



Leidsch β-congresch

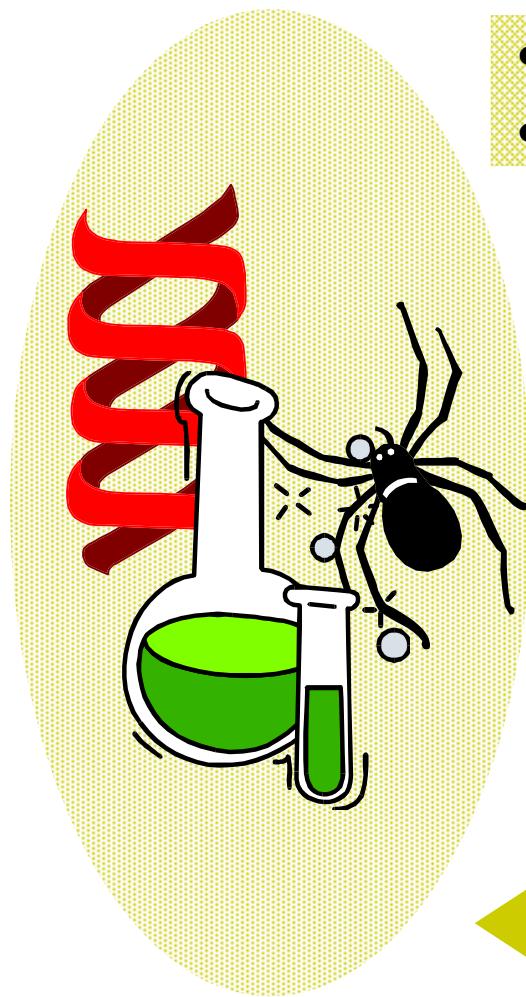
grenzen in de wetenschap

Computer in de Reageerbuis

DNA computing

Hendrik Jan Hoogeboom
informatica (LIACS)

natural computation



- genetische algoritmen
- neurale netwerken



DNA computing

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.

Nature News Service april 2003

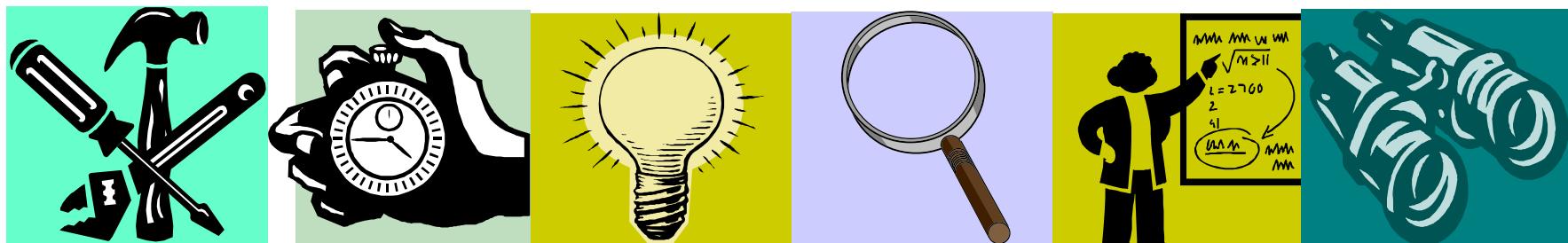
Physicists plunder life's tool chest

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.

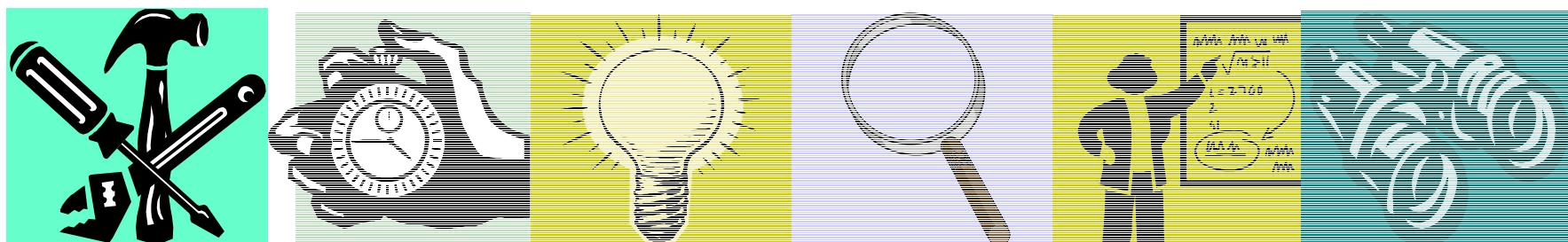
inhoudsopgave

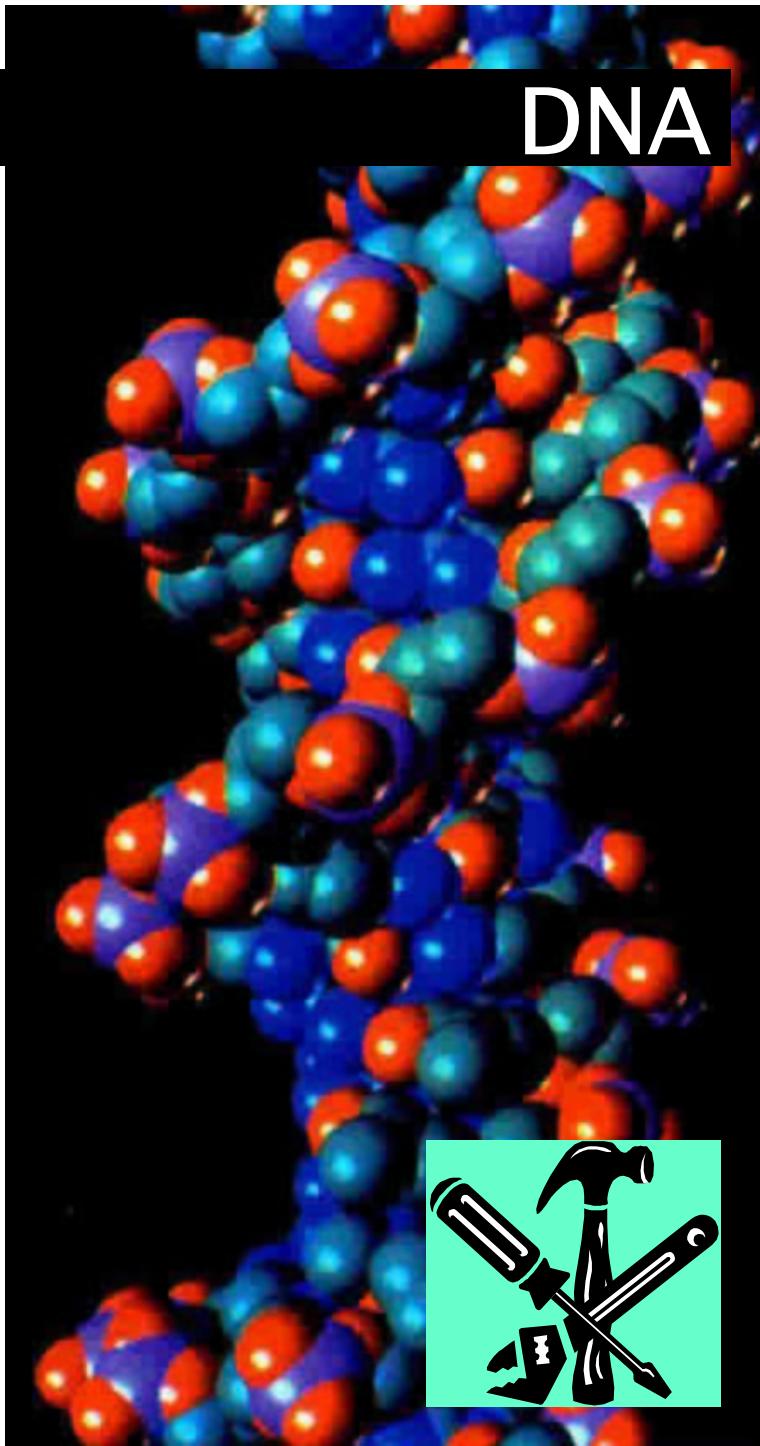
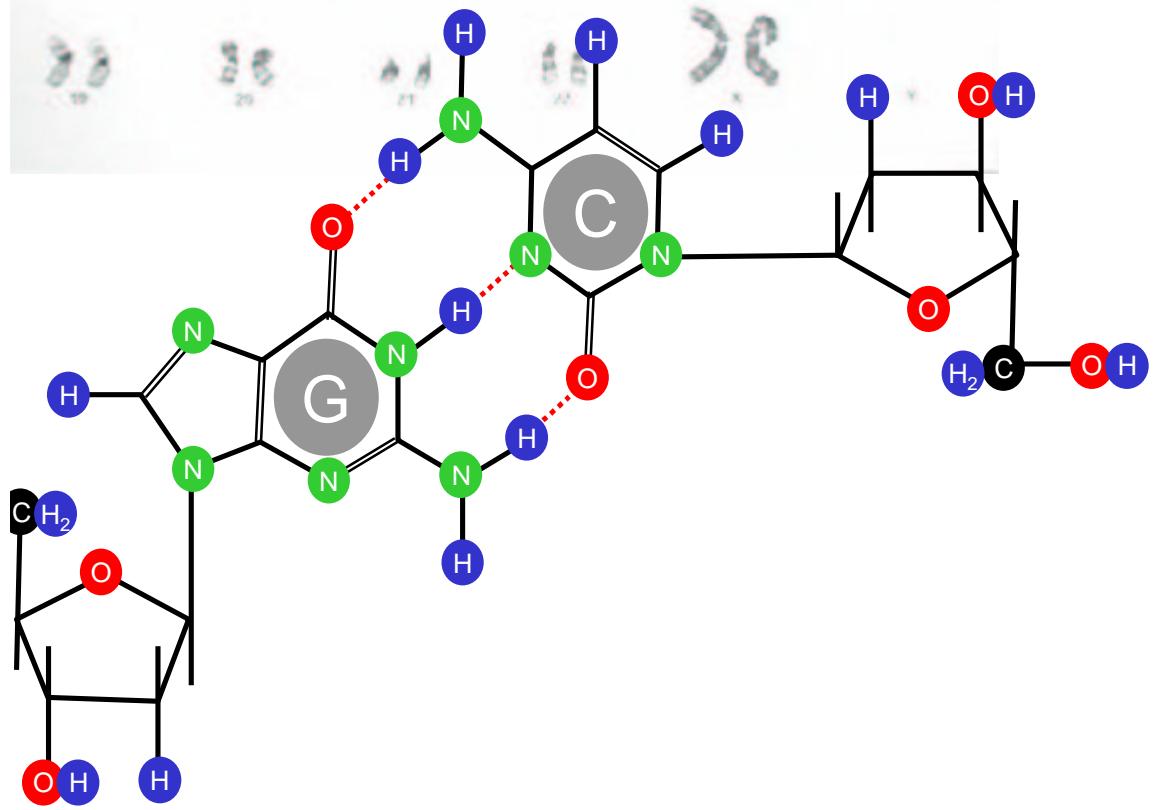
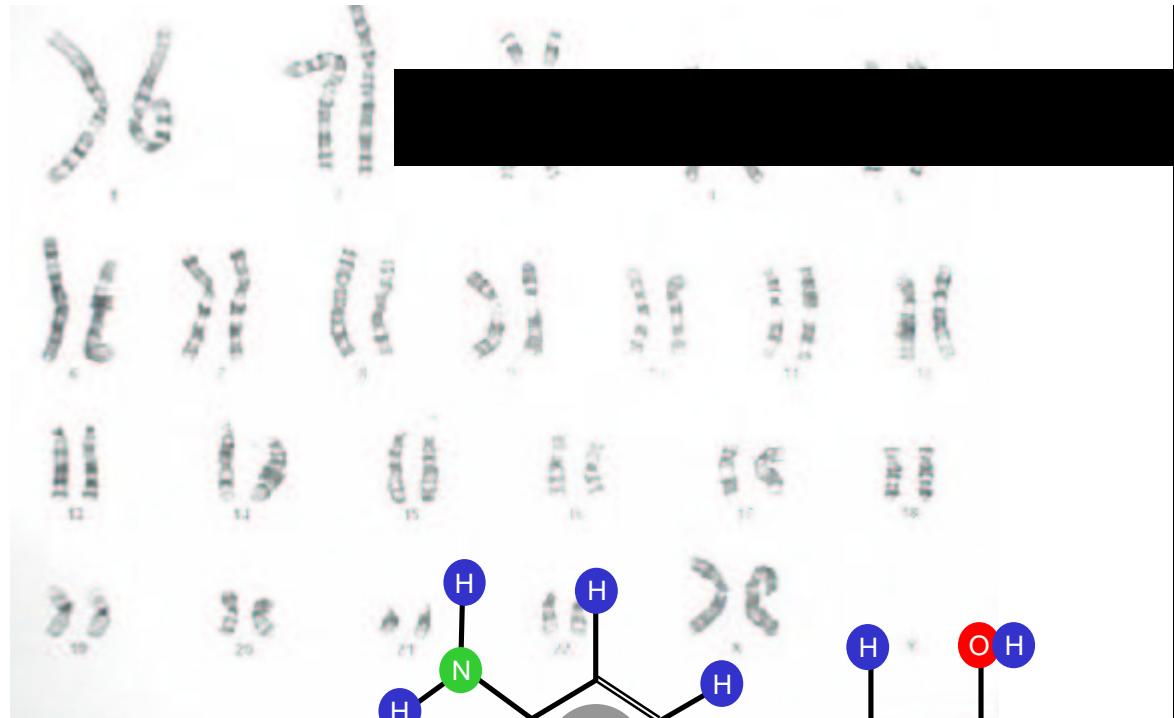
- \ DNA ... de gereedschapskist
- \ complexiteit van problemen ... P & NP
 - Hamilton Path Problem
- \ Adlemans algoritme
- \ commentaar
- \ theorie ... Turing machine
- \ recent werk + toekomstvisie

