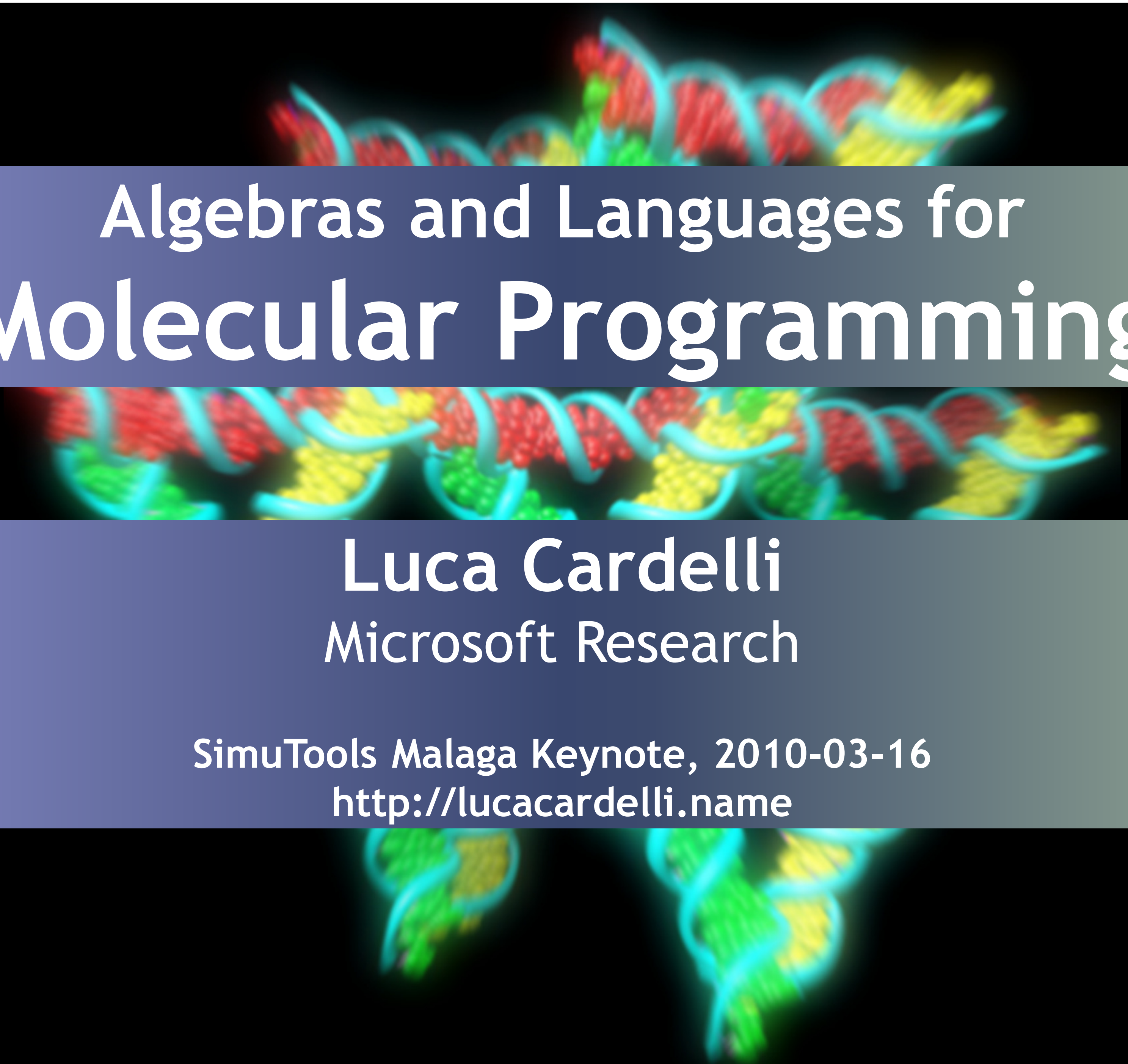


Algebras and Languages for
Molecular Programming

Luca Cardelli

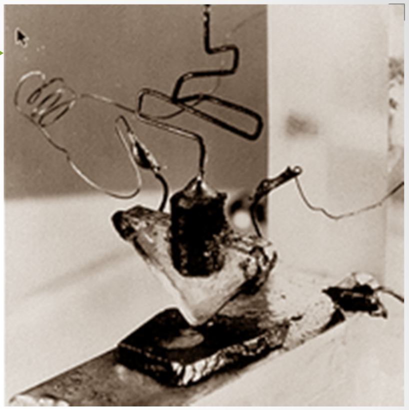
Microsoft Research

SimuTools Malaga Keynote, 2010-03-16

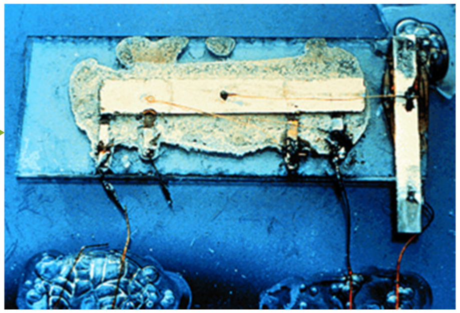
http://lucacardelli.name

Smaller and Smaller

Dec. 23, 1947. John Bardeen and Walter Brattain show the first working transistor.

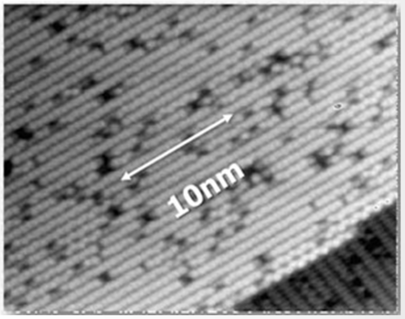


Sep. 1958. Jack Kilby builds the first integrated circuit.



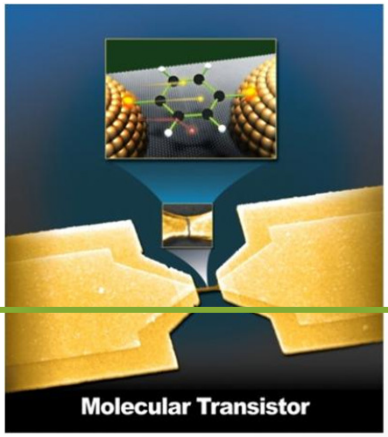
50 years later

Jan. 2010. Intel and Micron announce 25nm NAND flash.



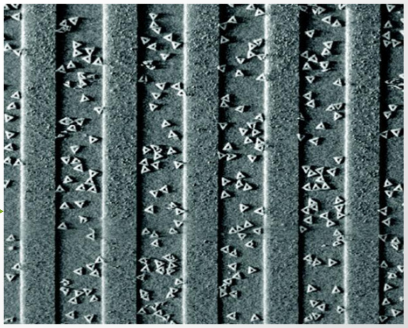
Scanning tunneling microscope image of a silicon surface showing 10nm is ~20 atoms across

Dec. 24, 2009. Working transistor made of a single molecule.



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

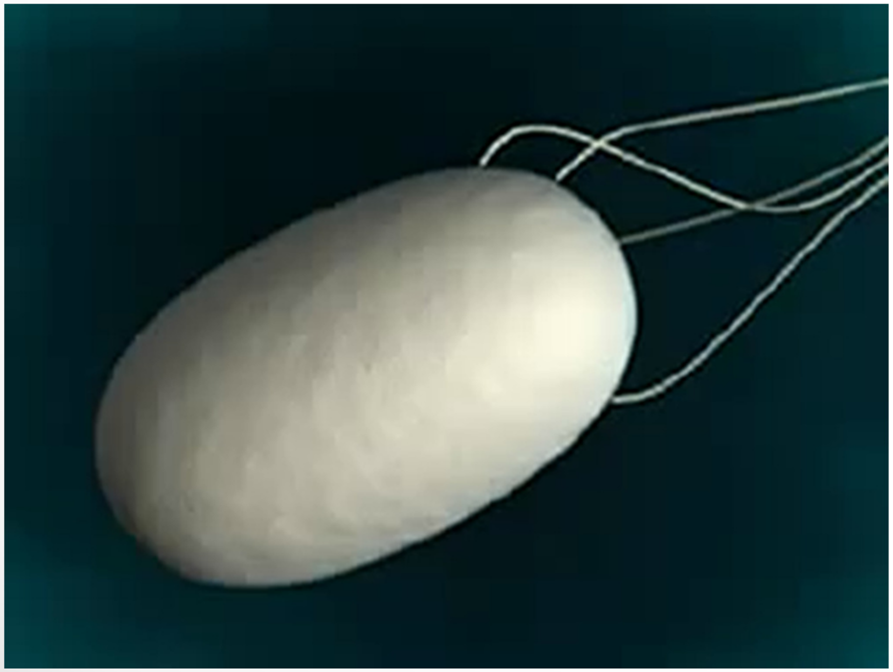
<10 iterations of Moore's Law left!
The race is on for *molecular scale integrated circuits*.



