

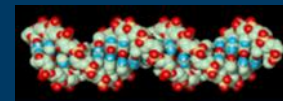
# Molecular Programming

Luca Cardelli

2013-05-15 Hasselt

# Objectives

- The promises of Molecular Programming:
  - In Science & Medicine
  - In Engineering
  - In Computing
- The current practice of Molecular Programming
  - DNA technology
  - Molecular languages and tools
  - Example of a molecular algorithm



# The Hardware Argument

Smaller and smaller things can be built

# Smaller and Smaller

## First working transistor

John Bardeen and Walter Brattain , Dec. 23, 1947

## First integrated circuit

Jack Kilby, Sep. 1958.

**50 years later**

## 25nm NAND flash

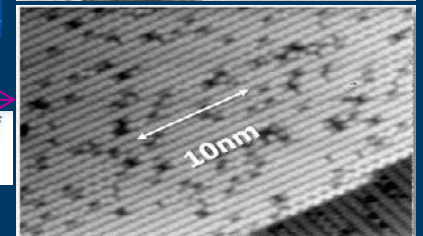
Intel&Micron, Jan. 2010. ~50atoms

## Single molecule transistor

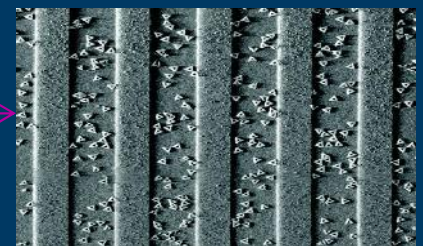
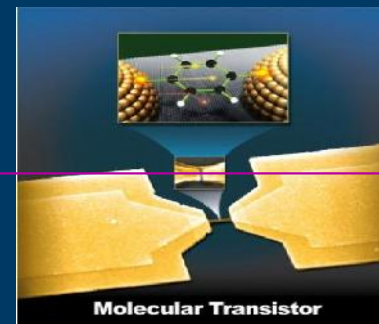
Observation of molecular orbital gating  
*Nature*, 2009; 462 (7276): 1039

## Molecules on a chip

**~10 Moore's Law cycles left!**



Scanning tunneling microscope image of a silicon surface showing 10nm is ~20 atoms across



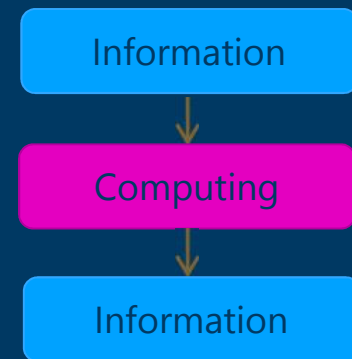
Placement and orientation of individual DNA shapes on lithographically patterned surfaces. *Nature Nanotechnology* 4, 557 - 561 (2009).

# The Software Argument

Smaller and smaller things can be programmed

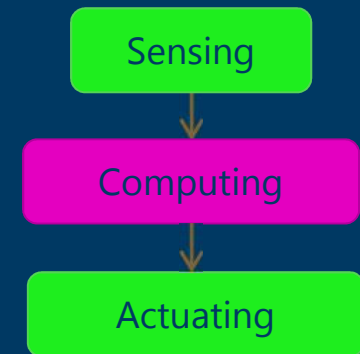
# We can program...

- Computers.
  - Completely!



# We can program...

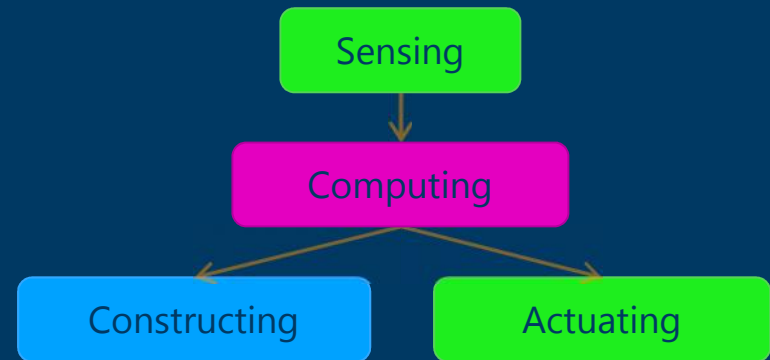
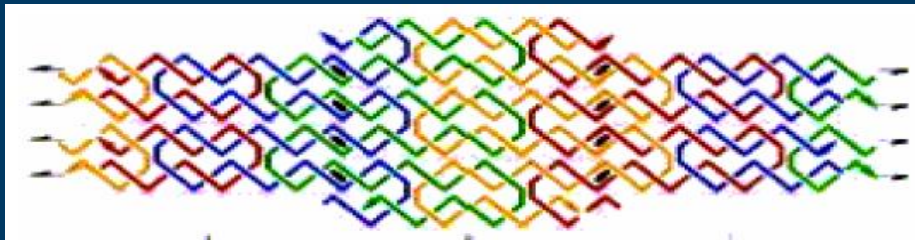
- Physical systems.
  - Completely!  
(Modulo sensors/actuators)



# We can program...

- **Matter**

- Completely and directly!
- Currently: only DNA/RNA.

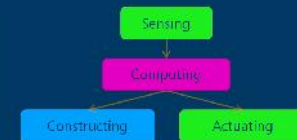
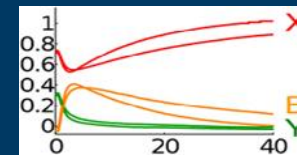
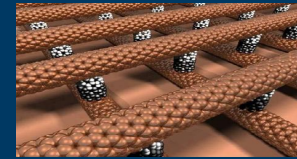


*It's like a 3D printer without the printer!*  
[Andrew Hellington]



# What can we do with “just” DNA?

- Organize ANY matter [caveats apply]
- Execute ANY kinetics [caveats: up to time scaling]
- Build Nano-Control Devices
- Interface to Biology

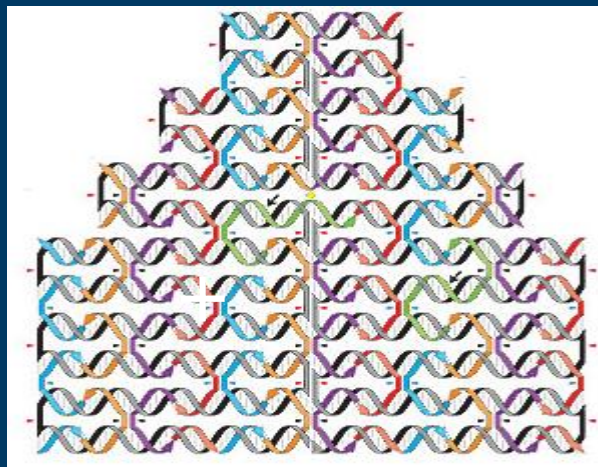


H.Lodish & al. Molecular Cell Biology 4<sup>th</sup> ed.