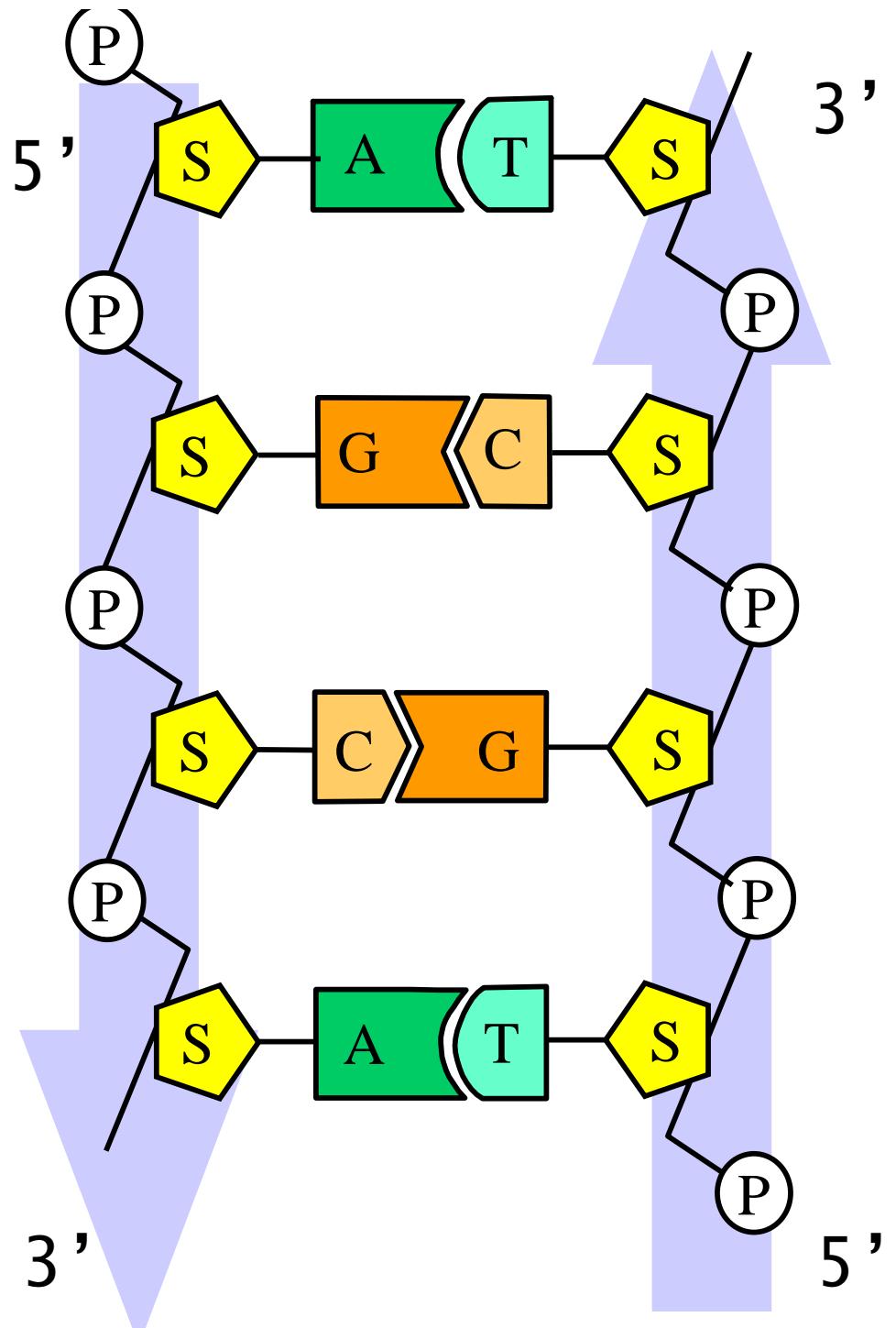


inhoudsopgave

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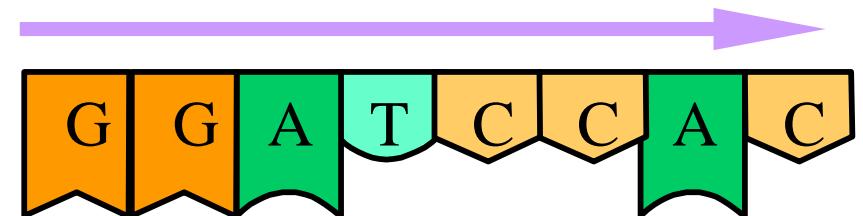


baseparen
Watson & Crick

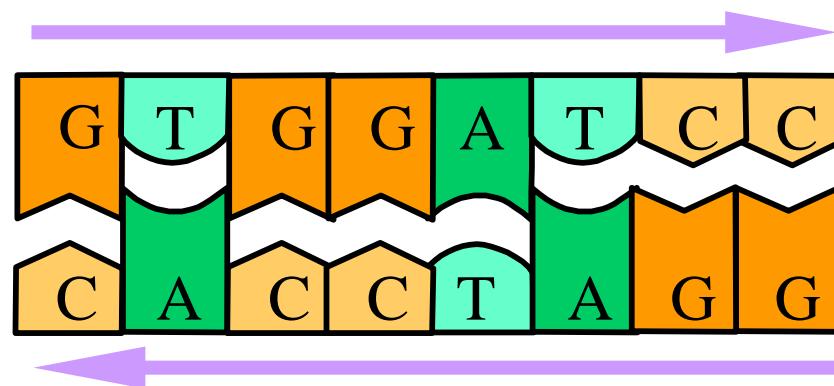
A=T
adenine - thymine
C≡G
guanine - cytosine