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

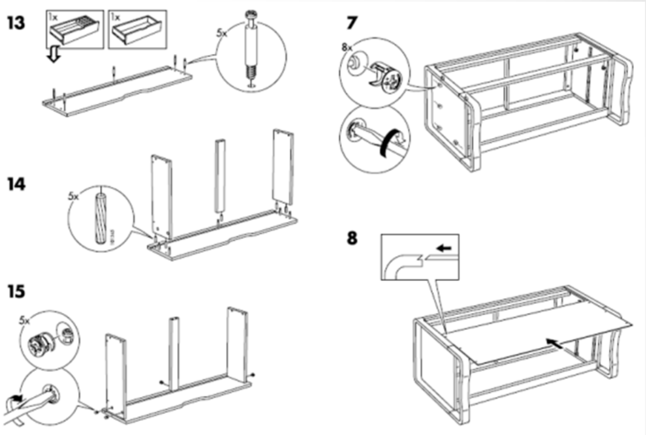
Building The Small*est* Things

- How do we build structures that are by definition smaller than your tools?
- Basic answer: you can't. Structures (and tools) should build themselves!
- By *programmed self-assembly*.

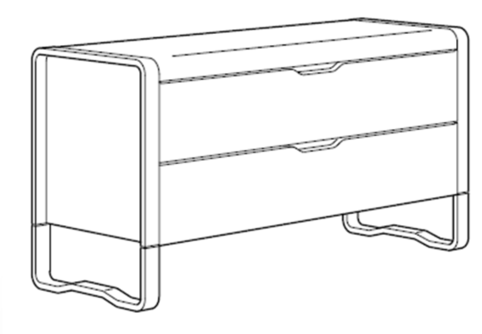


Molecular IKEA

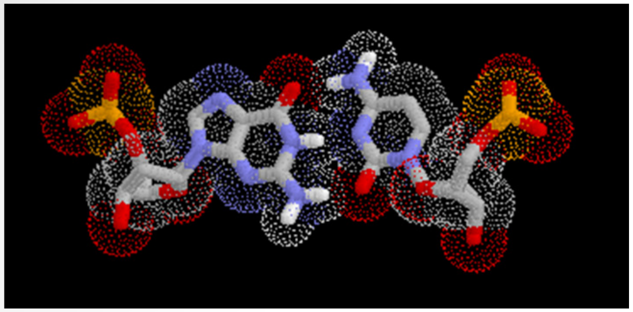
- Nature can self-assemble.
  Can we?
- *“Dear IKEA, please send me a chest of drawers that assembles itself.”*
- We need a magical material where the pieces are pre-programmed to fit into to each other.
- At the molecular scale many such materials exist; let’s pick one…