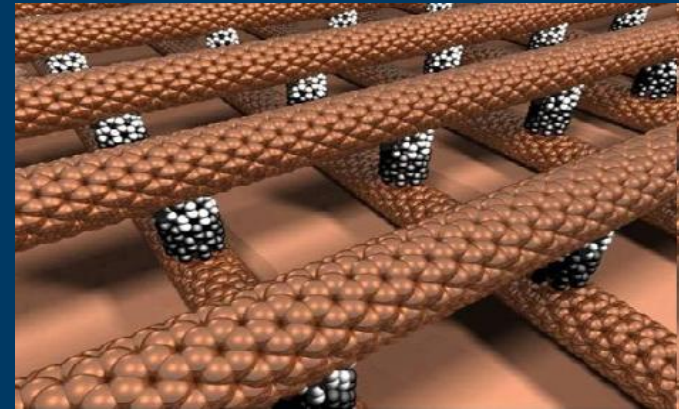
# Organizing Any Matter

- Use one kind of programmable matter (e.g. DNA).
- To organize (almost) ANY matter through it.

6 nm grid of individually addressable DNA pixels



PWK Rothemund, *Nature* 440, 297 (2006)



European Nanoelectronics Initiative Advisory Council

"What we are really making are tiny DNA circuit boards that will be used to assemble other components."

*Greg Wallraff, IBM*

# Executing Any Kinetics

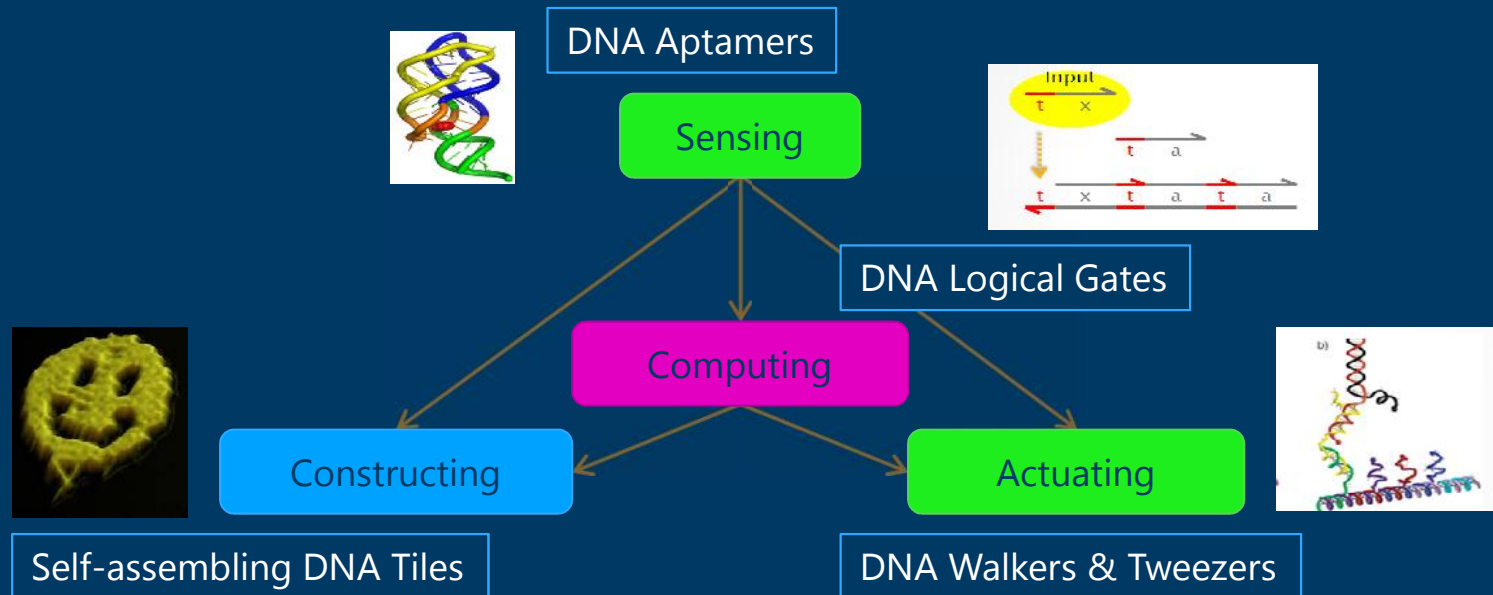
- The kinetics of any finite network of chemical reactions, can be implemented (physically) with especially programmed DNA molecules.
- Chemical reactions as an executable programming language for dynamical systems!

**DNA as a universal substrate for chemical kinetics**

David Soloveichik<sup>a,1</sup>, Georg Seelig<sup>a,b,1</sup>, and Erik Winfree<sup>c,1</sup>

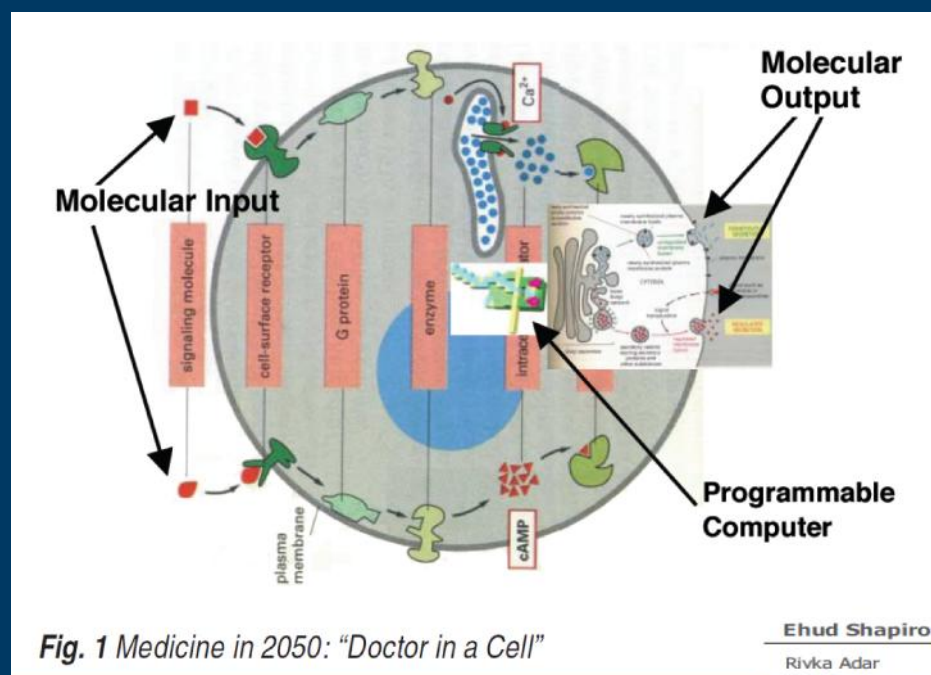
# Building Nano-Control Devices

- All the components of nanocontrollers can already be built entirely and solely with DNA, and interfaced to the environment