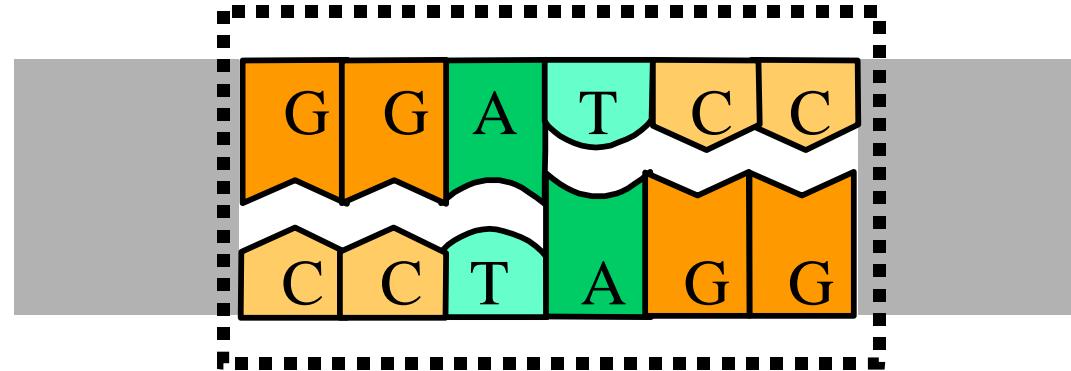
annealing & denaturing



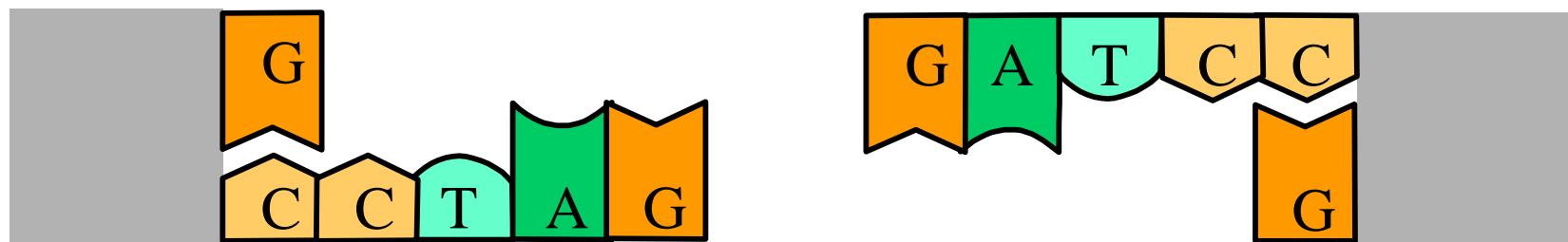
complementair



restriction enzymes



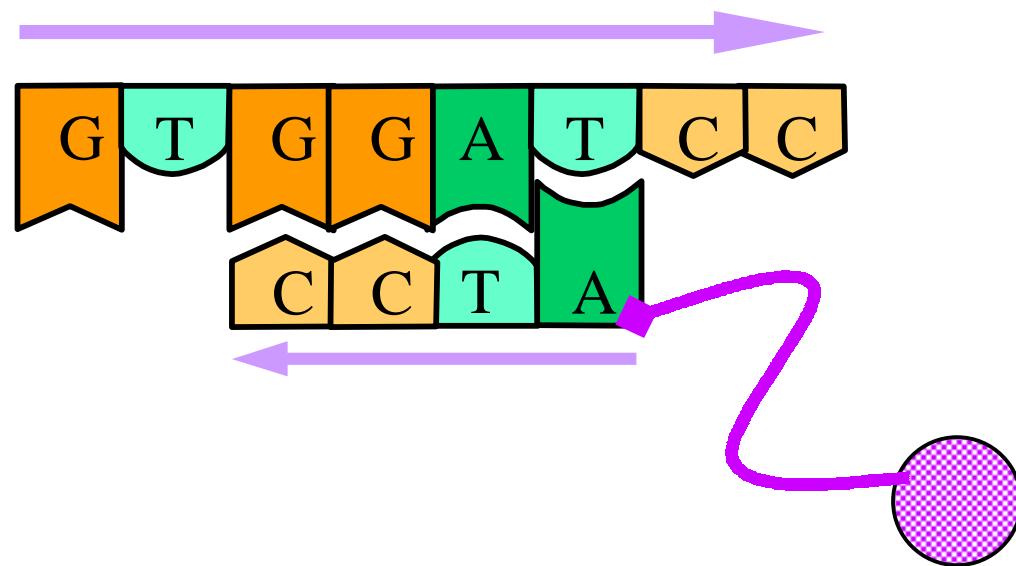
BamHI



sticky ends



selection

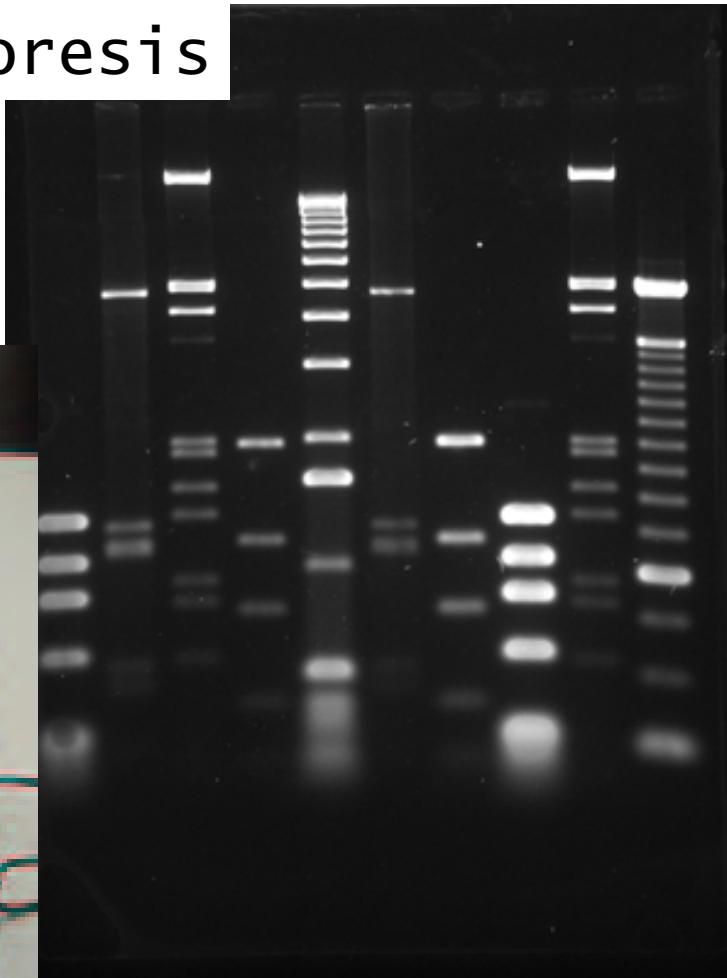
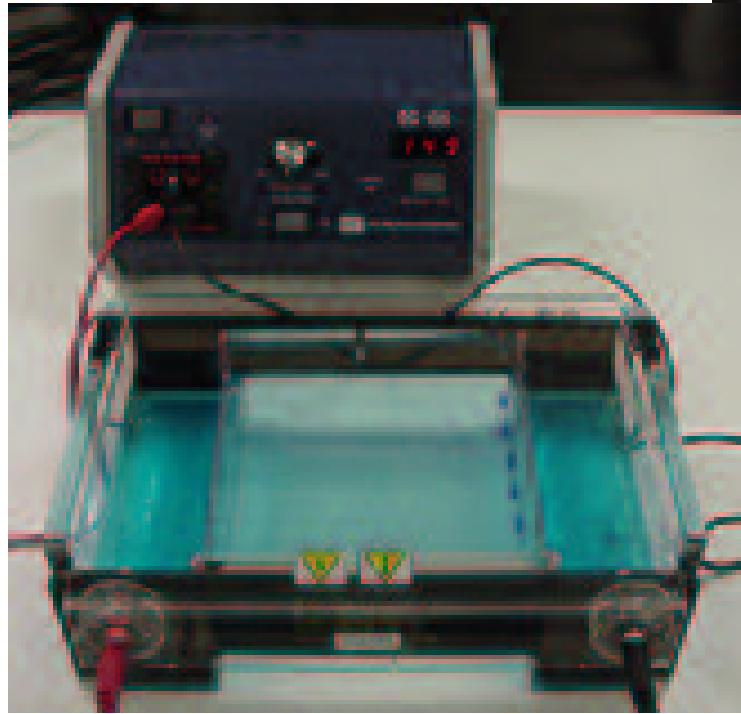


