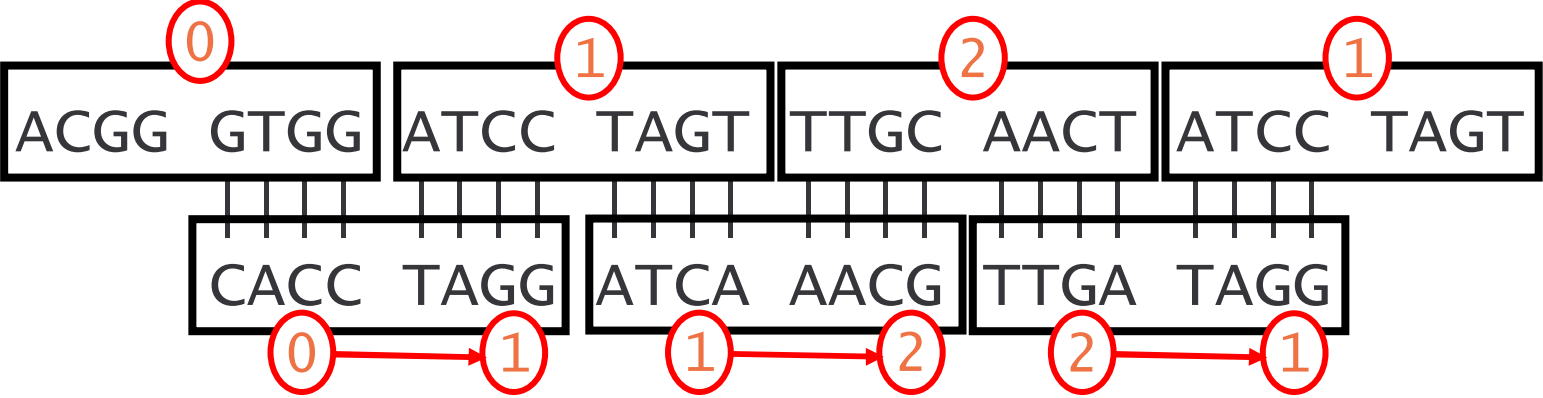
# evolutionary DNA computing



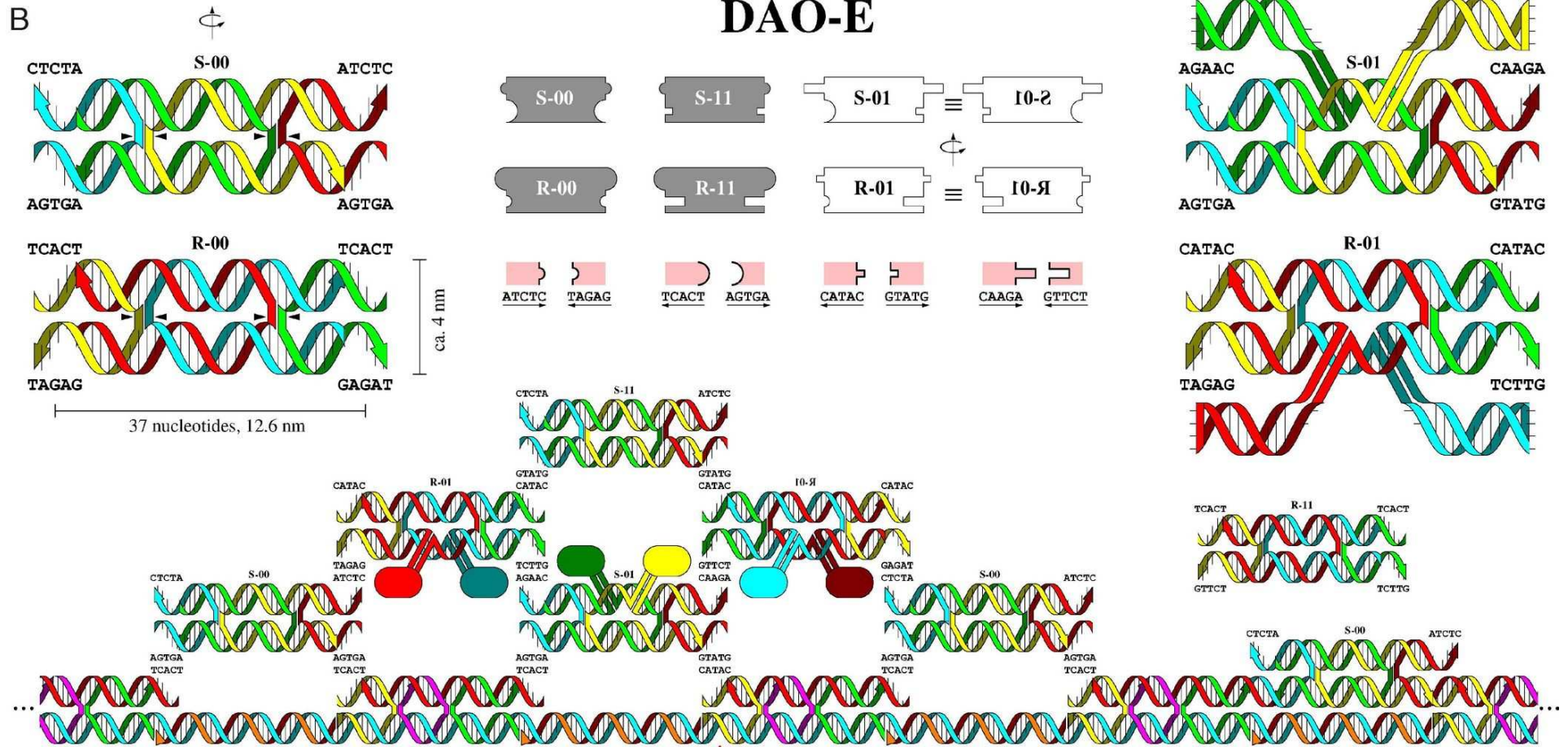
Cross-fertilization between evolutionary computation  
and DNA-based computing T.Back; J.N. Kok; G. Rozenberg  
Proceedings 1999 Evolutionary Computation.