# Interfacing to Biology

A doctor in each cell



Ehud Shapiro

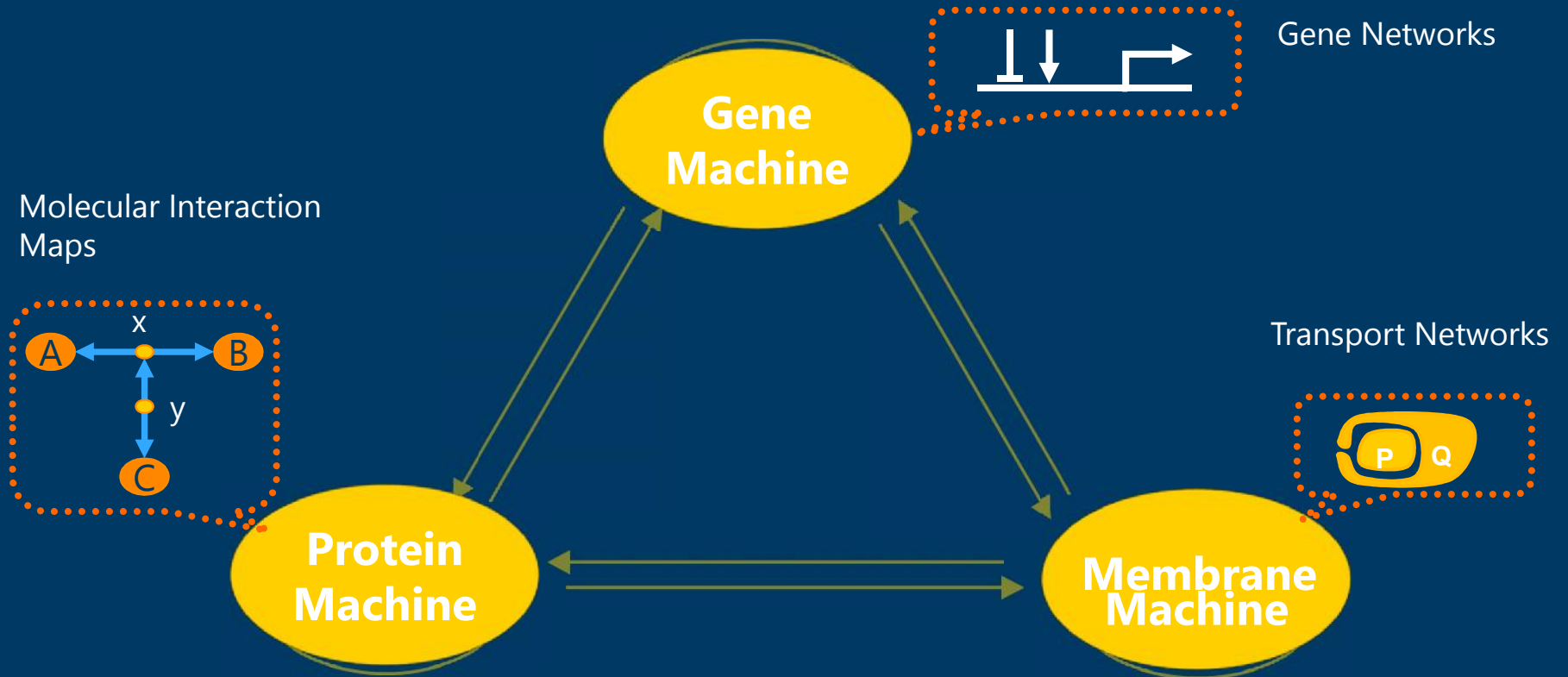
Rivka Adar  
Kobi Benenson  
Gregory Linshitz  
Aviv Regev  
William Silverman

**Molecules and  
computation**

# The Biological Argument

Biological systems are already  
'molecularly programmed'

# Biological Languages



## But ...

- Biology is programmable, but not by us!
- Still work in progress:
  - Gene networks are being programmed in synthetic biology, but using existing 'parts'
  - Protein networks are a good candidate, unfortunately we cannot yet effectively design proteins
  - Transport networks are being looked at for programming microfluidic devices manipulating vesicles



# Molecular Languages

... that **we** can execute

# Action Plan

- Building a full software/hardware pipeline for a new fundamental technology
  - **Mathematical Foundations** [~ concurrency theory in the 80's]
  - **Programming Languages** [~ software engineering in the 70's]
  - **Analytical Methods and Tools** [~ formal methods in the 90's]
  - **Device Architecture and Manufacturing** [~ electronics in the 60's]
- To realize the potential of Molecular Programming
- This is largely a 'software problem' even when working on device design

# The role of DNA Computing

- Non-goals
  - Not to solve NP-complete problems with large vats of DNA
  - Not to replace silicon
- Bootstrapping a carbon-based technology
  - To precisely control the organization and dynamics of matter and information at the molecular level
  - DNA is our engineering material
    - Its biological origin is "accidental" (but convenient)
    - It is an information-bearing programmable material
    - It is possible that other such materials will be developed

# Domains

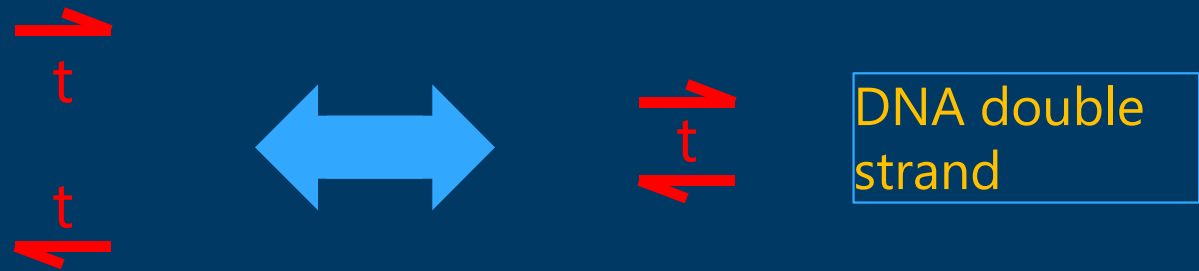
- Subsequences on a DNA strand are called **domains**
  - *provided* they are “independent” of each other



oriented DNA  
single strand

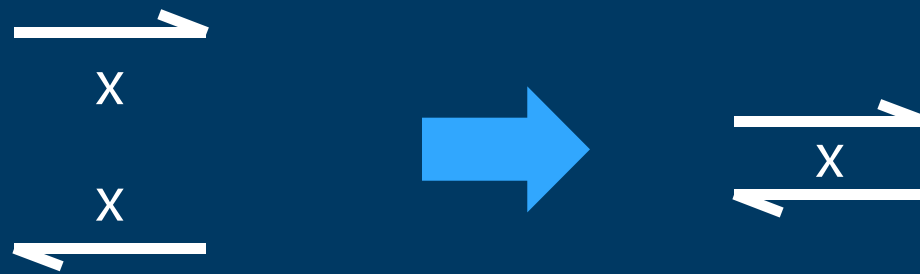
- That is, differently named domains must not **hybridize**
  - With each other, with each other’s complement, with subsequences of each other, with concatenations of other domains (or their complements), etc.