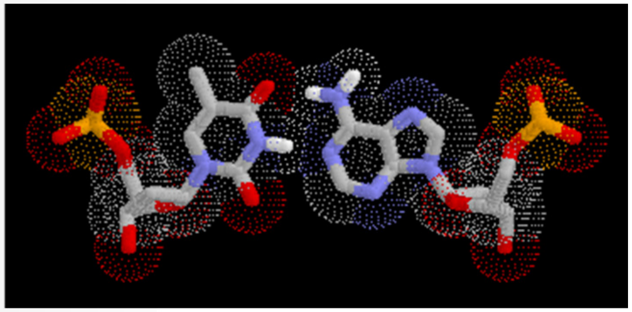
Add water



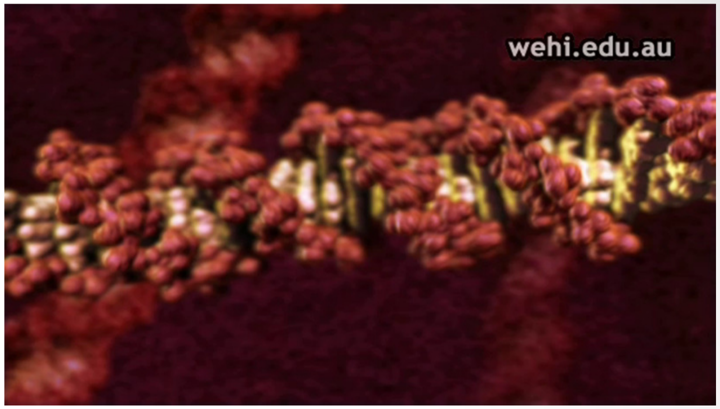
DNA



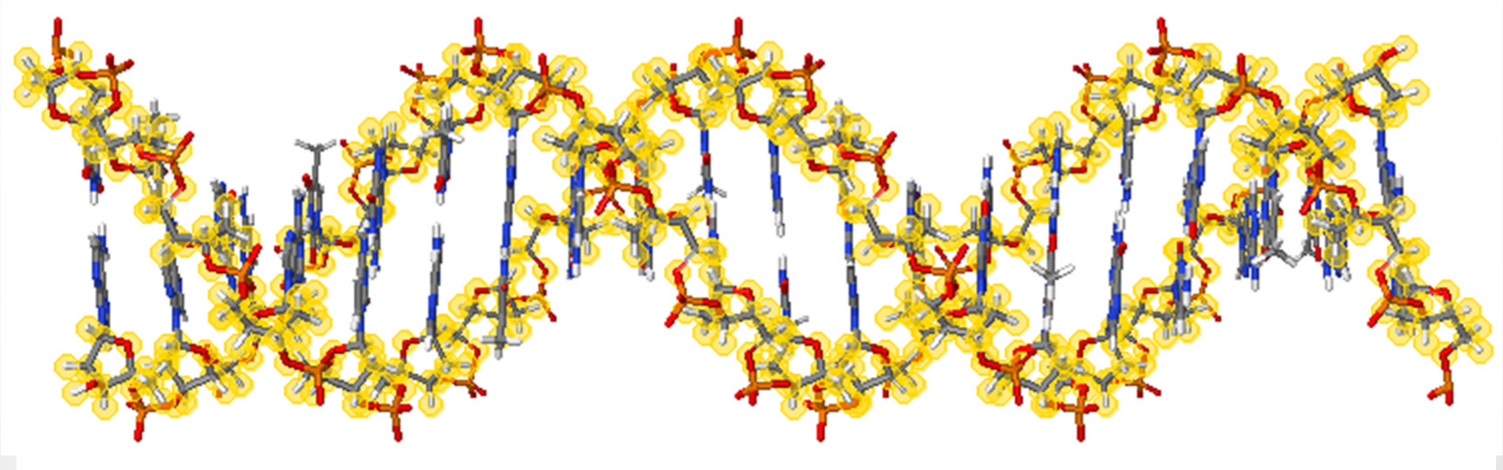
GC Base Pair
Guanine-Cytosine



TA Base Pair
Thymine-Adenine



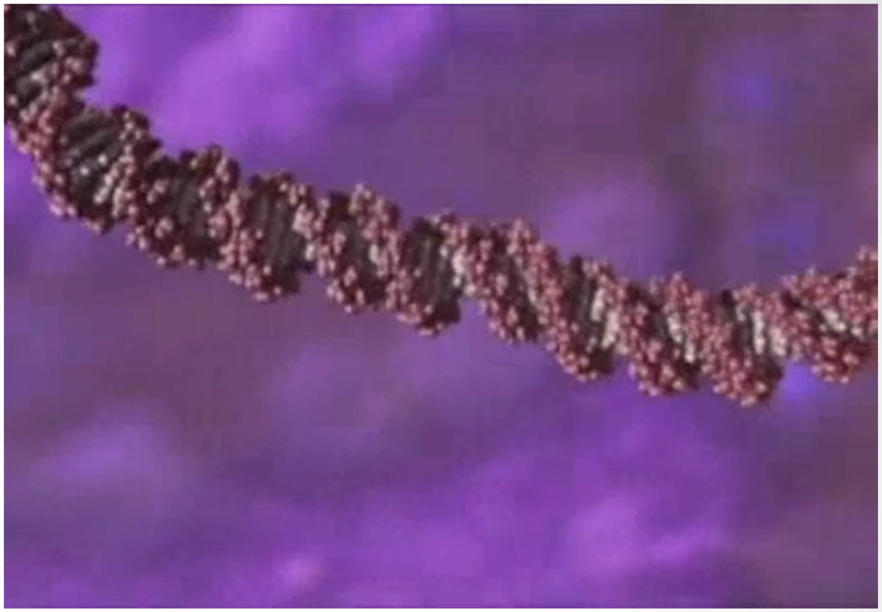
Interactive DNA Tutorial
(http://www.biosciences.bham.ac.uk/labs/minchin/tutorials/dna.html)



Sequence of Base Pairs (GACT alphabet)

Robust, and *Long*

- DNA in each human cell:
    - 3 billion base pairs
    - **2 meters long**, 2nm thick
    - folded into a 6μm ball
    - 750 MegaBytes
- A huge amount for a cell
    - Every time a cell replicates it has to copy *2 meters of DNA* reliably.
    - To get a feeling for the scale disparity, compute:
- DNA in human body
    - 10 trillion cells
    - 133 Astronomical Units long
    - 7.5 OctaBytes
- DNA in human population
    - 20 million light years long

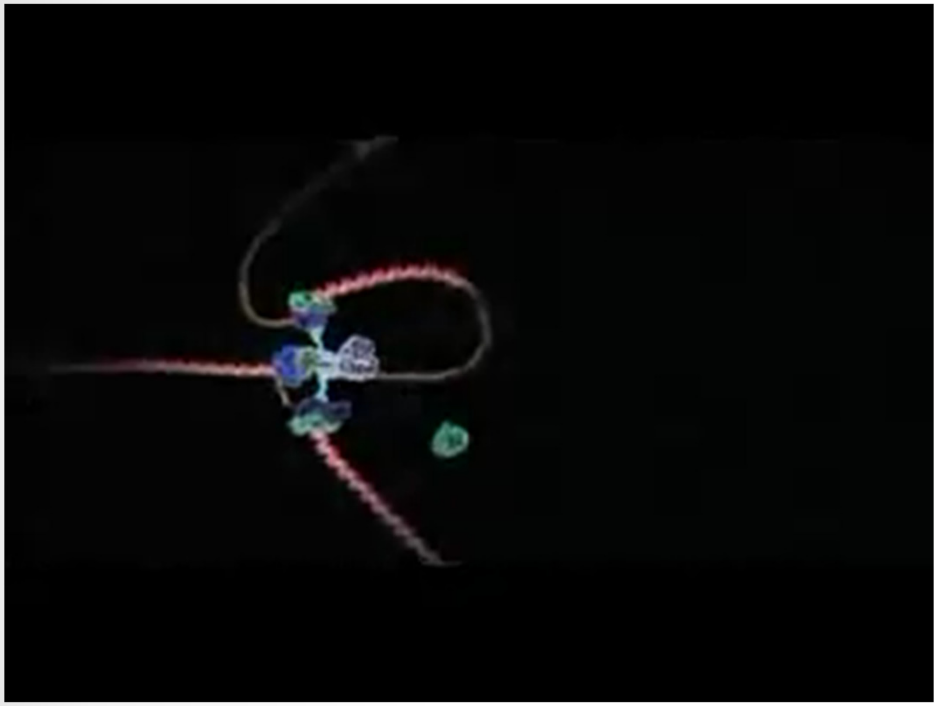


DNA wrapping into chromosomes

Andromeda Galaxy
2.5 million light years

Zipping Along

- DNA can support structural and computational complexity.



DNA replication in *real time*

In Humans: 50 nucleotides/second
Whole genome in a few hours (with parallel processing)

In Bacteria: 1000 nucleotides/second
(higher error rate)