magnetic beads

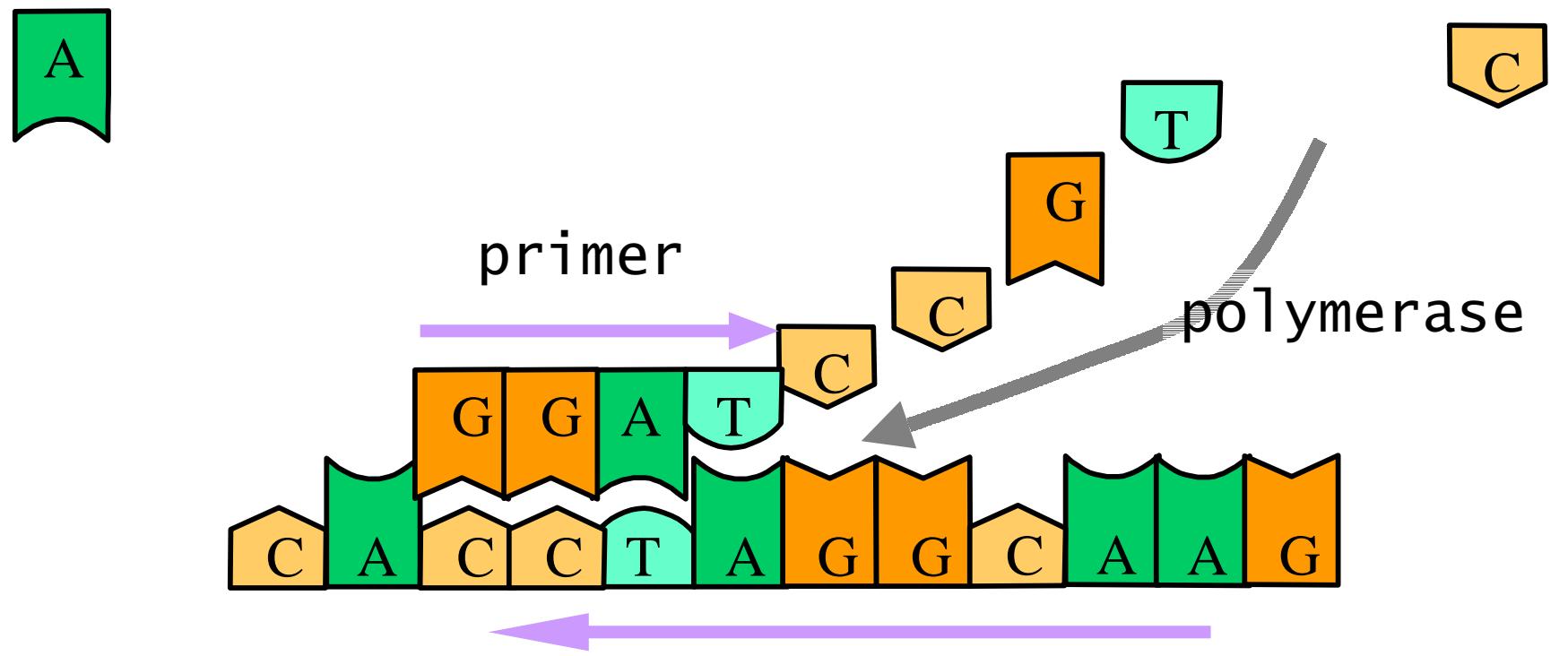


separation on length

DNA gel electrophoresis

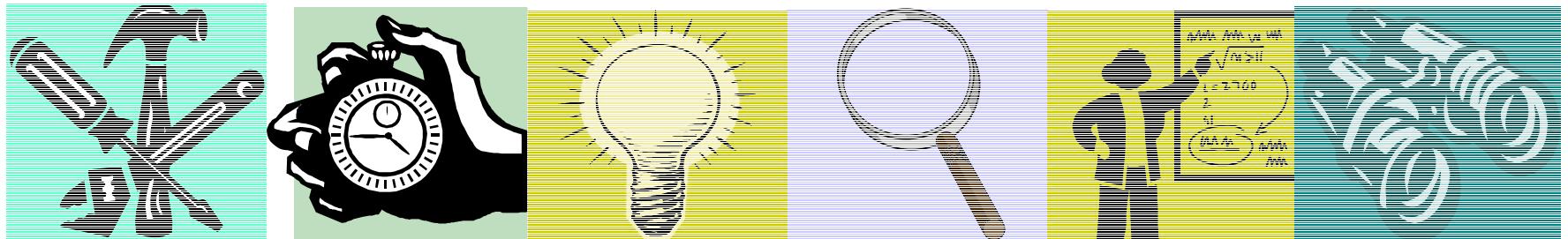


multiplication / amplification



inhoudsopgave

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grenzen: complexiteit

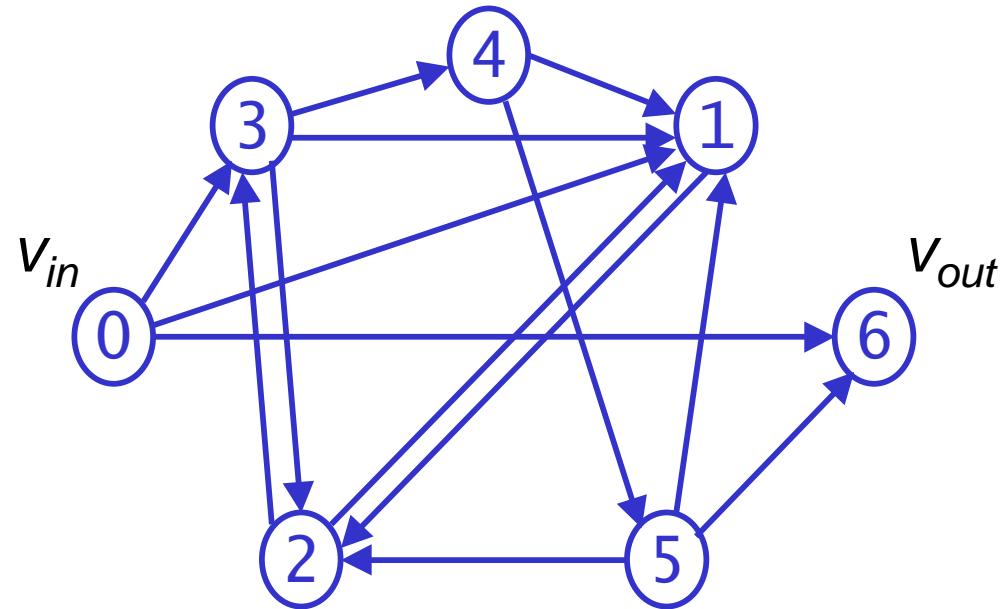
	n=10	30	50	60	second minute day year century
n	$10^{-5}s$	$3 \times 10^{-5}s$	$5 \times 10^{-5}s$	$6 \times 10^{-5}s$	
n^2	$10^{-4}s$	$9 \times 10^{-4}s$	$2 \times 10^{-3}s$	$4 \times 10^{-3}s$	
n^5	$10^{-1}s$	24 s	1.7 m	13 m	
2^n	$10^{-3}s$	18 m	13 d	366 c	
3^n	$6 \times 10^{-2}s$	6.5 y	3855 c	$10^{13}c$	

polynomiaal vs.
exponentieel

	nu	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

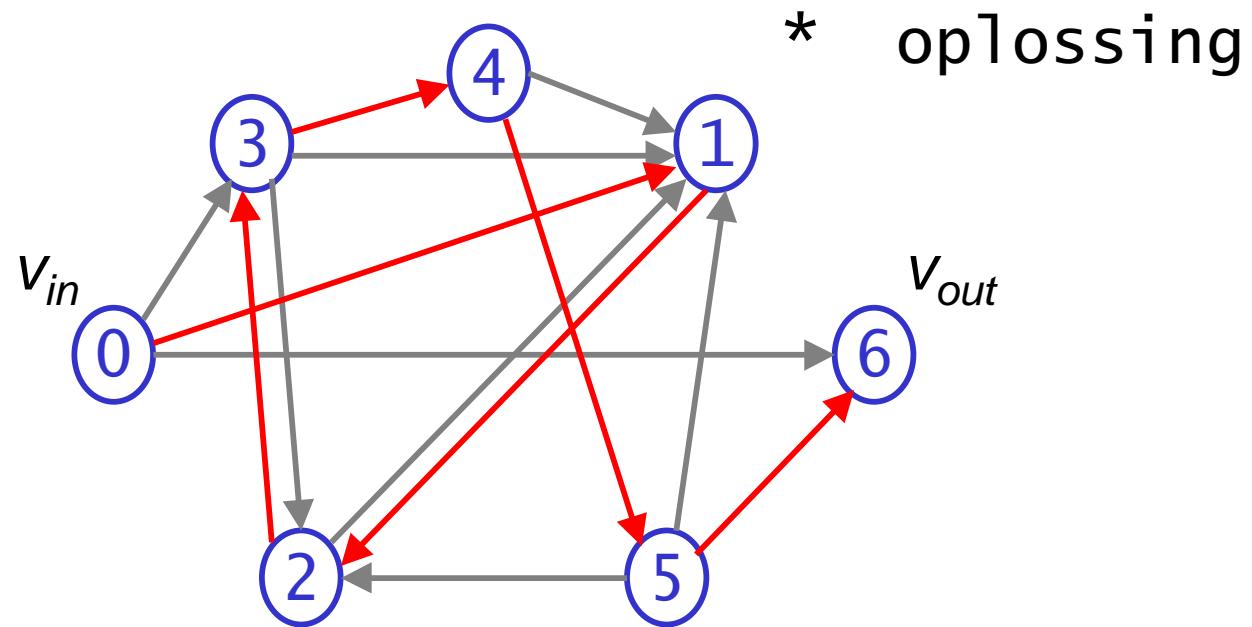


*'travelling
salesman'*

gegeven: knopen en verbindingen
vraag: bestaat er een wandeling die
elke knoop **precies één keer** aandoet ?



HPP: Hamilton Path Problem



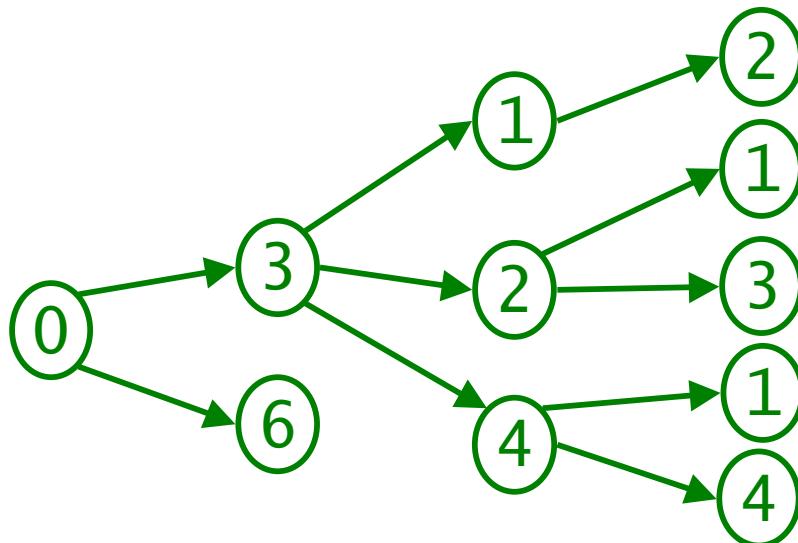
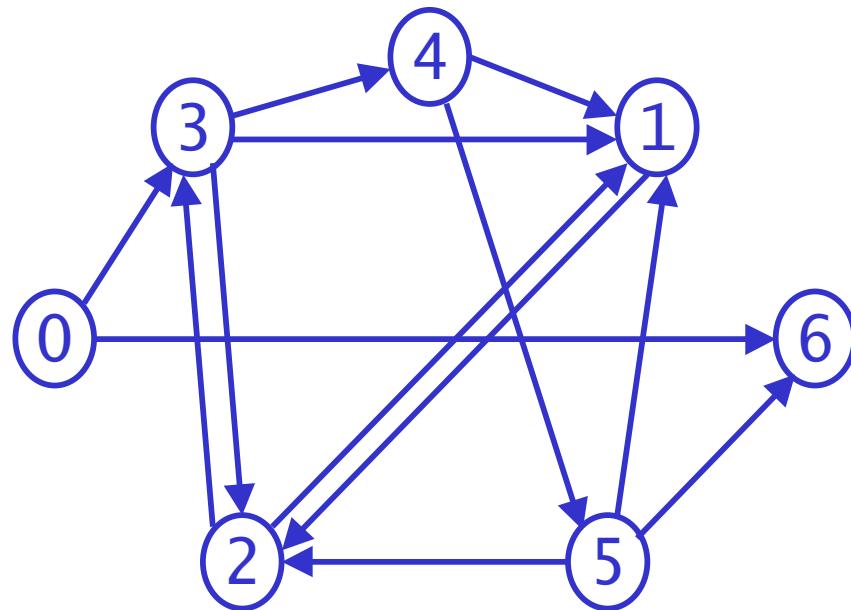
* oplossing

*'travelling
salesman'*

gegeven: knopen en verbindingen
vraag: bestaat er een wandeling die
elke knoop **precies één keer** aandoet ?