# Short Domains



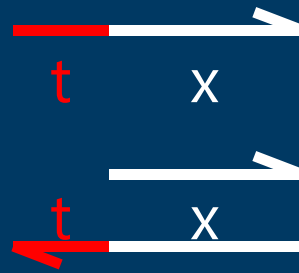
Reversible Hybridization

# Long Domains



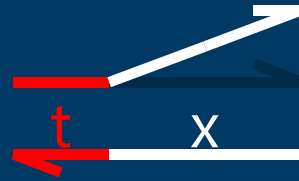
Irreversible Hybridization

# Strand Displacement



“Toehold Mediated”

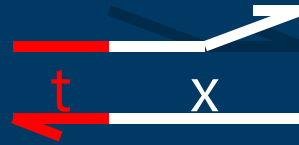
# Strand Displacement



Toehold Binding

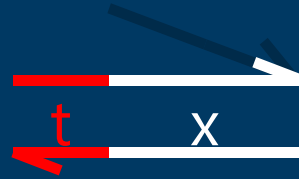


# Strand Displacement



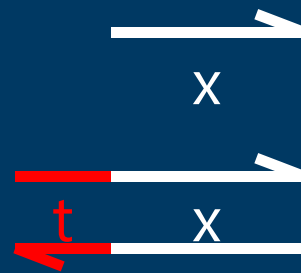
Branch Migration

# Strand Displacement



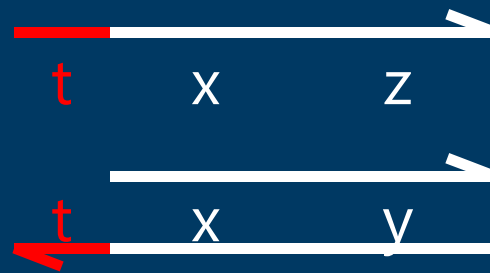
Displacement

# Strand Displacement

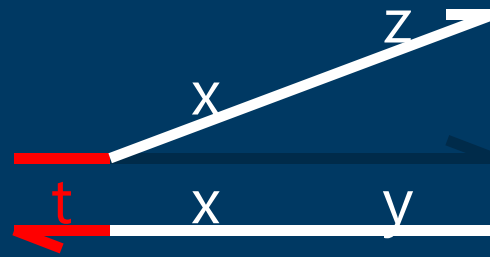


Irreversible release

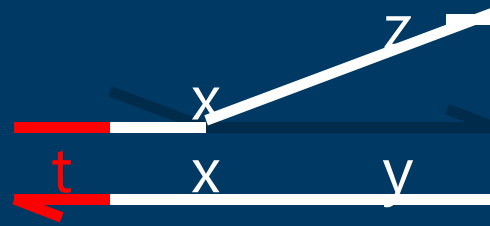
# Bad Match



# Bad Match



# Bad Match



# Bad Match



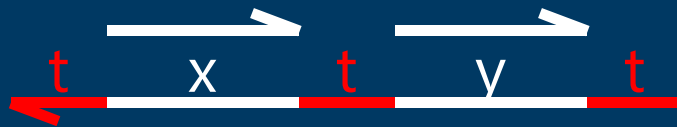
Cannot proceed  
Hence will undo

# Two-Domain Architecture

- Signals: 1 toehold + 1 recognition region



- Gates: “top-nicked double strands” with open toeholds



Garbage collection  
“built into” the gates

## Two-Domain DNA Strand Displacement

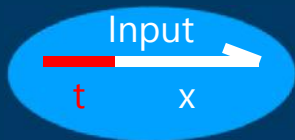
*Luca Cardelli*

In S. B. Cooper, E. Kashefi, P. Panangaden (Eds.):  
Developments in Computational Models (DCM 2010).  
EPTCS 25, 2010, pp. 33-47. May 2010.

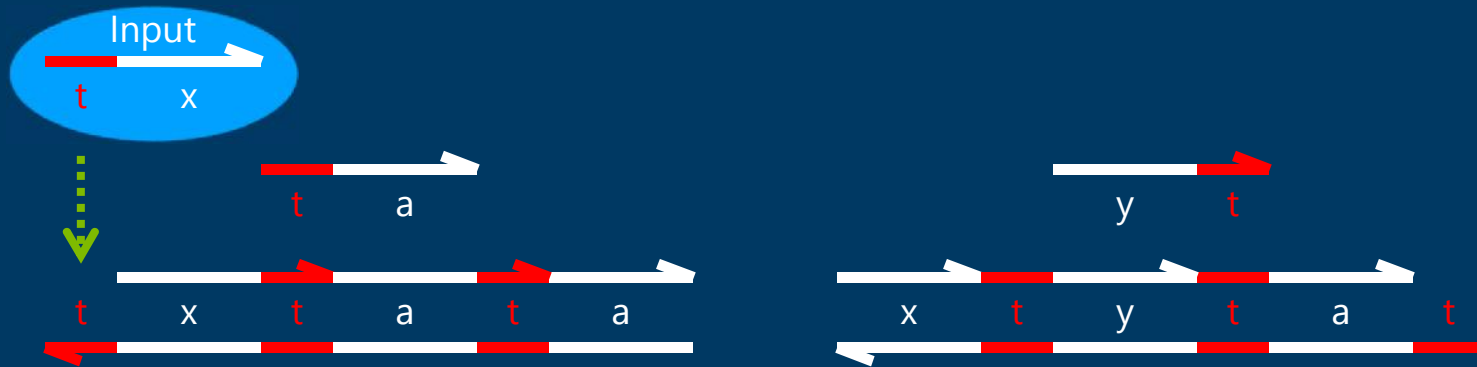


# Transducer

# Transducer $x \rightarrow y$



# Transducer $x \rightarrow y$



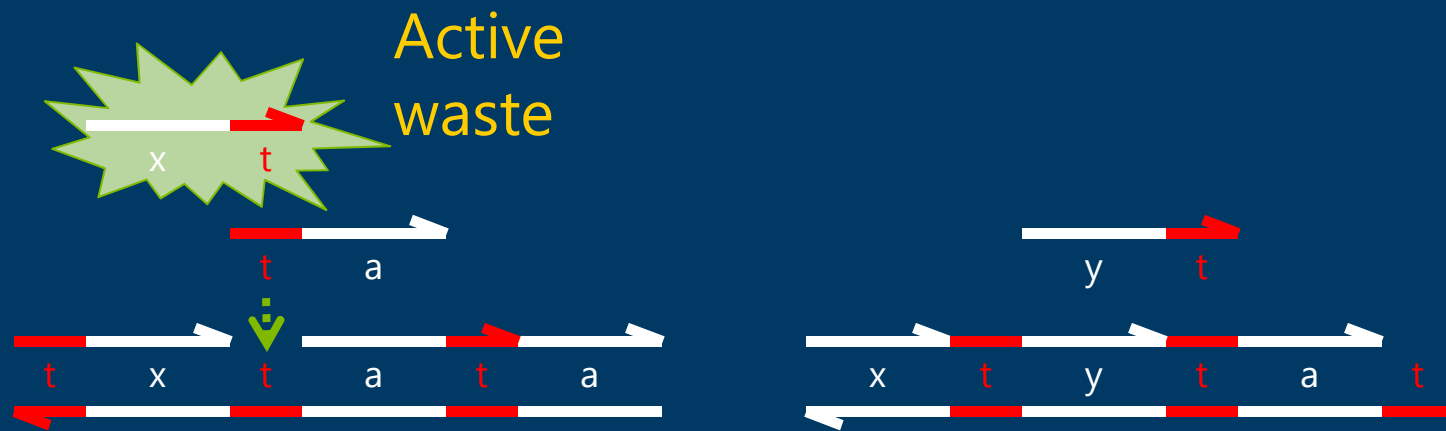
Built by self-assembly!