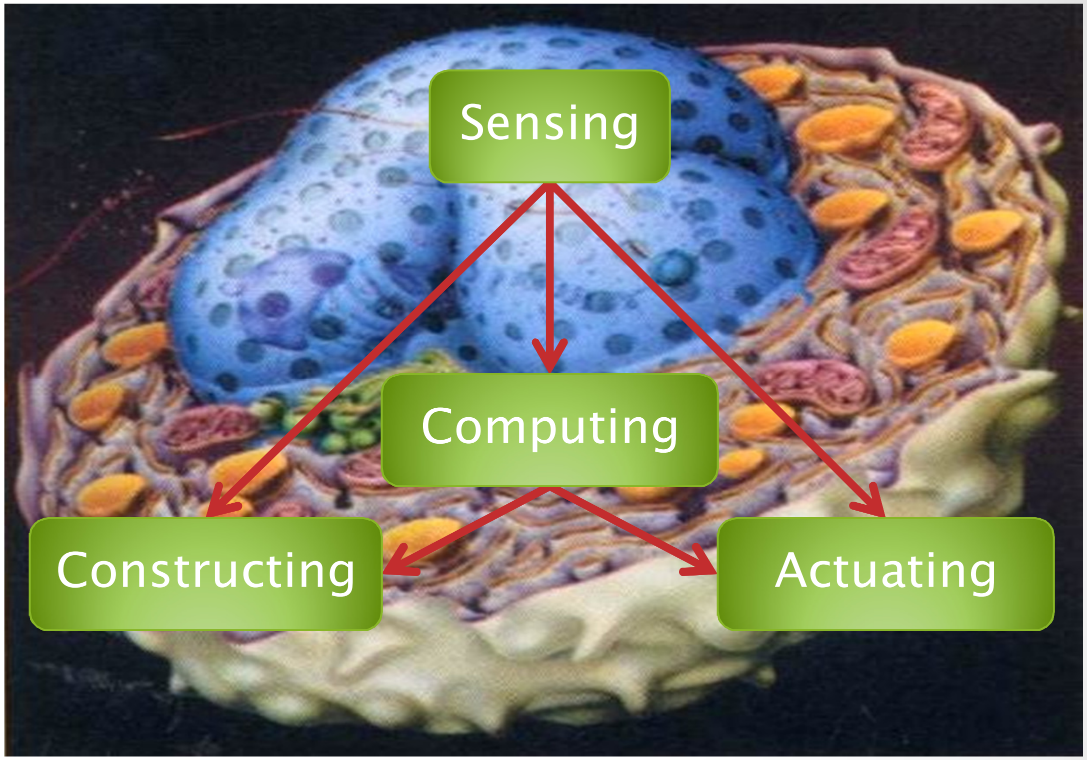
DNA transcription in *real time*

RNA polymerase II: 15-30 base/second

Drew Berry
http://www.wehi.edu.au/wehi-tv

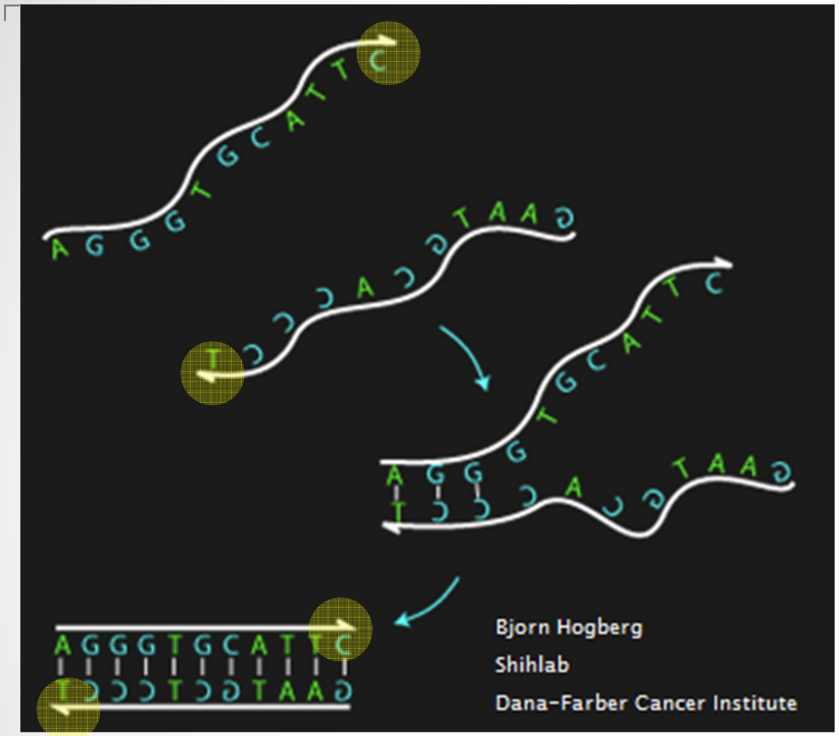
Nanoscale Engineering

- Sensing
  - Reacting to forces
  - Binding to molecules
- Actuating
  - Releasing molecules
  - Producing forces
- Constructing
  - Chassis
  - Growth
- Computing
  - Signal Processing
  - Decision Making

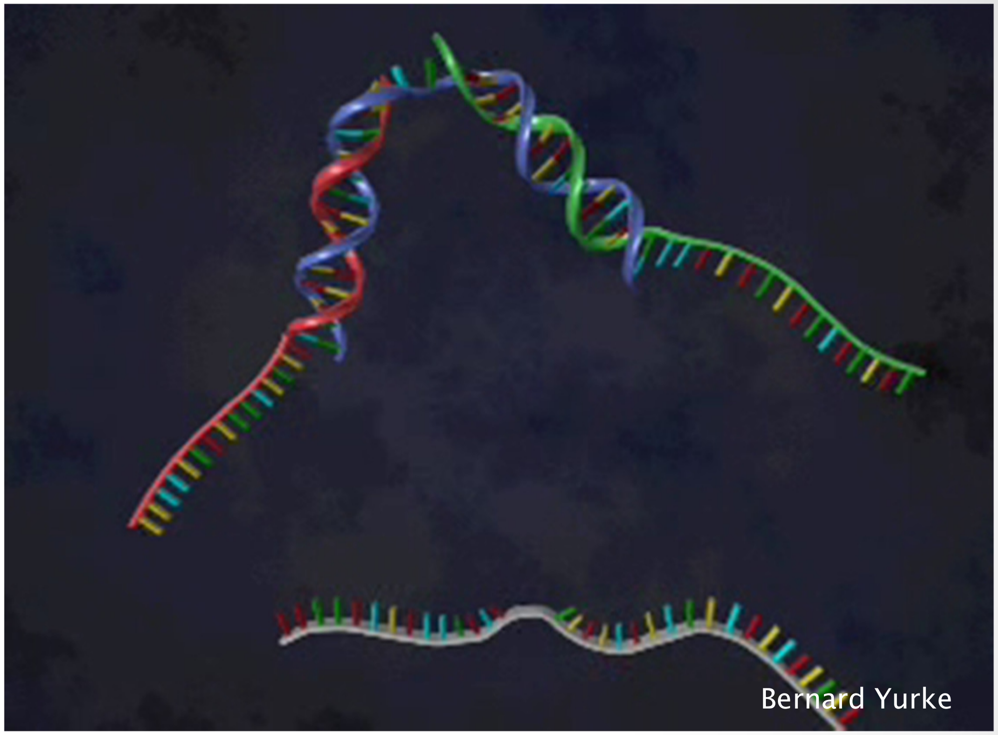


Nucleic Acids can do all this.
And interface to biology.

Hybridization

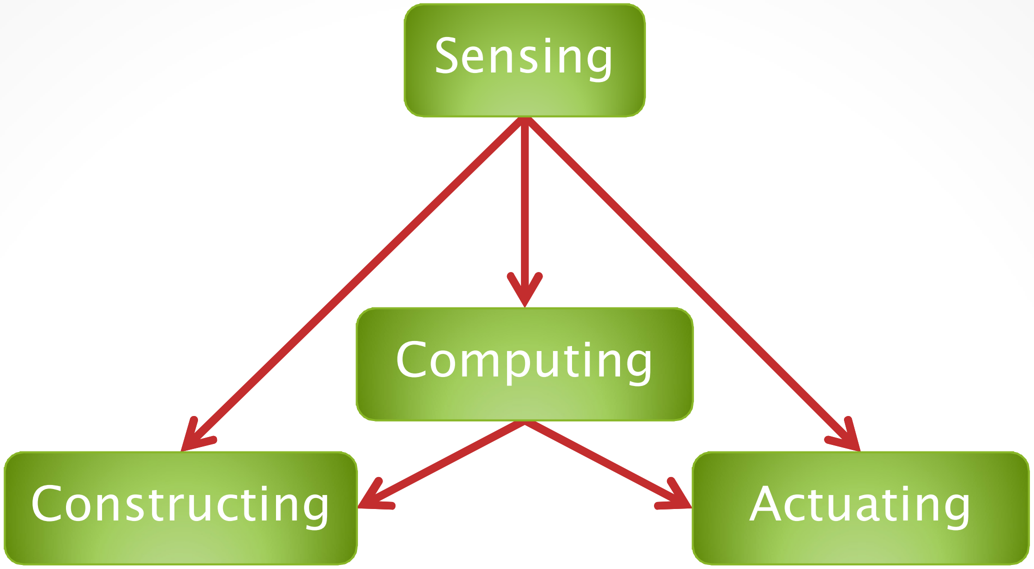


Bjorn Hogberg
Shihlab
Dana-Farber Cancer Institute



Bernard Yurke

- Strands with **opposite orientation** and **complementary base pairs** stick to each other (Watson-Crick duality).
- This is all we are going to use
  - We are not going to exploit DNA replication, transcription, translation, **restriction and ligation enzymes**, etc., which enable other classes of tricks.