# self assembly



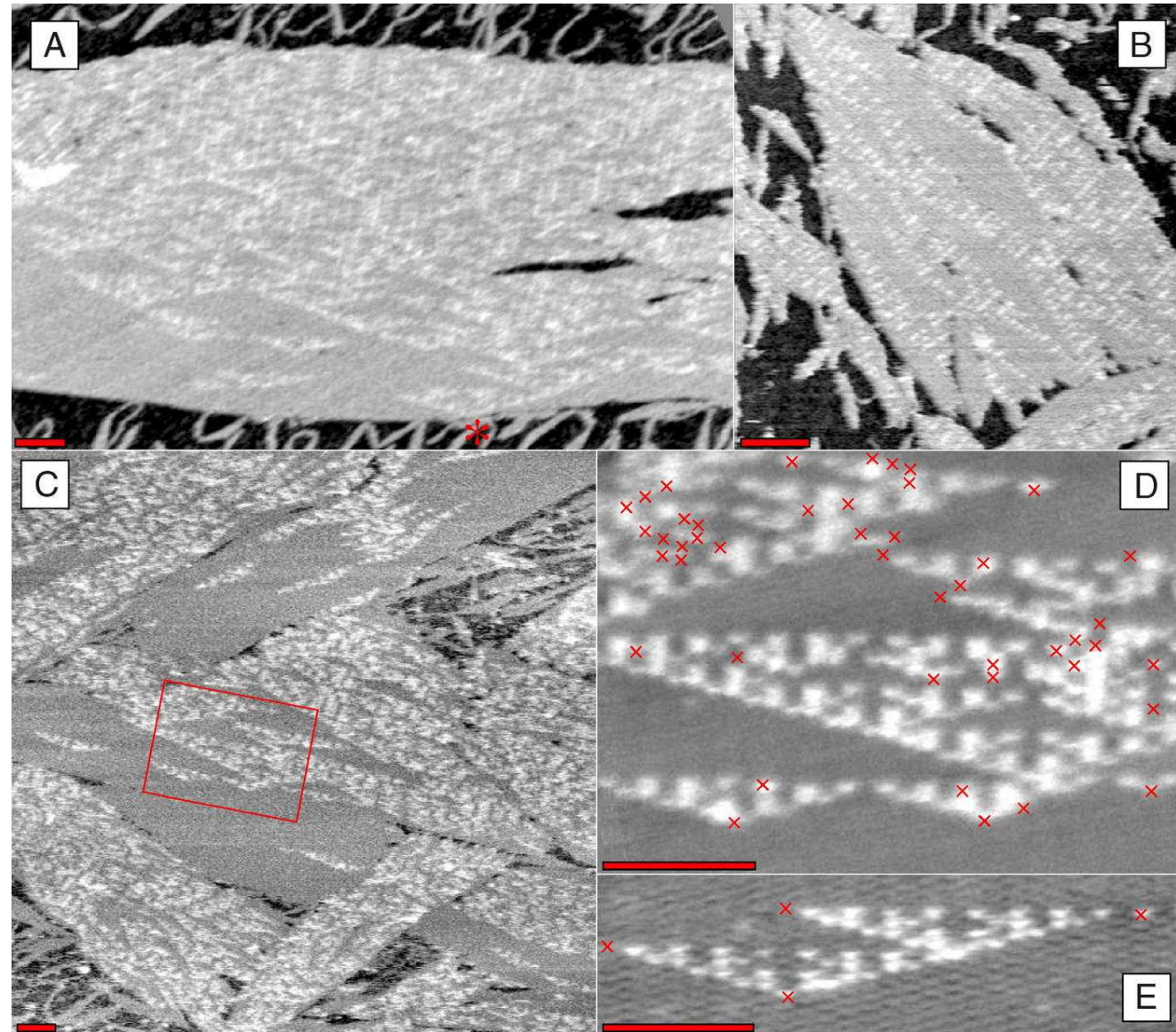
# self assembly



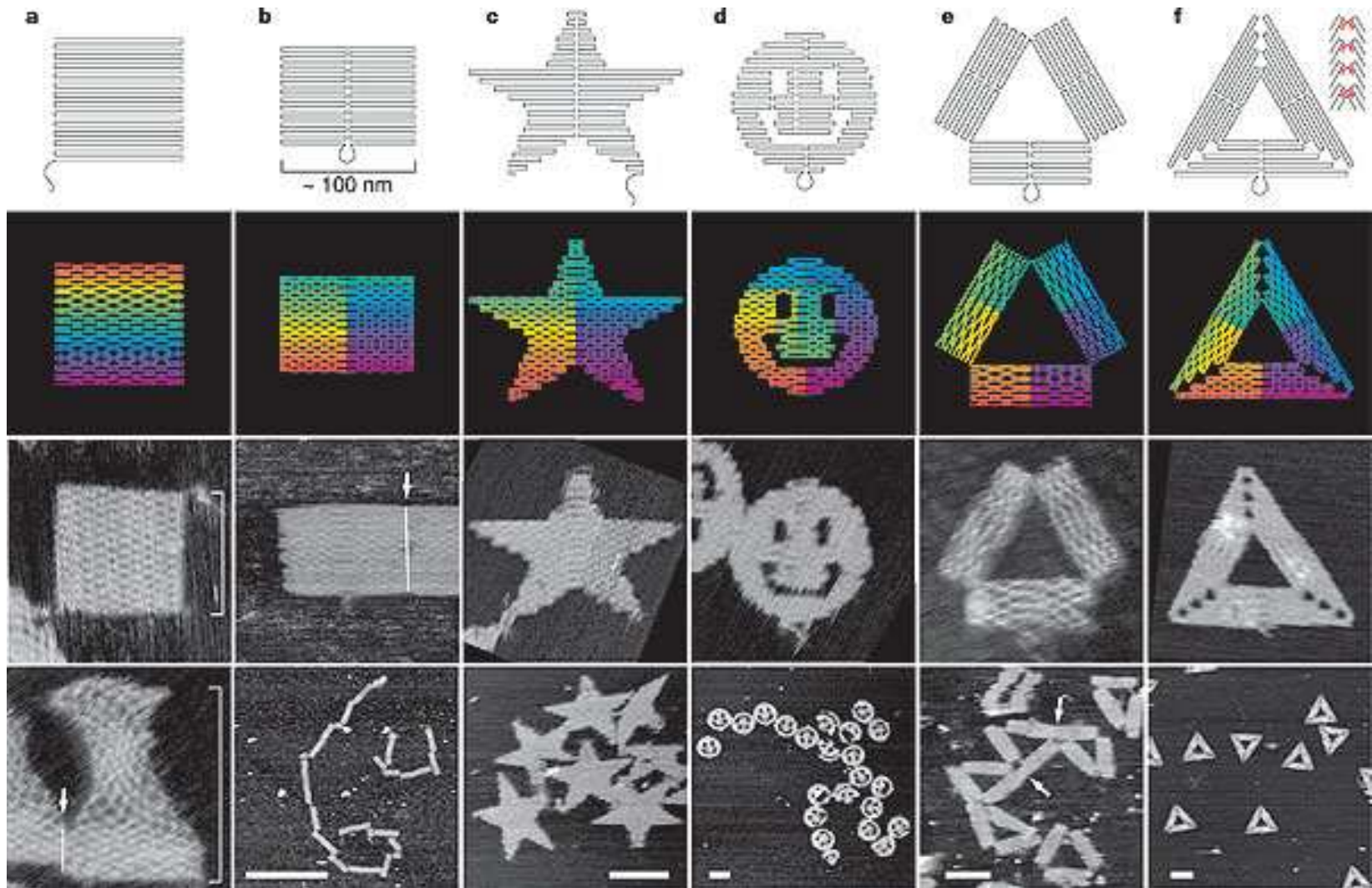
<http://dx.doi.org/10.1371/journal.pbio.0020424>  
Algorithmic Self-Assembly of DNA Sierpinski Triangles  
Rothemund, Papadakis, Winfree; PLOS Biology (2004)



# self assembly



# self assembly: DNA origami



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