**ta** is a *private* signal (a different 'a' for each  $xy$  pair)

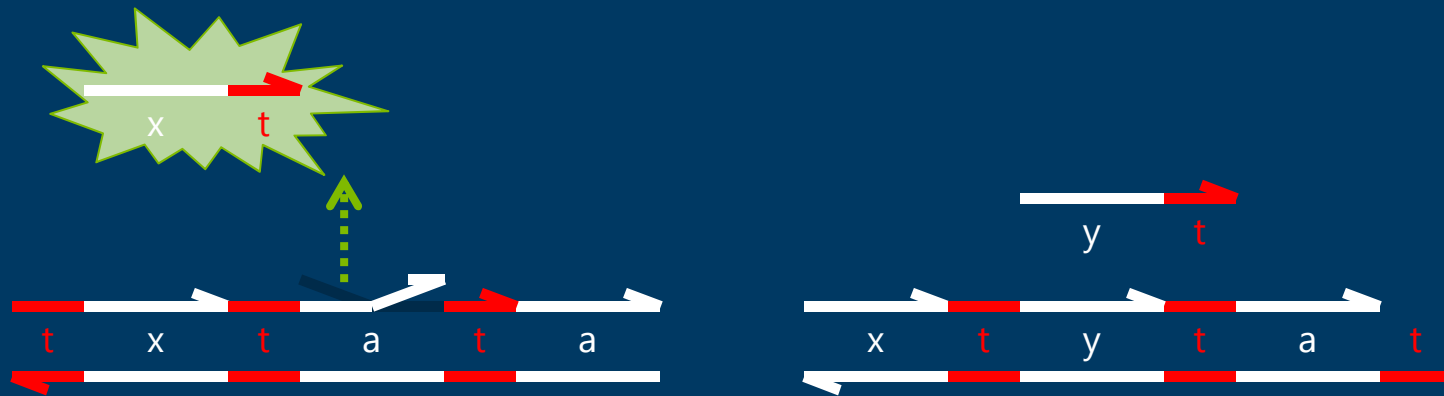
# Transducer $x \rightarrow y$



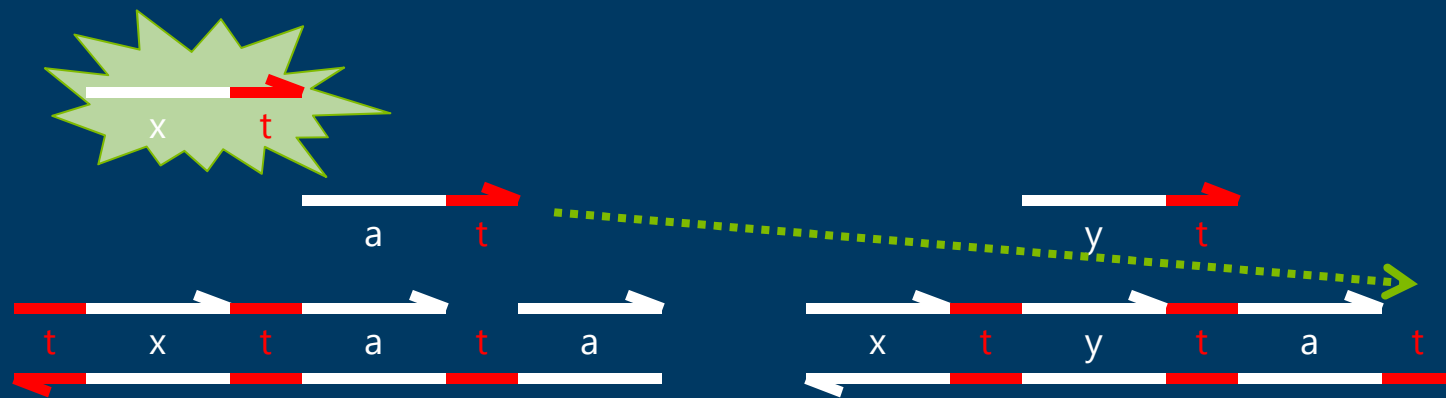
# Transducer $x \rightarrow y$



# Transducer $x \rightarrow y$



# Transducer $x \rightarrow y$



So far, a **tx** signal has produced an **at** cosignal.  
But we want signals as output, not cosignals.