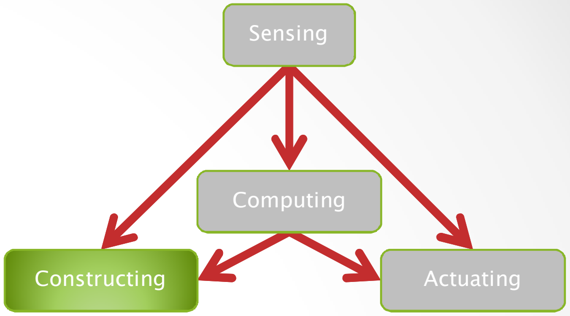

Sensing

Computing

Constructing

Actuating

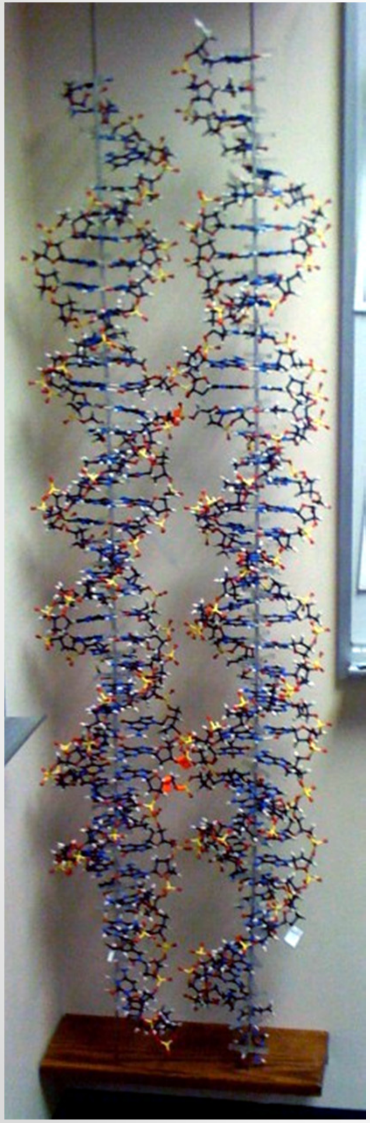
Hybridization Tricks

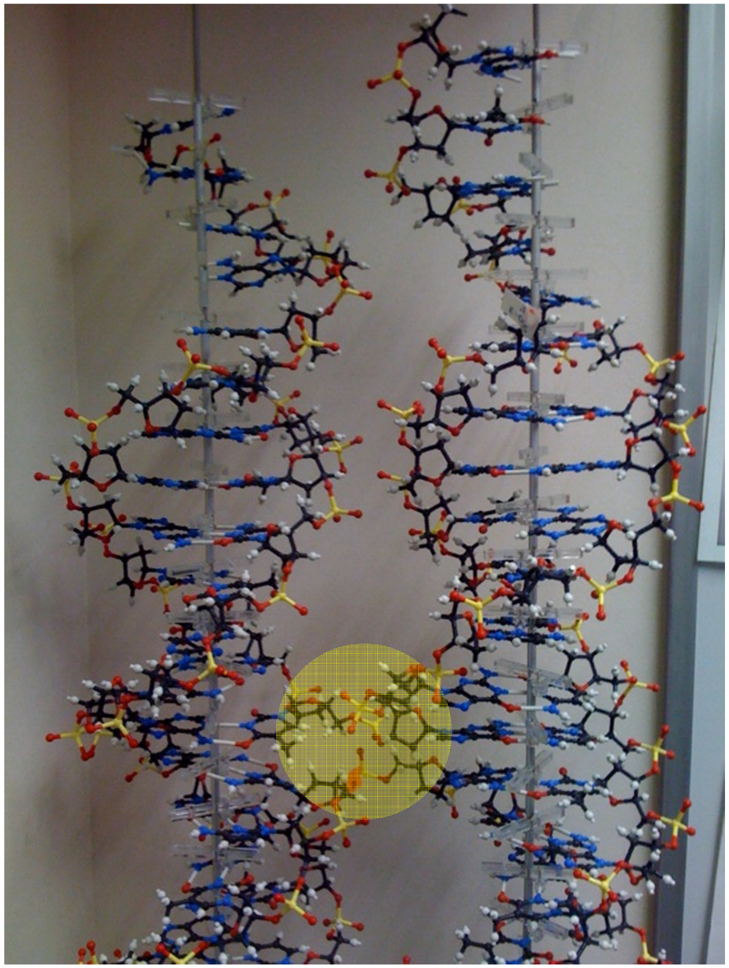


Constructing

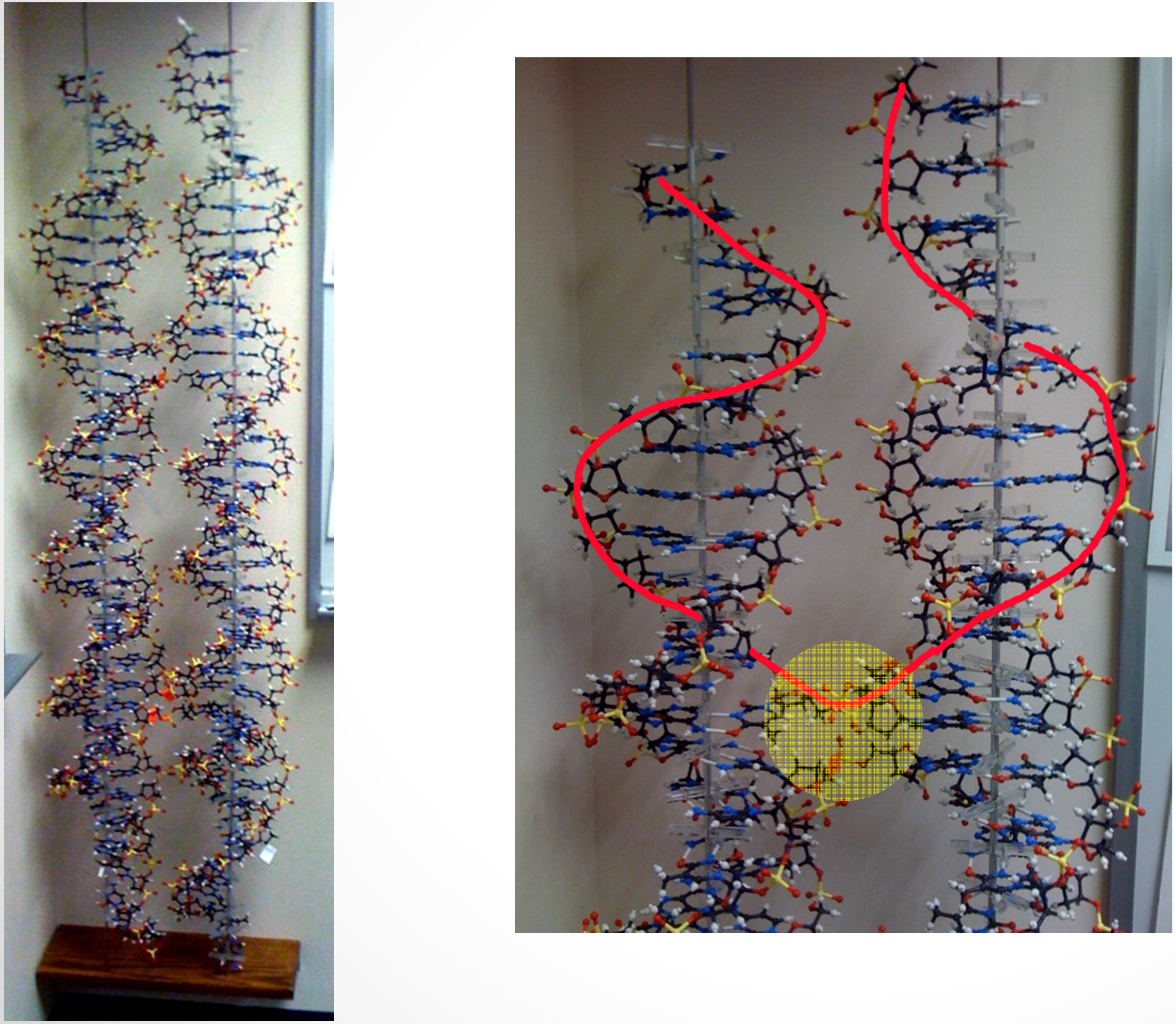
• • •

Crosslinking

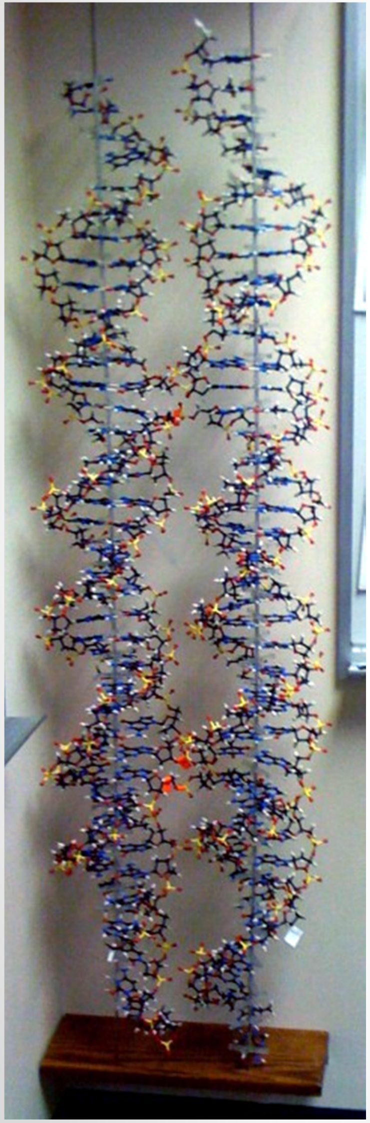


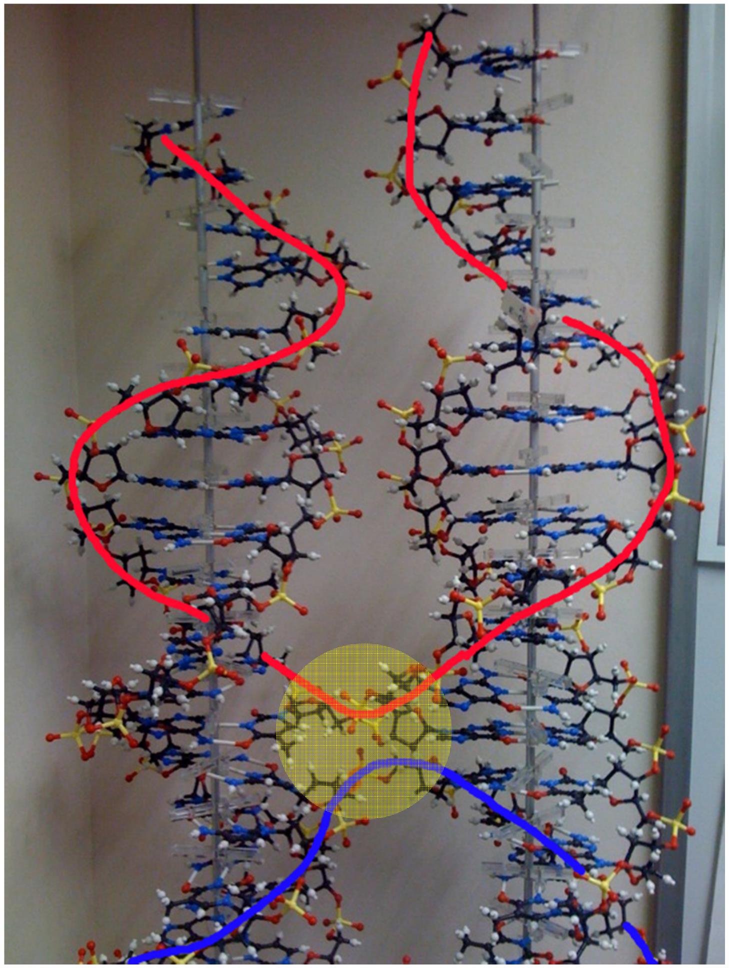


Crosslinking



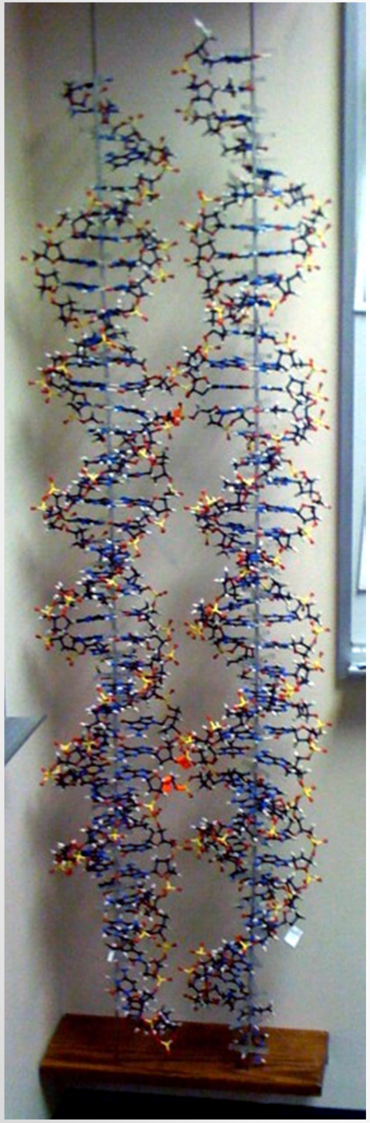