the end ...



perhaps not a computer ...  
but still some cool science!

PS ...

# DNA for cocktail parties



National Centre for Biotechnology Education  
<http://www.ncbe.reading.ac.uk/DNA50/cocktail.html>



# DNA for cocktail parties



Moisten the rim of a large test tube with lime juice then dip the rim into icing sugar.

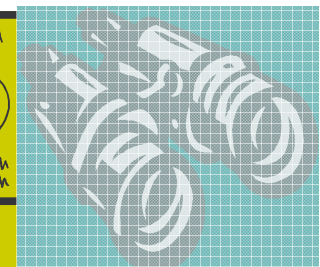
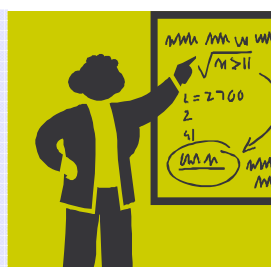
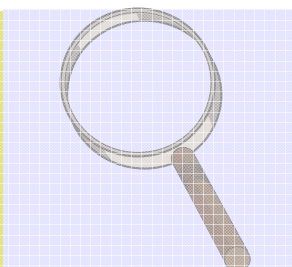
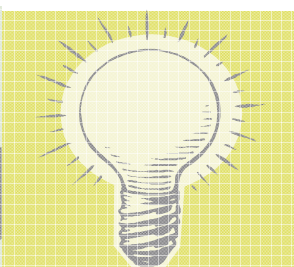
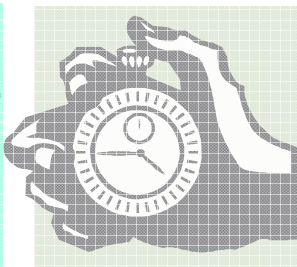
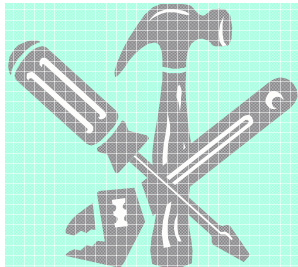
Add about 10ml of blue curaçao to the tube.