HPP: Hamilton Path Problem



* geen oplossing?

exponentiële tijd:
alle mogelijkheden
proberen

representatief:
'NP compleet'

heuristieken



grenzen (theorie) - P vs. NP

P

polynomiaal algoritme
om oplossing te bepalen

NP

polynomiaal algoritme
om oplossing te verifiëren

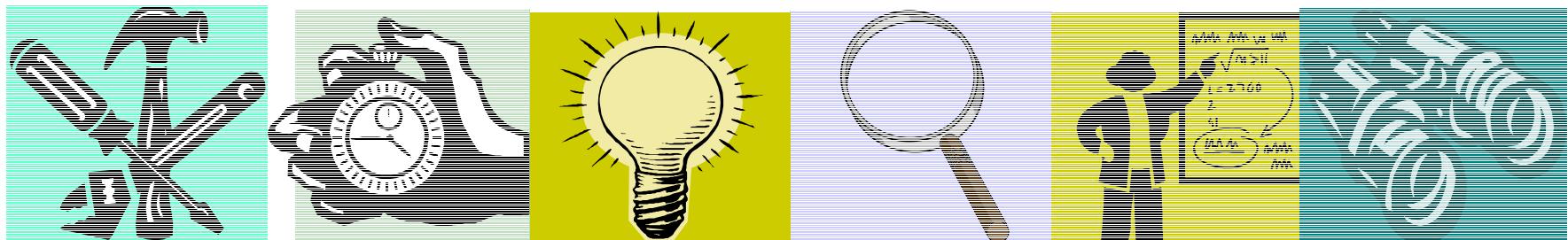
NP-compleet

millenium prize problem P=NP
www.claymath.org/Millennium_Prize_Problems/

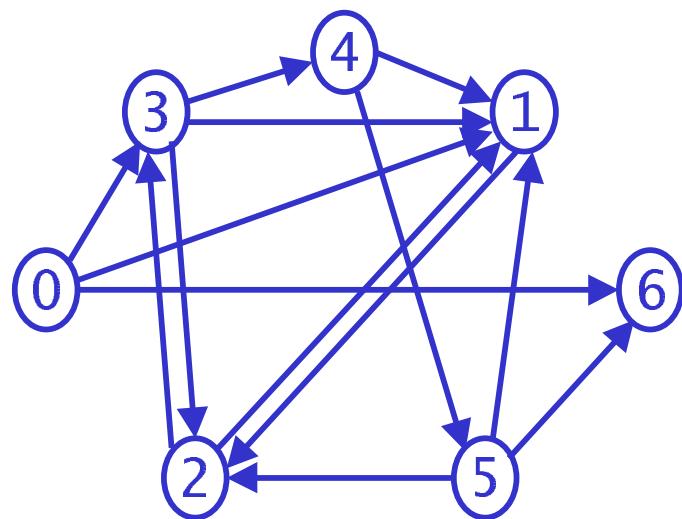


inhoudsopgave

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Adleman's algorithm



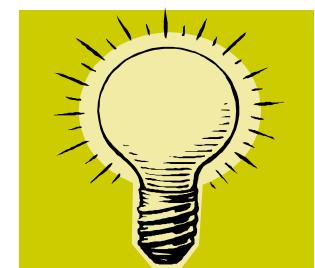
1. generate 'all' paths
- keep only paths
2. ... from v_{in} to v_{out}
3. ... that enter n vertices
4. ... that enter all vertices
5. if any path remains OK

máár

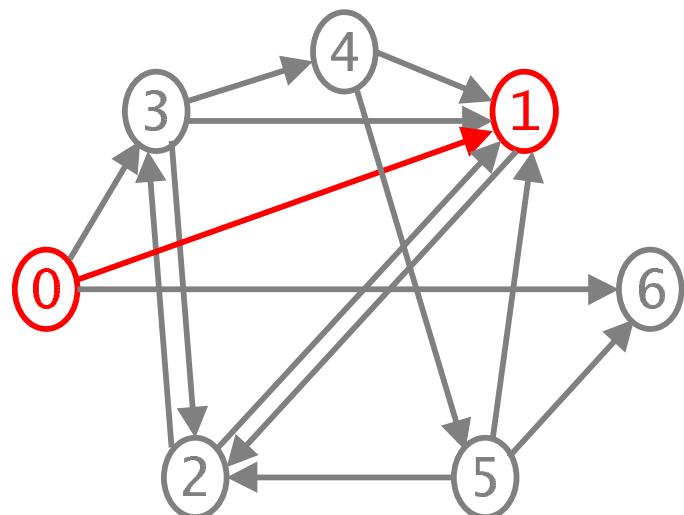
... in DNA

... alle paden parallel

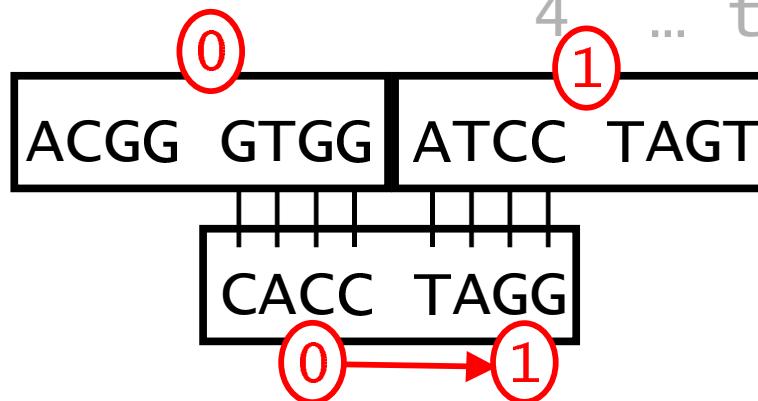
'massive parallelism'



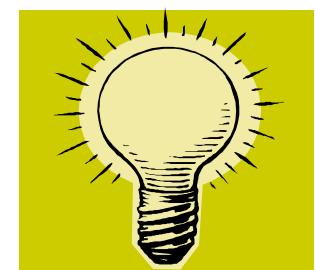
Adleman's algorithm



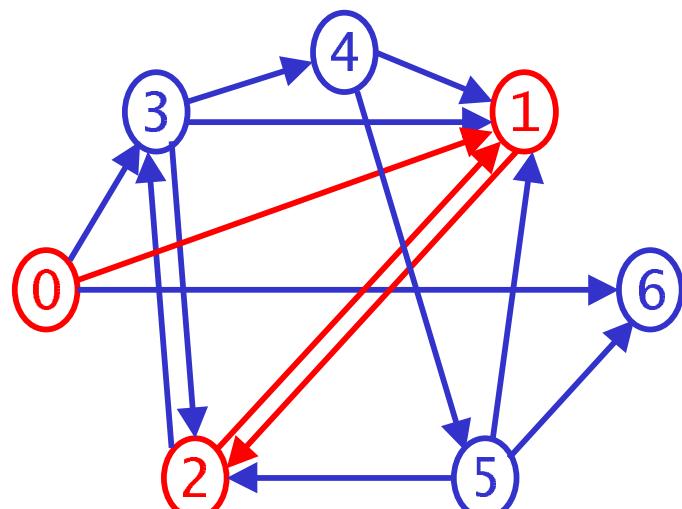
0. coding the graph
1. generate 'all' paths
- keep only paths
2. ... from v_{in} to v_{out}
3. ... that enter n vertices
4. ... that enter all vertices



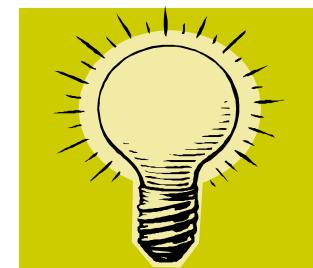
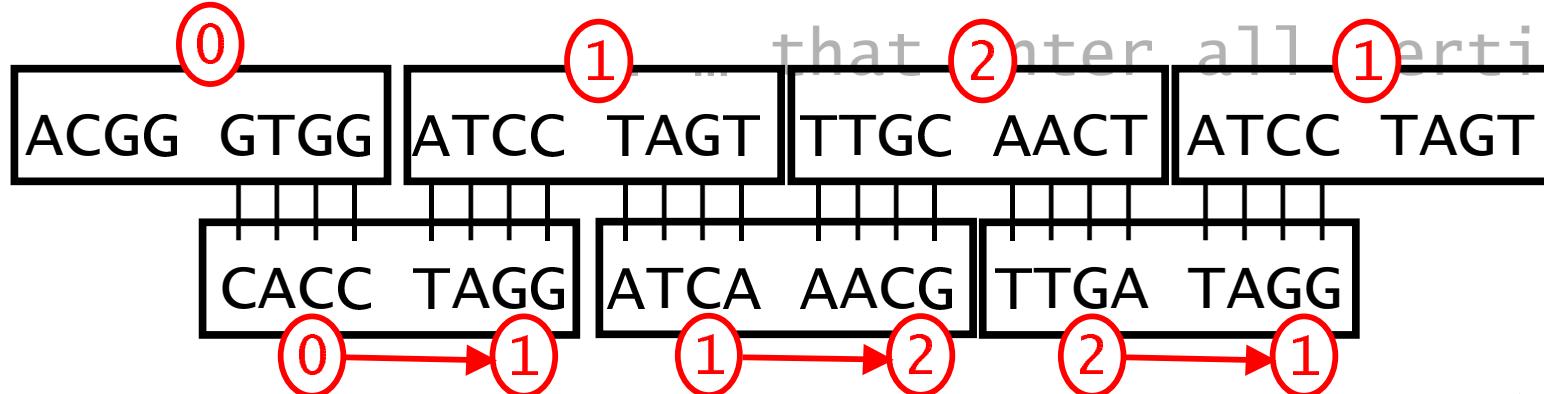
any path remains OK