Crosslinking

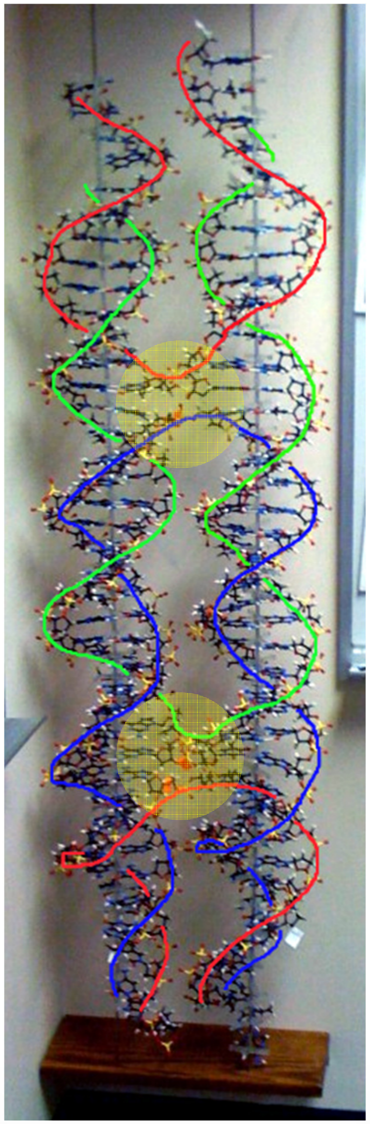




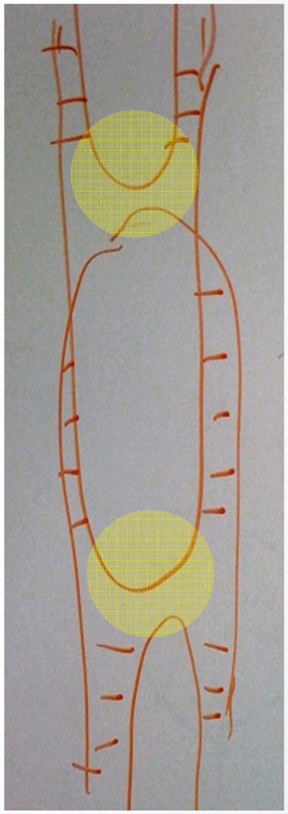
Crosslinking

Crosslinking



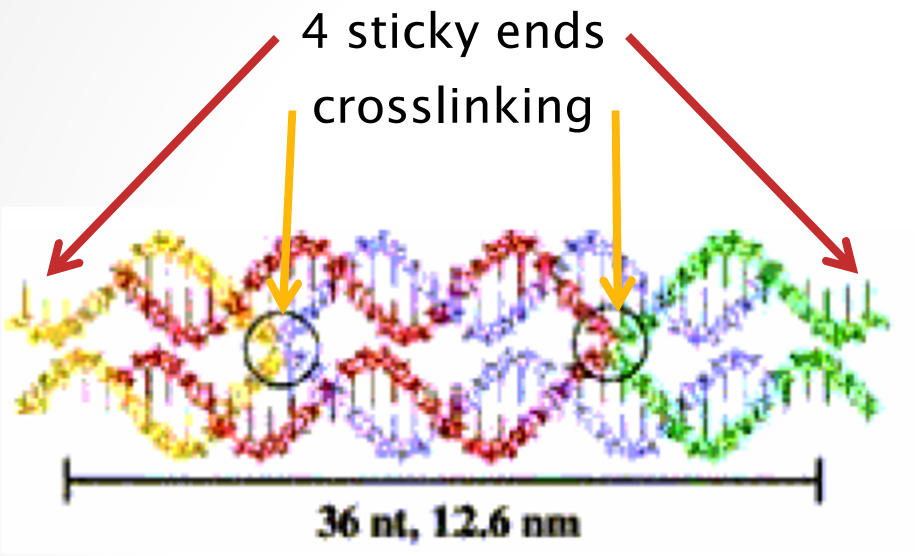


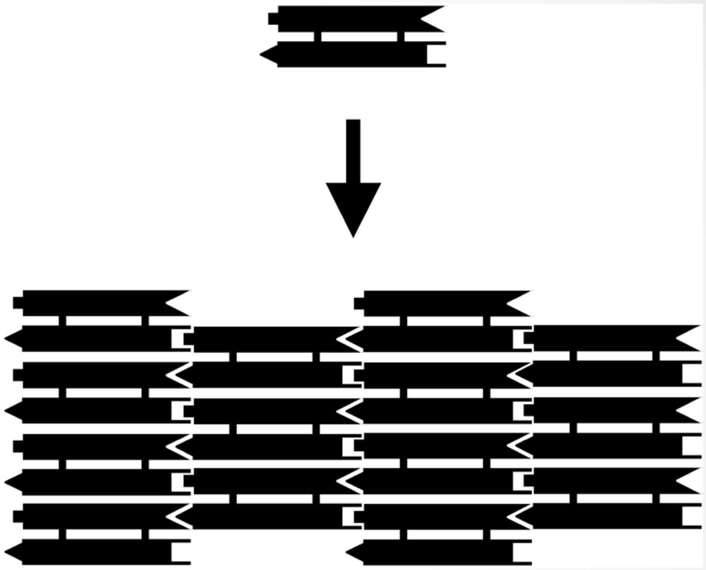
In nature, crosslinking is deadly (blocks DNA replication).

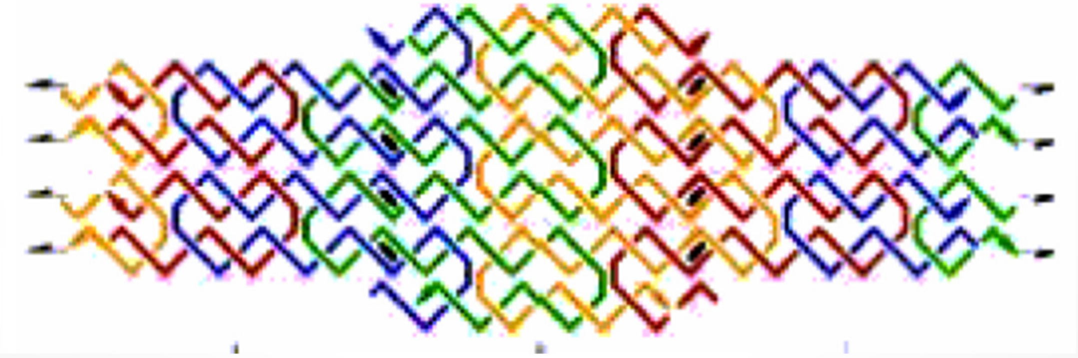


In engineering, crosslinking is the key to using DNA as a construction material.