# Transducer $x \rightarrow y$

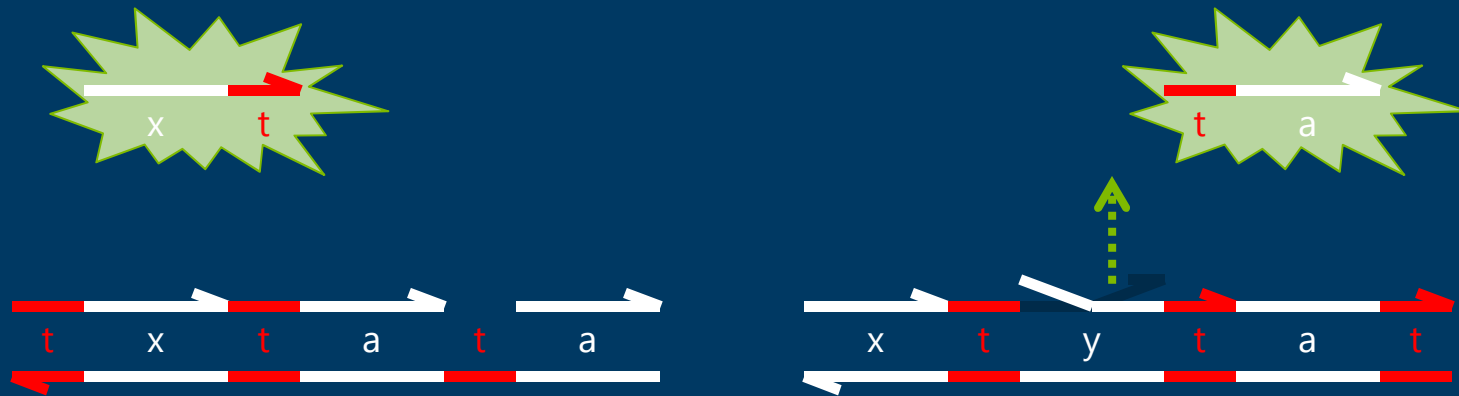




# Transducer $x \rightarrow y$



# Transducer $x \rightarrow y$



# Transducer $x \rightarrow y$



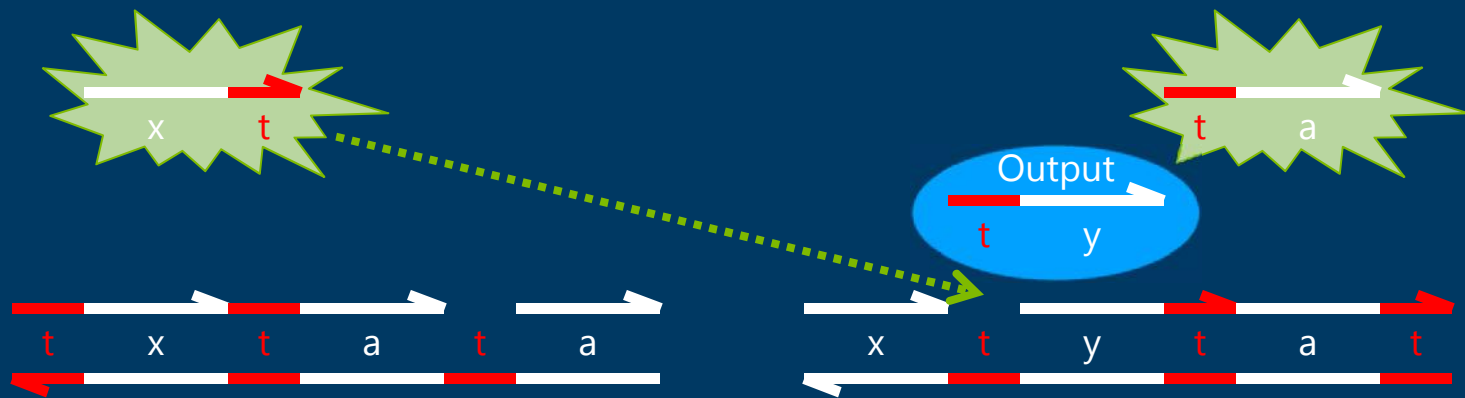
Here is our output **ty** signal.

But we are not done yet:

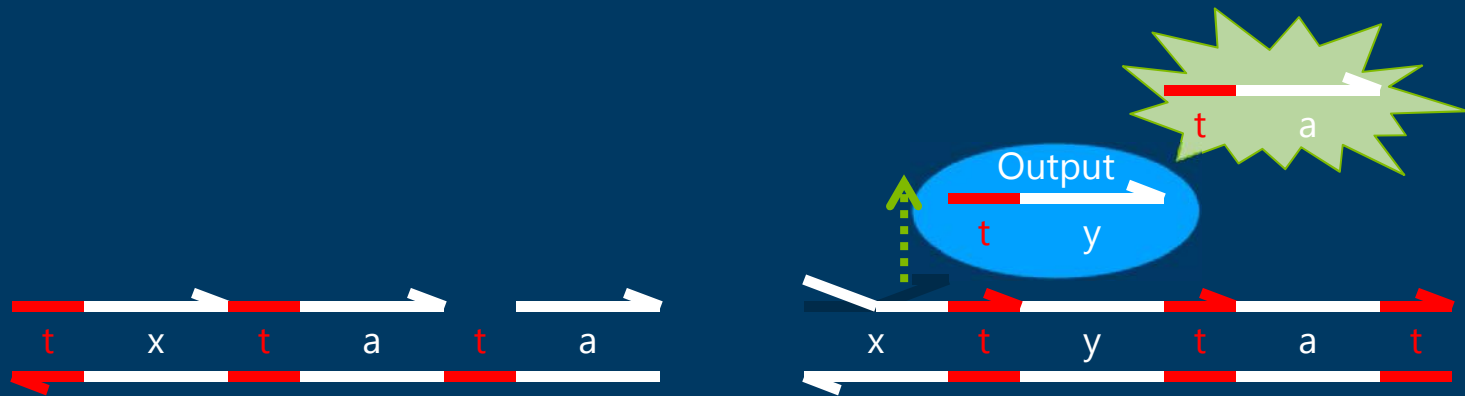
- 1) We need to make the output irreversible.
- 2) We need to remove the garbage.

We can use (2) to achieve (1).

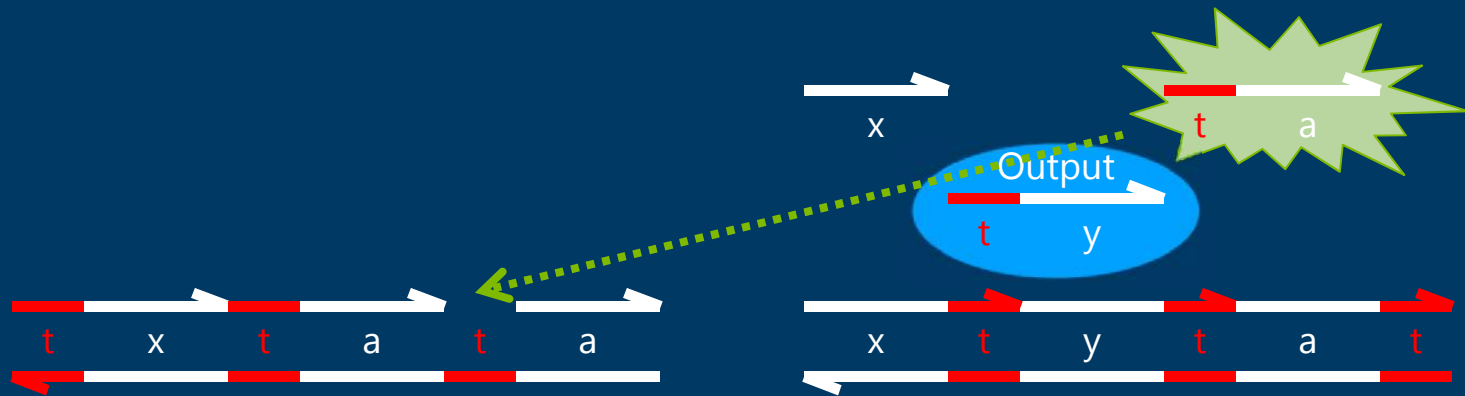
# Transducer $x \rightarrow y$



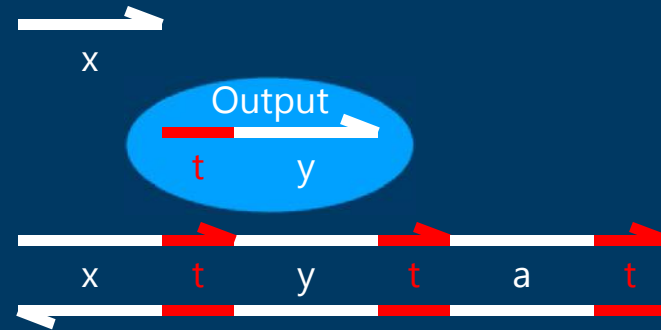
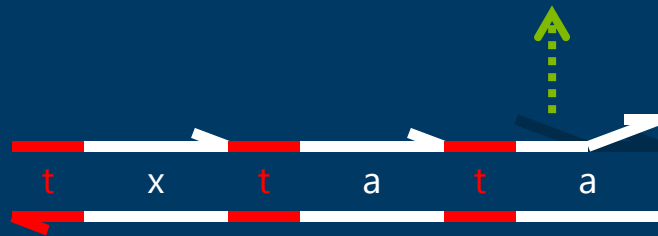
# Transducer $x \rightarrow y$