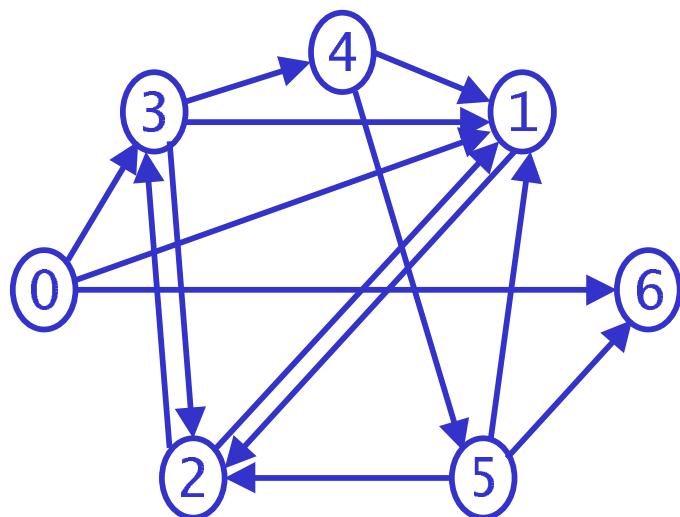
Adleman's algorithm



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

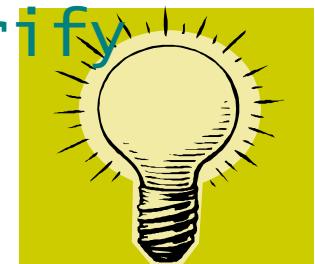
5. if any path remains OK

- PCR with v_{in} and v_{out} primers

- gel: separate on length, amplify & purify

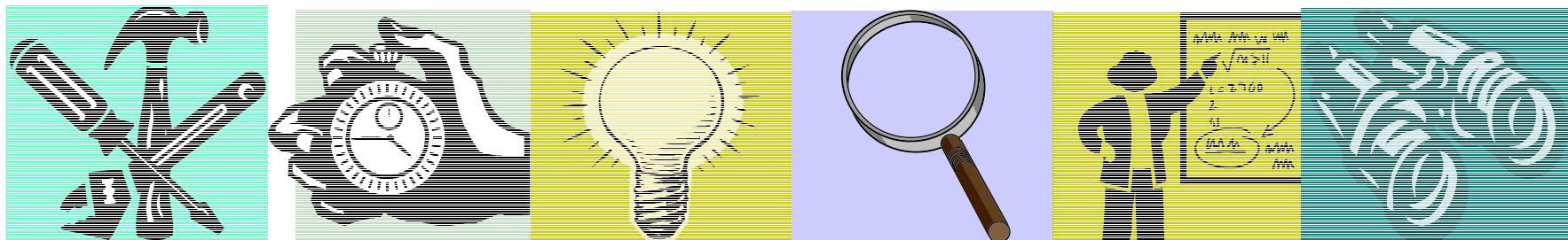
- magnetic beads: select strands

- PCR amplification & gel



inhoudsopgave

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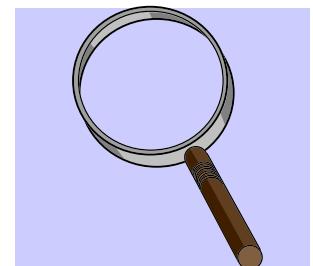
comments ...

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



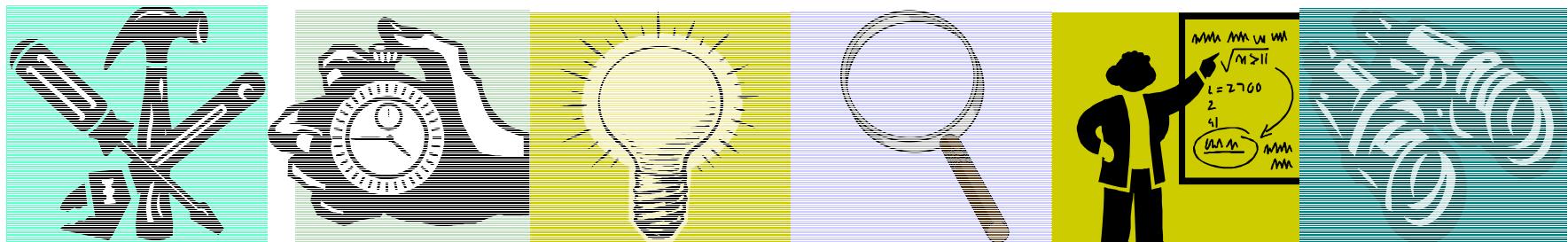
comments ...

- D “power of this method of computation”
 - 10^{14} operations 10^{20} plausible
 - exceed supercomputers by thousandfold
- D “not clear whether ... used to solve real computational problems”
 - . multiplying 100 digit numbers
- D potential: massively parallel searches

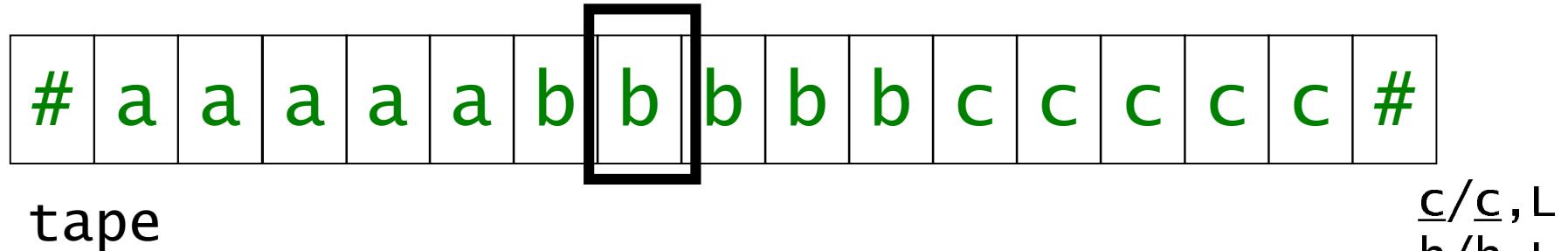


inhoudsopgave

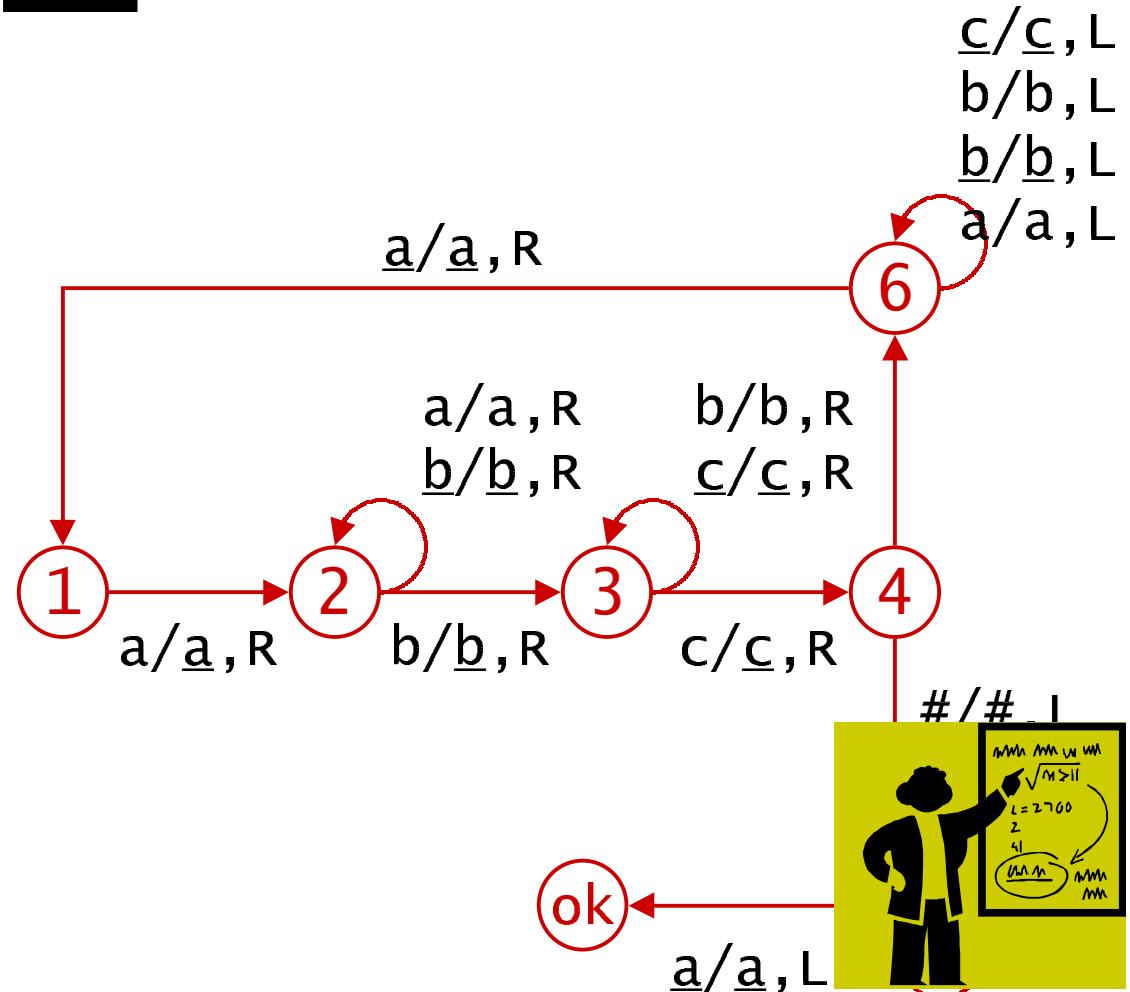
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Turing machine



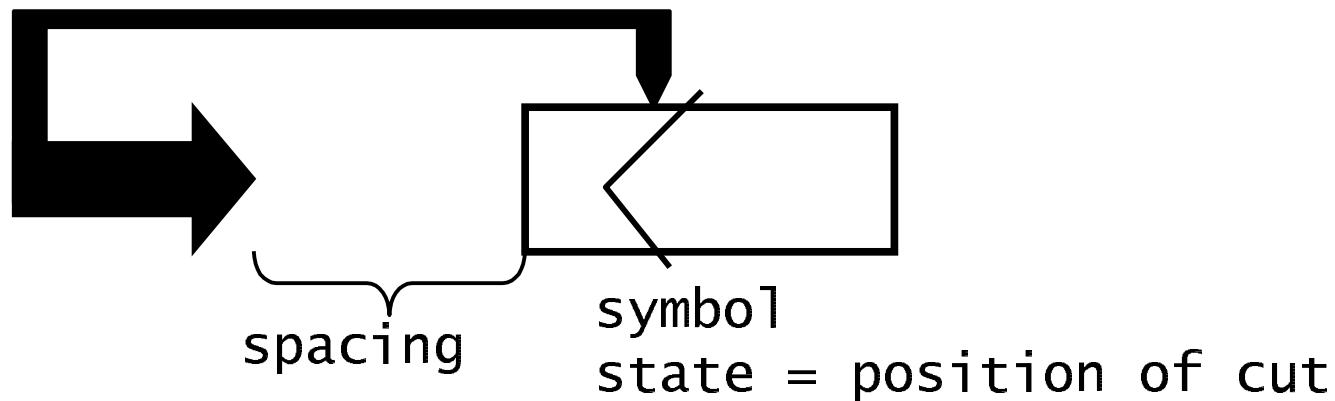
1. mark a
2. move to b's
mark b
3. move to c's
mark c
4. if another c
5. then back to a's
goto 1.
else back to a's
6. check marks
stop