DNA Tiling



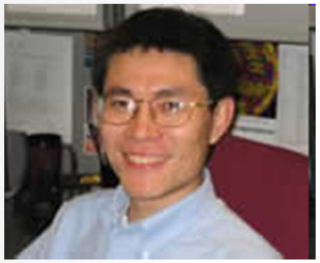




Construction and manipulation of DNA tiles in free space

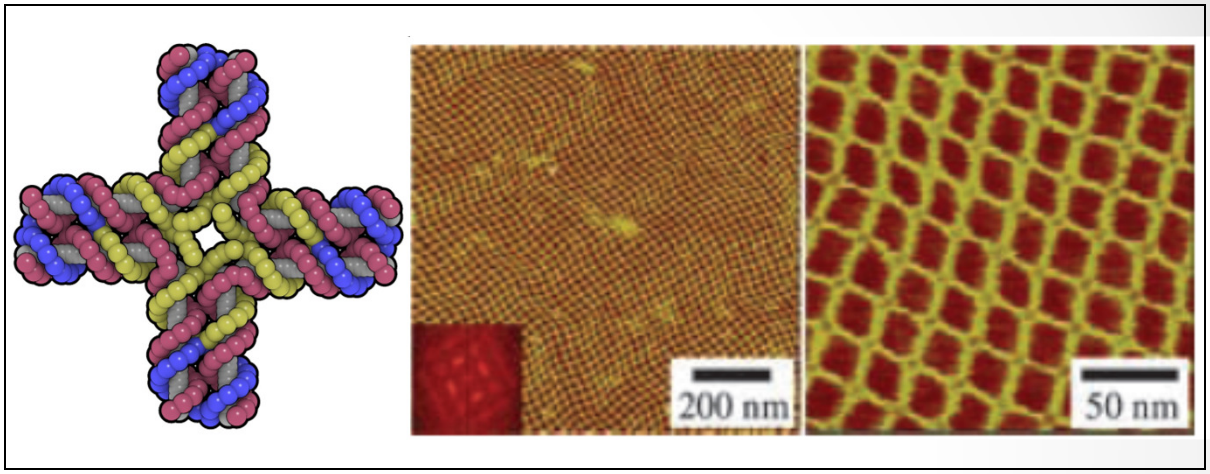
Pankhudi

2D DNA Lattices

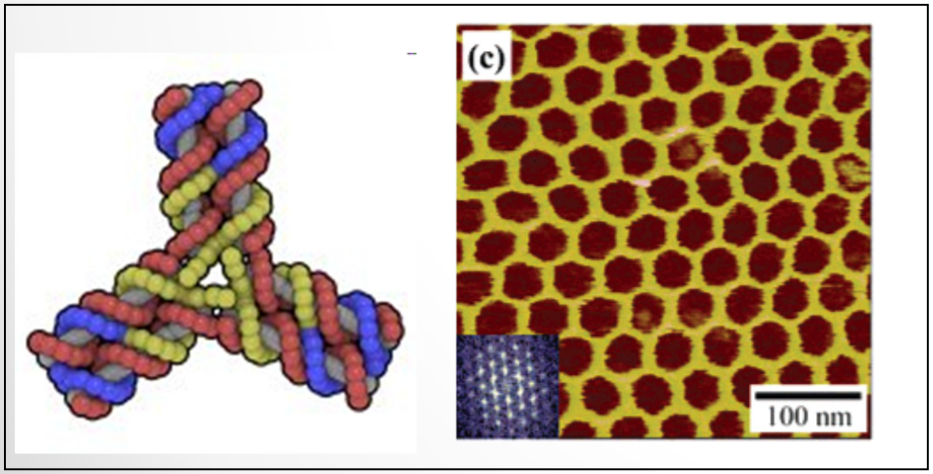


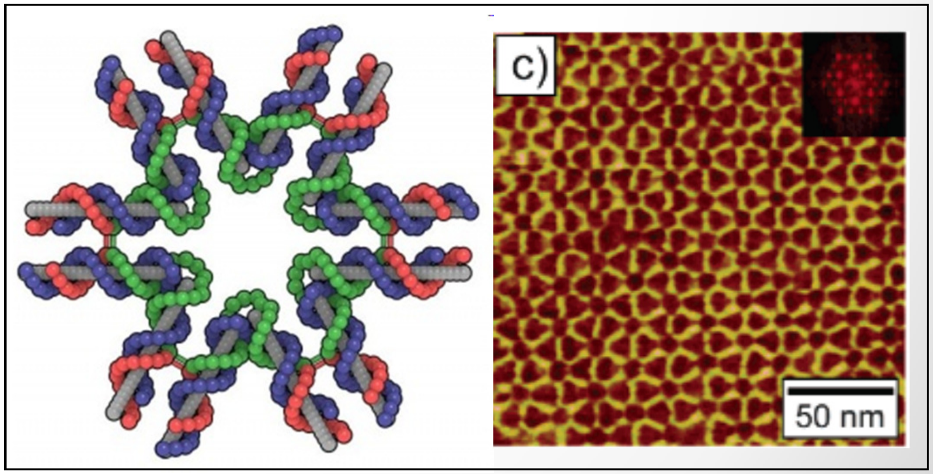
Chengde Mao

Purdue University, USA



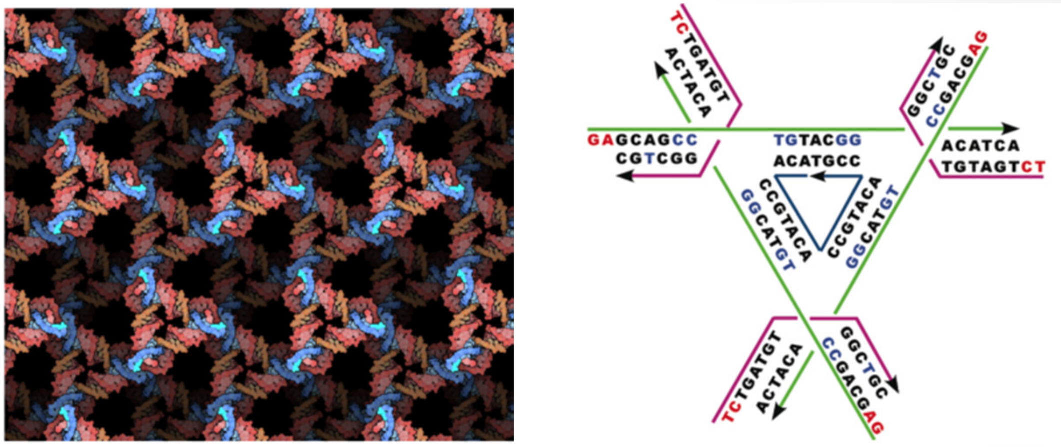
N-point Stars





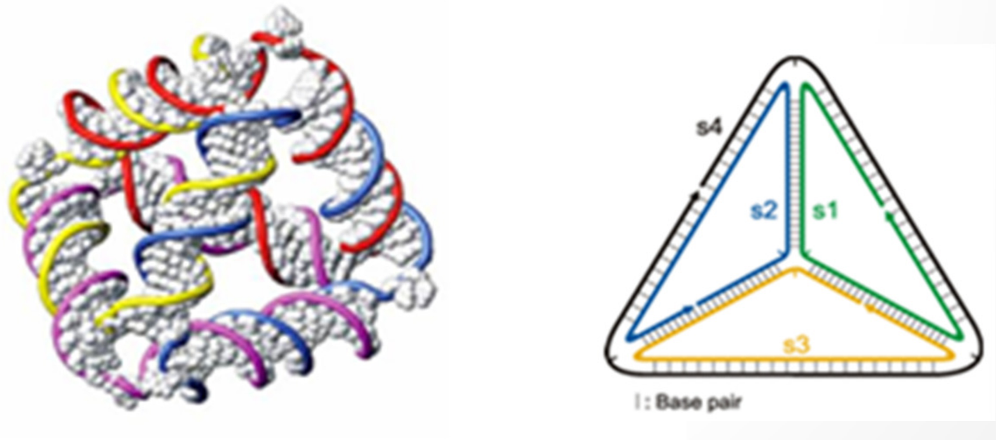
3D DNA Structures

Ned Seeman
NYU



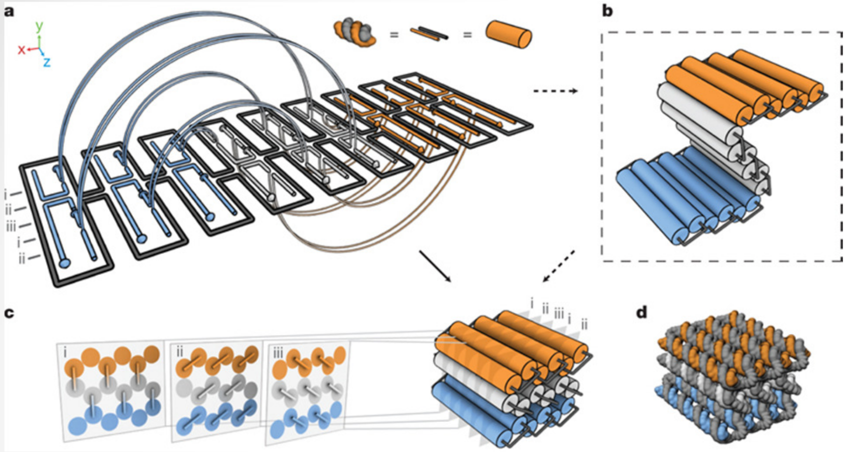
3D Cyrstal

AndrewTuberfield
Oxford



Tetrahedron

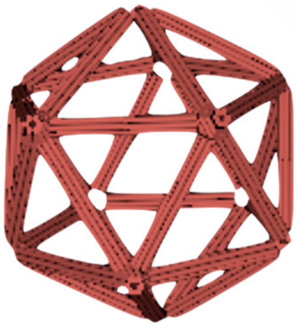