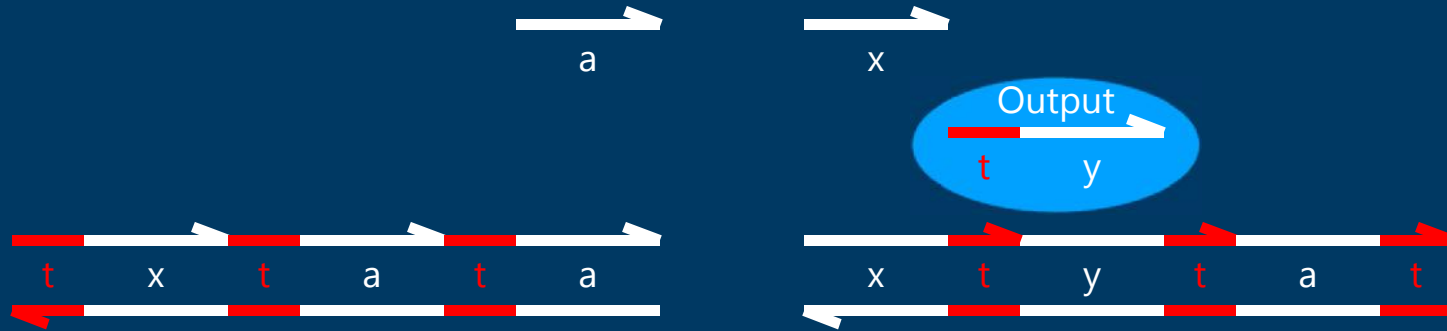
# Transducer $x \rightarrow y$



# Transducer $x \rightarrow y$



# Transducer $x \rightarrow y$





# Transducer $x \rightarrow y$



Done.

N.B. the gate is consumed: it is the energy source





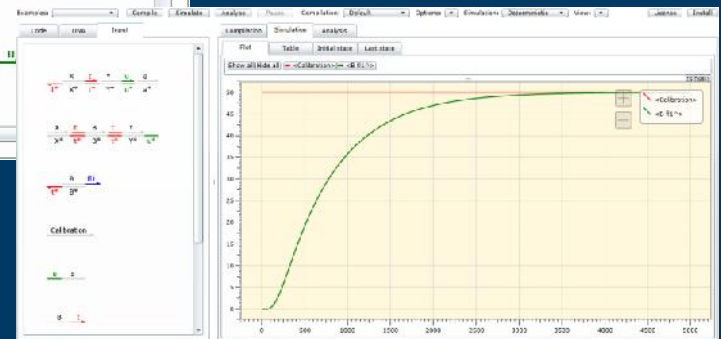
# Development Tools

## MSRC Bio Computation Group

The screenshot shows the Interface software interface. On the left, a code editor displays the following code:

```
def bind = kT1.0e+3 (* /invs Y)  
def unbind = kL*exu_DeltaE_over_RT (* /s *)  
new t@bind,unbind  
new u@bind,unbind  
new f@0.0,0.0  
  
def cnsx = 50.0  
  
(* x - y -> y + z *)  
def Cat(N, X, Y, Z) =  
  new C  
  ( (1.5*M) * f*[X+Y][Y+Z]:[X]  
    | (1.5*M) * f*[X+Z][Y+Z]:[Y]  
    | (2.0*M) * cnsx * a  
    | (2.0*M) * cnsx * b  
  )  
  
def hcp(N,X,Z) =  
  ((1.0*M) * f*[X+Z]:[X])  
  
( cnsx = <calibration>  
  | cat(nex,K,Y,Z)  
  | Rep(cnsx,0,[1])  
  | area * <L^X>  
  | cnsx * <L^Y>  
)
```

The code is highlighted with a red box. The main window displays several reaction diagrams showing the interaction of species X, Y, Z, U, and A, with various rate constants and binding/unbinding processes.



JOURNAL OF THE ROYAL SOCIETY

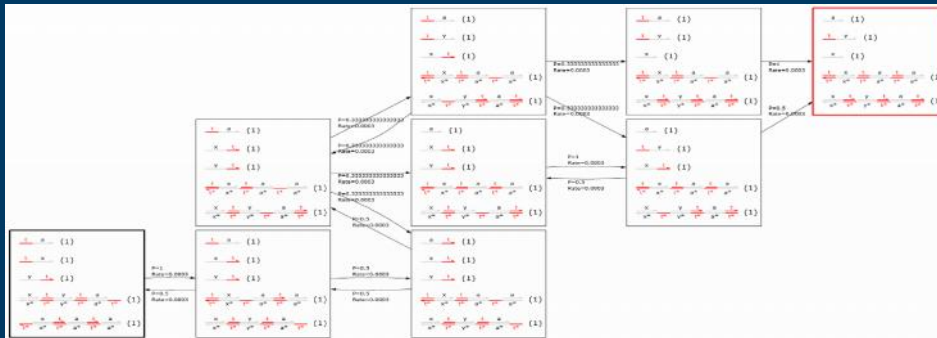
Interface

A programming language for composable DNA circuits

Andrew Phillips and Luca Cardelli

# Analytical Methods

- Probabilistic modelchecking (complete state space exploration) to test system correctness.



JOURNAL OF THE ROYAL SOCIETY **Interface**

Design and analysis of DNA strand displacement devices using probabilistic model checking

Matthew R. Lakin<sup>1,2,†</sup>, David Parker<sup>2,†</sup>, Luca Cardelli<sup>1</sup>, Marla Kwiatkowska<sup>2</sup> and Andrew Phillips<sup>1,\*</sup>

- Quantitative theories of system equivalence and approximation.