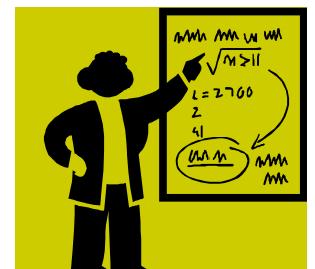
'universal' Turing machine

GGATGnnnnnnnn
CCTACnnnnnnnnnnnn

Rothemund
Foki
circular DNA

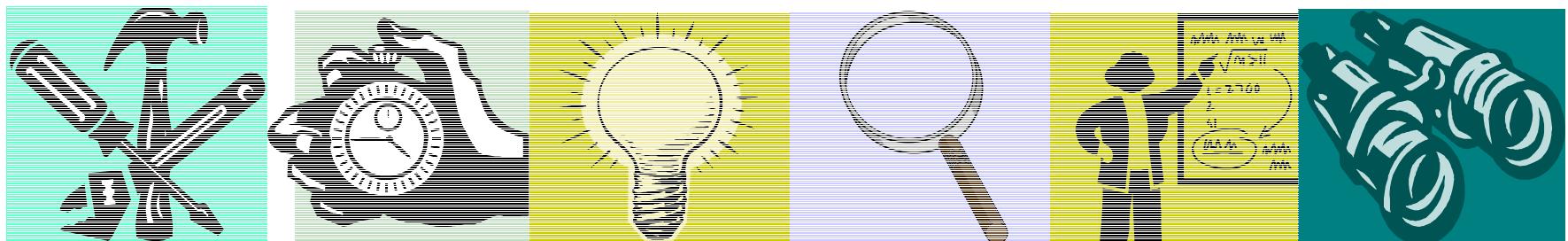


- cut states with restriction enzyme
- mix 'instructions' with 'tape'
- 'activate' instructions (cut protected end)
- ligate to form circles
- cut old symbol
- recircularize

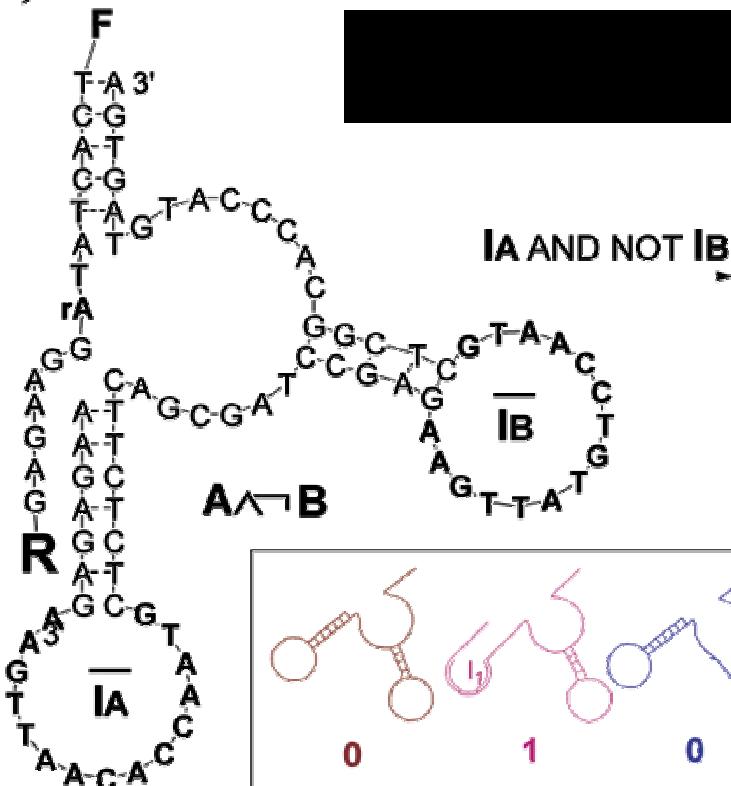


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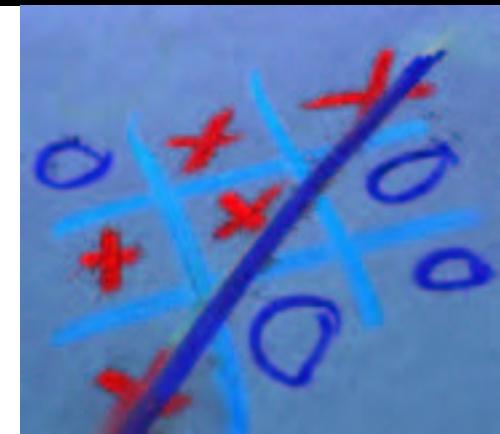
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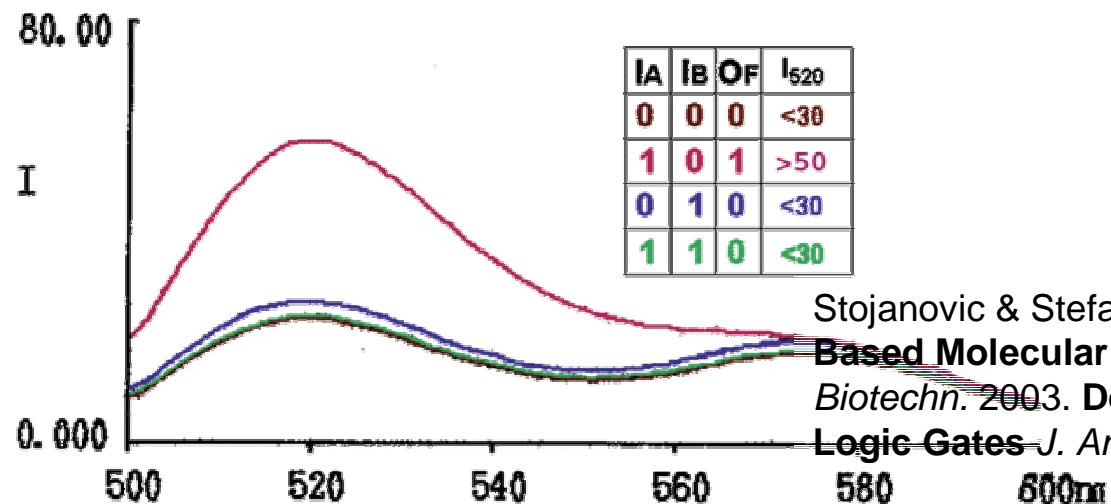
(a)



recently in Nature



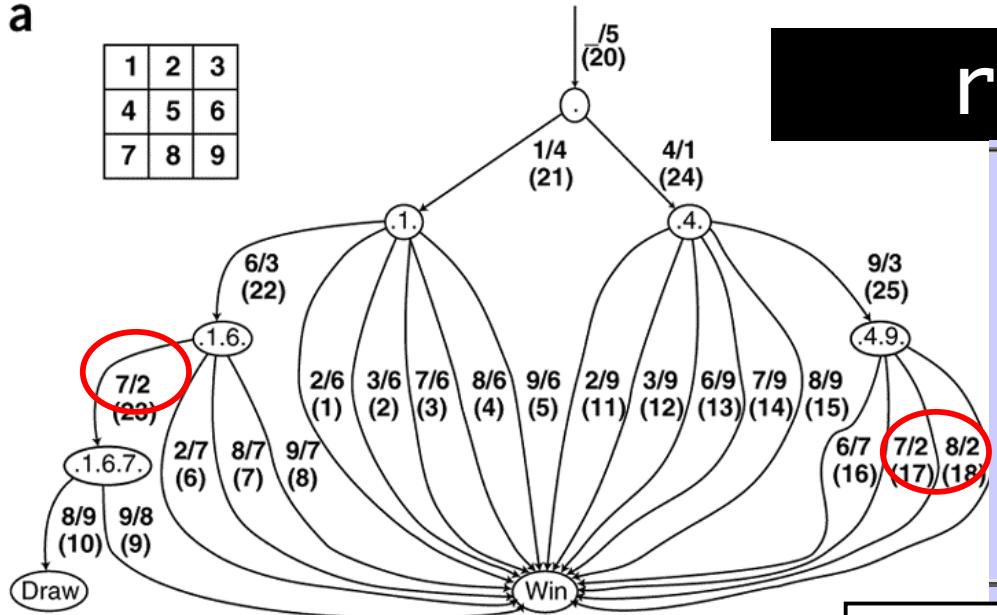
(b)