Tilt the tube then with great care, pour about 20ml of ice-cold gin down the side of the tube to form a layer above the blue curaçao.

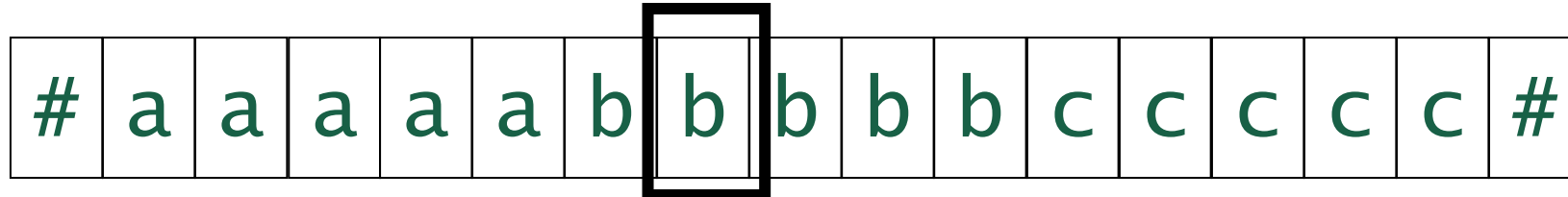
Blend the strawberries and pineapple juice for 10 seconds, then drop the purée on top of the gin. Wisps of strawberry D.N.A. will precipitate into the gin (see figure).

# contents

- ❖ DNA ... the tool chest
- ❖ problem complexity ... P & NP  
Hamilton Path Problem
- ❖ Adleman's algorithm
- ❖ comments
- ❖ theory ... Turing machine
- ❖ recent work + future