CONTINUOUS MARKOVIAN LOGICS  
AXIOMATIZATION AND QUANTIFIED METATHEORY

RADU MARDARE, LUCA CARDELLI, AND KIM G. LARSEN

# Approximate Majority Algorithm

- Given two populations of agents (or molecules)
  - Randomly communicating by radio (or by collisions)
  - Reach an agreement about which population is in majority
  - By converting all the minority to the majority  
[Angluin et al., Distributed Computing, 2007]
- Could also be used to restore a digital signal to full strength

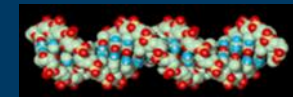
- 3 rules of agent (or molecule) interaction

•  $X + Y \rightarrow B + B$

•  $B + X \rightarrow X + X$

•  $B + Y \rightarrow Y + Y$

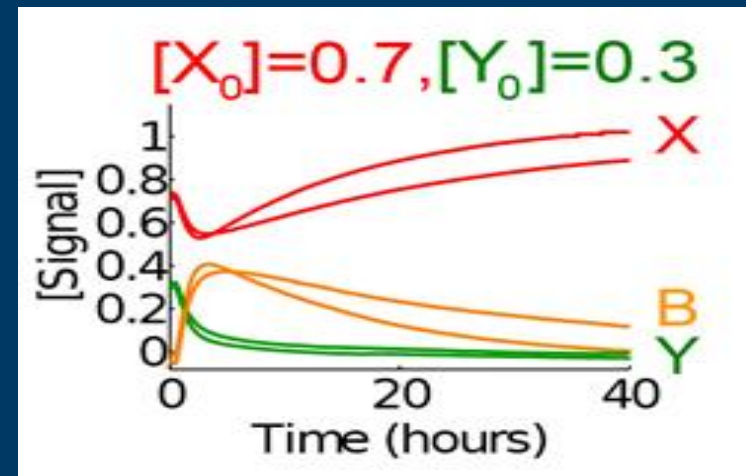
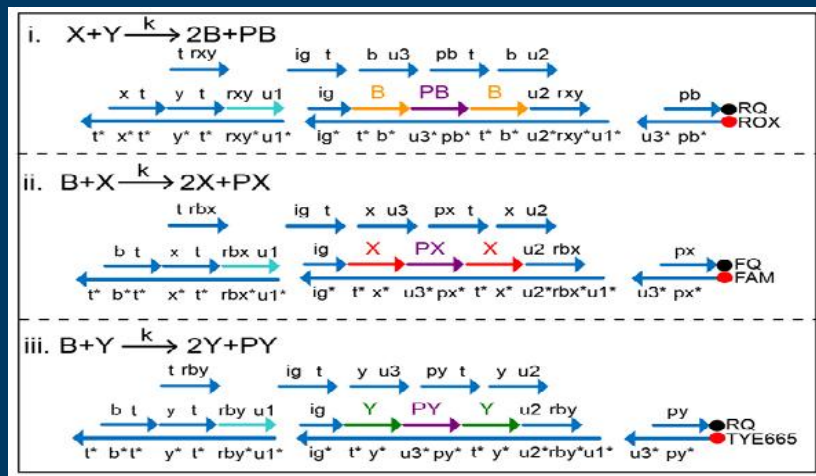
"our program"  $\rightarrow$



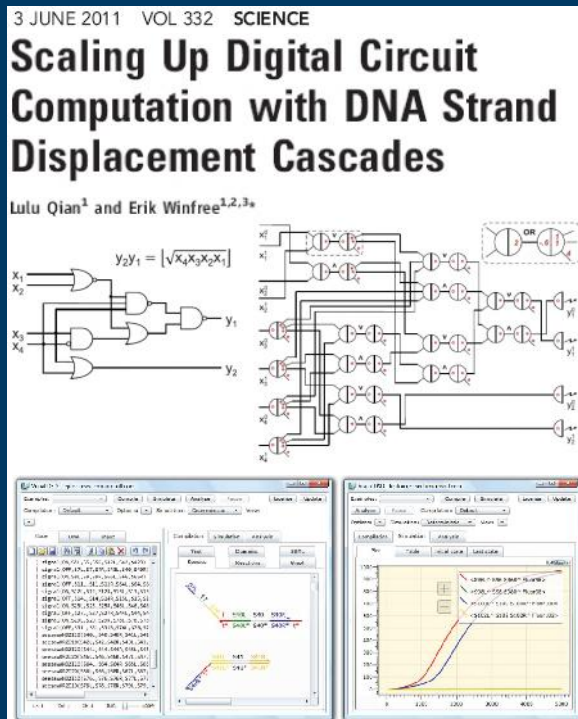
# DNA Implementation, at U.W.

- A DNA Realization of Chemical Reaction Networks

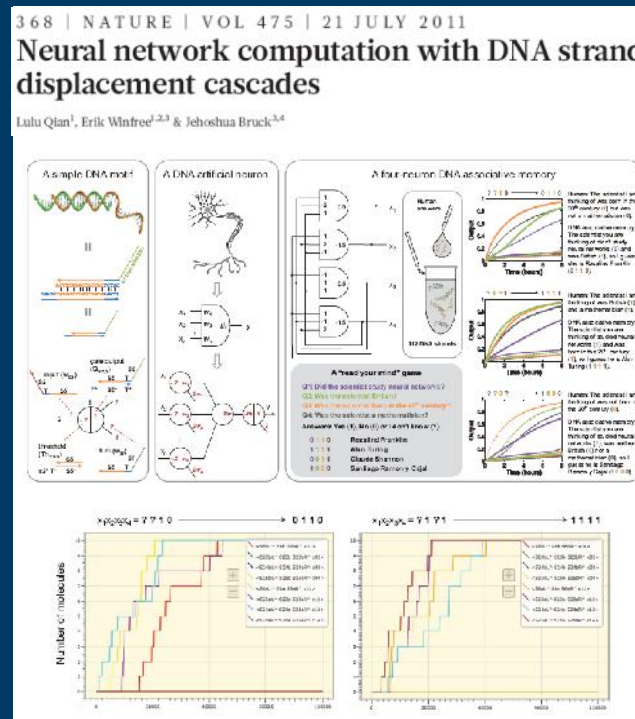
[Yuan-Jyue Chen, Neil Dalchau, Niranjana Srinivas, Andrew Phillips, Luca Cardelli, David Soloveichik and Georg Seelig]



# Related Work Supporter by our Tools



Square root of a 4-bit number



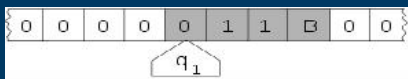
Associative memory



# Final Remarks

# Outlook: A Brief History of DNA

Turing Machine, 1936



Transistor, 1947



~~Digital Computers~~

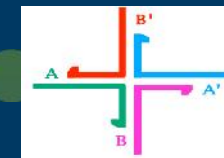
Computer programming

20<sup>th</sup> century

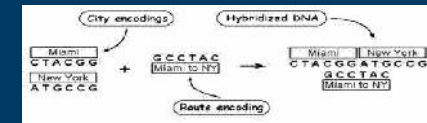
DNA, -3,800,000,000



Structural DNA, 1982



DNA Algorithm, 1994



**Software**  
*systematic  
manipulation  
of information*

**<??>**  
*systematic  
manipulation  
of matter*

~~DNA Computers~~

Molecular programming

21<sup>th</sup> century



©2013 Microsoft Corporation. All rights reserved.