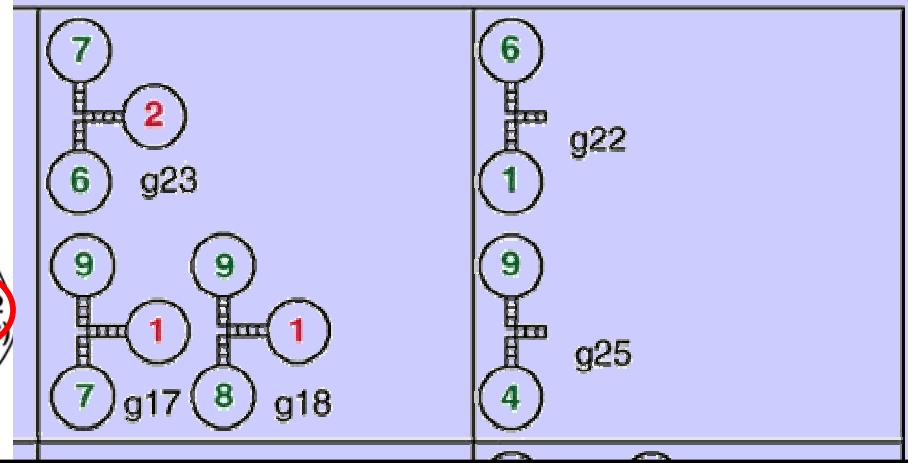
logische schakeling
fluorcentie

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



a

recently in Nature

**b**

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

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

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

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

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

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

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

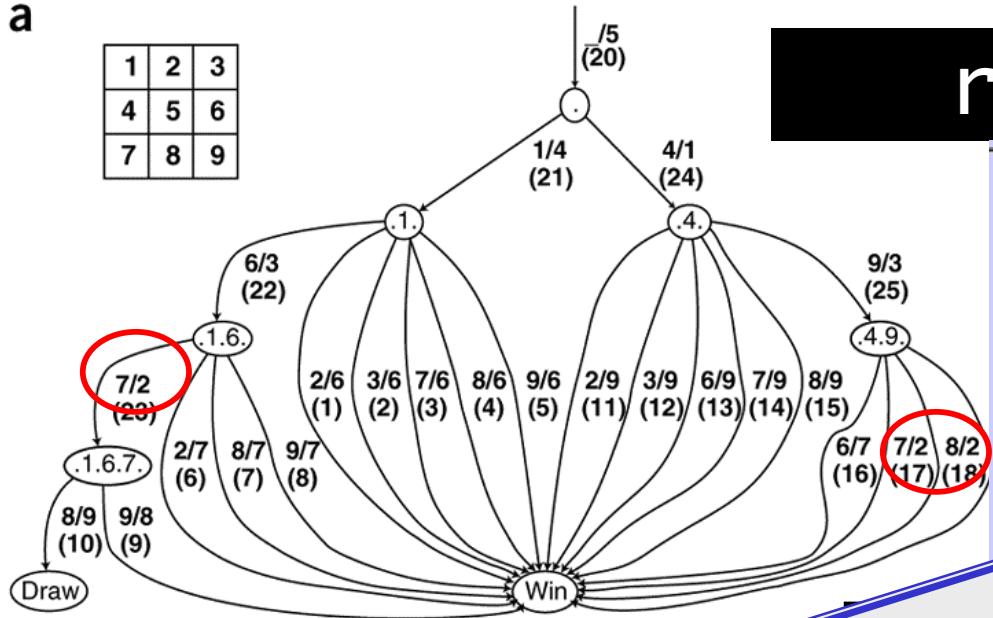
$$o_8 = \underbrace{i_9 \wedge i_7 \wedge \neg i_4}_{\text{edge (9)}}$$

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

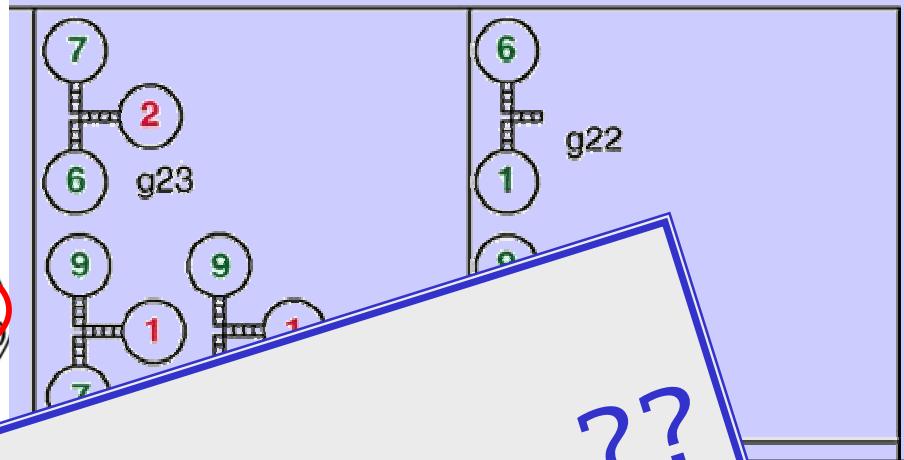
$$O_2 = (i_6 \wedge i_7 \wedge \neg i_2) \vee (i_7 \wedge i_9 \wedge \neg i_1) \vee (i_8 \wedge i_9 \wedge \neg i_1)$$

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

recently in Nature

**b**

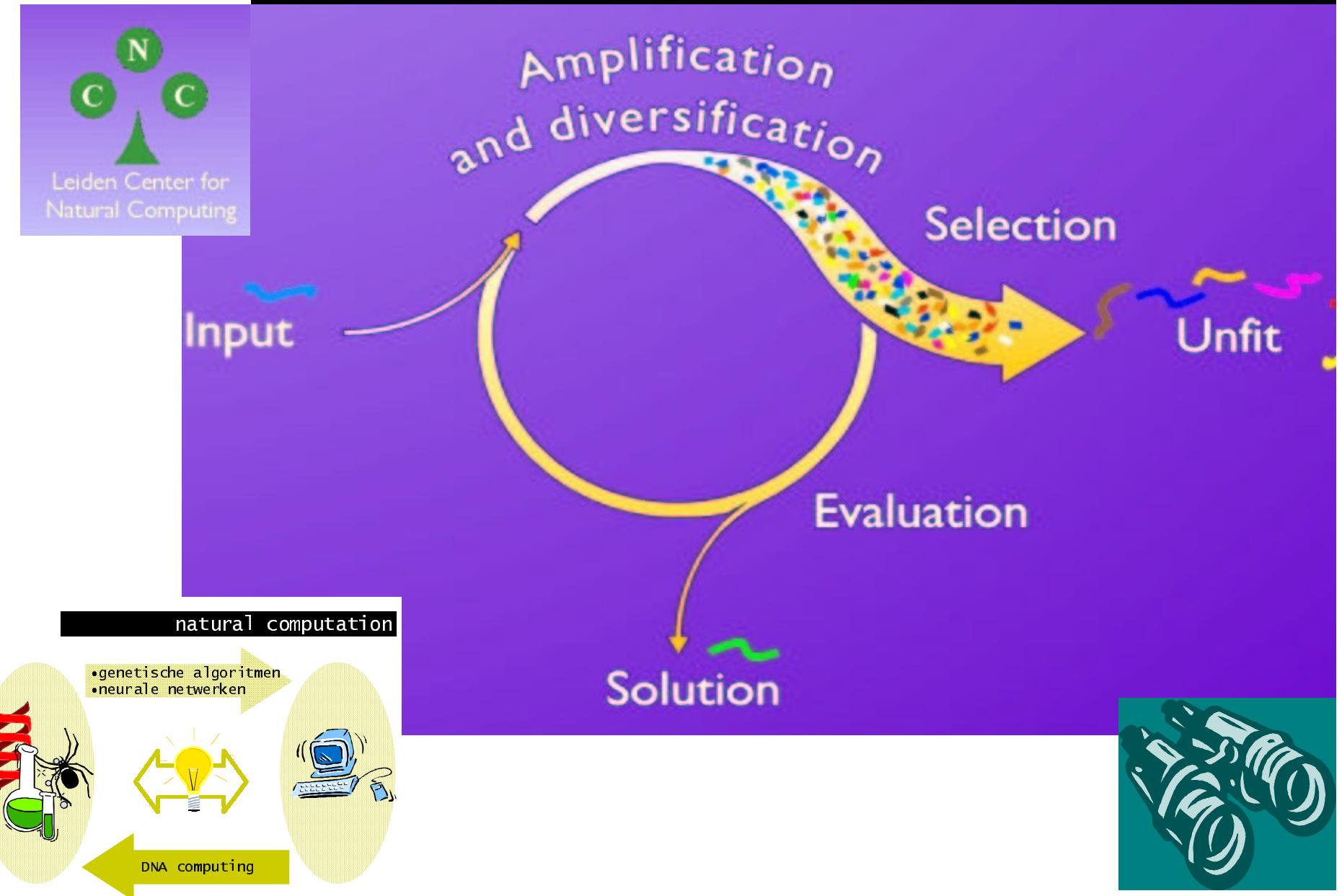
$$\begin{aligned}
 o_1 &= \underbrace{i_4}_{\text{edge (24)}} \\
 o_2 &= \underbrace{(i_6 \wedge i_7 \wedge \neg i_2)}_{\text{edge (23)}} \vee \underbrace{(i_6 \wedge i_8 \wedge \neg i_2)}_{\text{edge (23)}} \\
 o_3 &= \underbrace{(i_1 \wedge i_6)}_{\text{edge (22)}} \vee \underbrace{(i_4 \wedge i_9)}_{\text{edge (25)}} \\
 o_4 &= \underbrace{i_1}_{\text{edge (21)}} \\
 o_5 &= \underbrace{1}_{\text{edge (20)}} \\
 o_6 &= \underbrace{(i_1 \wedge i_2 \wedge \neg i_6)}_{\text{edge (1)}} \vee \underbrace{(i_1 \wedge i_3 \wedge \neg i_6)}_{\text{edge (2)}} \vee \underbrace{(i_1 \wedge i_7 \wedge \neg i_6)}_{\text{edge (3)}} \vee \underbrace{(i_1 \wedge i_8 \wedge \neg i_6)}_{\text{edge (4)}} \vee \underbrace{(i_1 \wedge i_9 \wedge \neg i_6)}_{\text{edge (5)}} \vee \underbrace{(i_1 \wedge i_{10} \wedge \neg i_6)}_{\text{edge (6)}} \\
 o_7 &= \underbrace{(i_2 \wedge i_6 \wedge \neg i_7)}_{\text{edge (6)}} \vee \underbrace{(i_6 \wedge i_8 \wedge \neg i_7)}_{\text{edge (7)}} \vee \underbrace{(i_6 \wedge i_9 \wedge \neg i_7)}_{\text{edges (8) and (16)}} \vee \underbrace{(i_9 \wedge i_2 \wedge \neg i_1)}_{\text{edge (19)}} \\
 o_8 &= \underbrace{i_9 \wedge i_7 \wedge \neg i_4}_{\text{edge (9)}} \\
 o_9 &= \underbrace{(i_7 \wedge i_8 \wedge \neg i_4)}_{\text{edge (10)}} \vee \underbrace{(i_4 \wedge i_2 \wedge \neg i_9)}_{\text{edge (11)}} \vee \underbrace{(i_4 \wedge i_3 \wedge \neg i_9)}_{\text{edge (12)}} \vee \underbrace{(i_4 \wedge i_6 \wedge \neg i_9)}_{\text{edge (13)}}
 \end{aligned}$$

maar ... is dit een 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



evolutionary DNA computing



grenzen (praktijk)

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

...

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