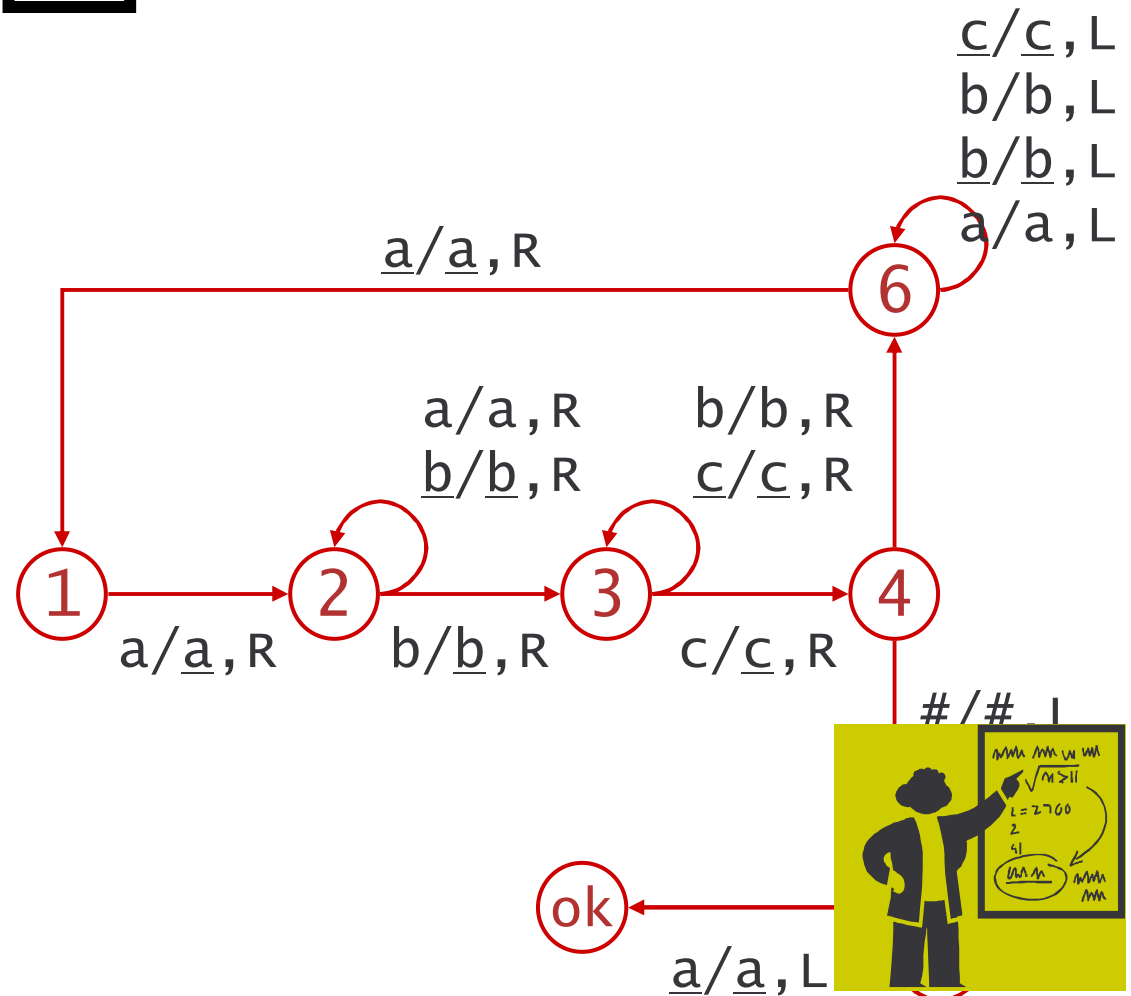


# Turing machine



tape

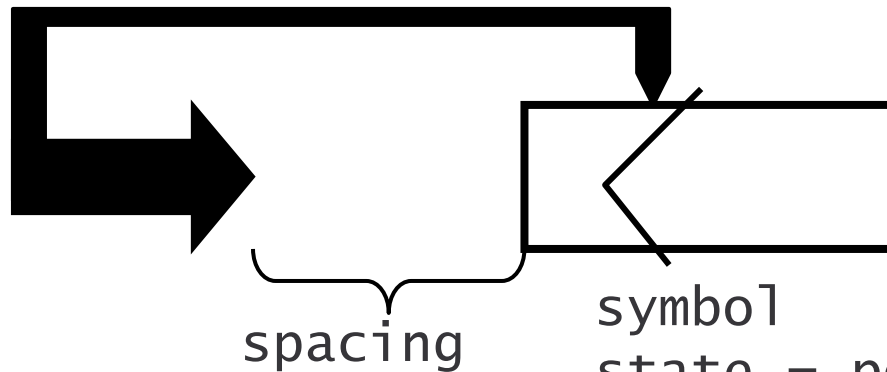
1. mark a
2. move to b's  
mark b
3. move to c's  
mark c
4. if another c
5. then back to a's  
goto 1.
6. check marks  
stop



# 'universal' Turing machine

GGATGnnnnnnnnnnnn  
CCTACnnnnnnnnnnnnnnnn

Rothemund  
*FokI*  
circular DNA



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