CADnano



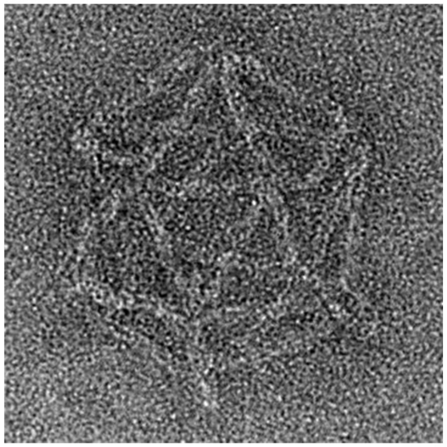
Folding DNA into Twisted and Curved Nanoscale Shapes

Hendrik Dietz, Shawn M. Douglas, & William M. Shih

Science, 325:725–730, 7 August 2009.



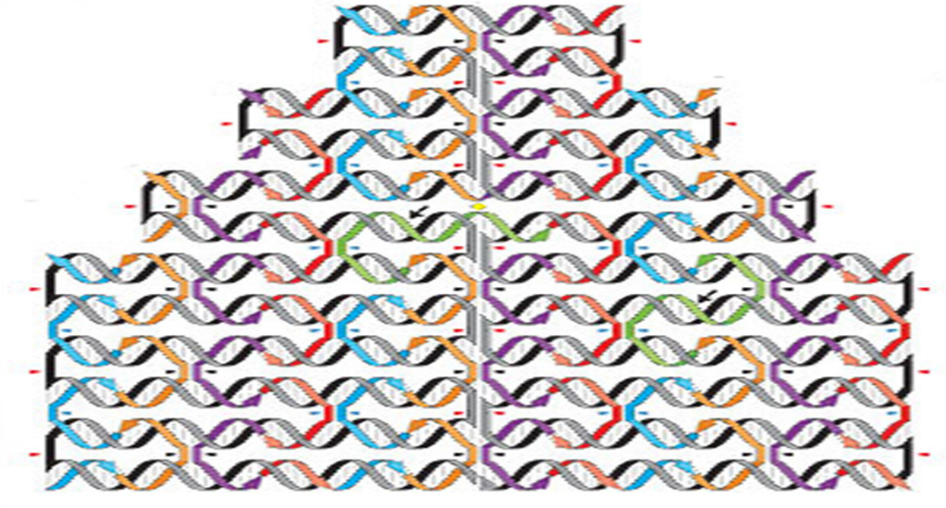
William Shih
Harvard



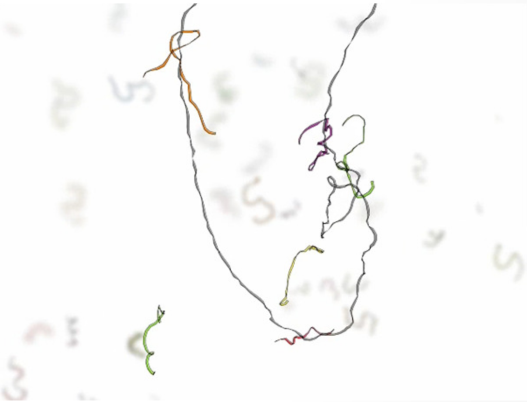
S.M. Douglas, H. Dietz, T. Liedl, B. Högberg, F. Graf and W. M. Shih
Self-assembly of DNA into nanoscale three-dimensional shapes, Nature (2009)

DNA Origami

- *Folding* long (7000bp) naturally occurring (viral) ssDNA
- By lots of short 'staple' strands that constrain it

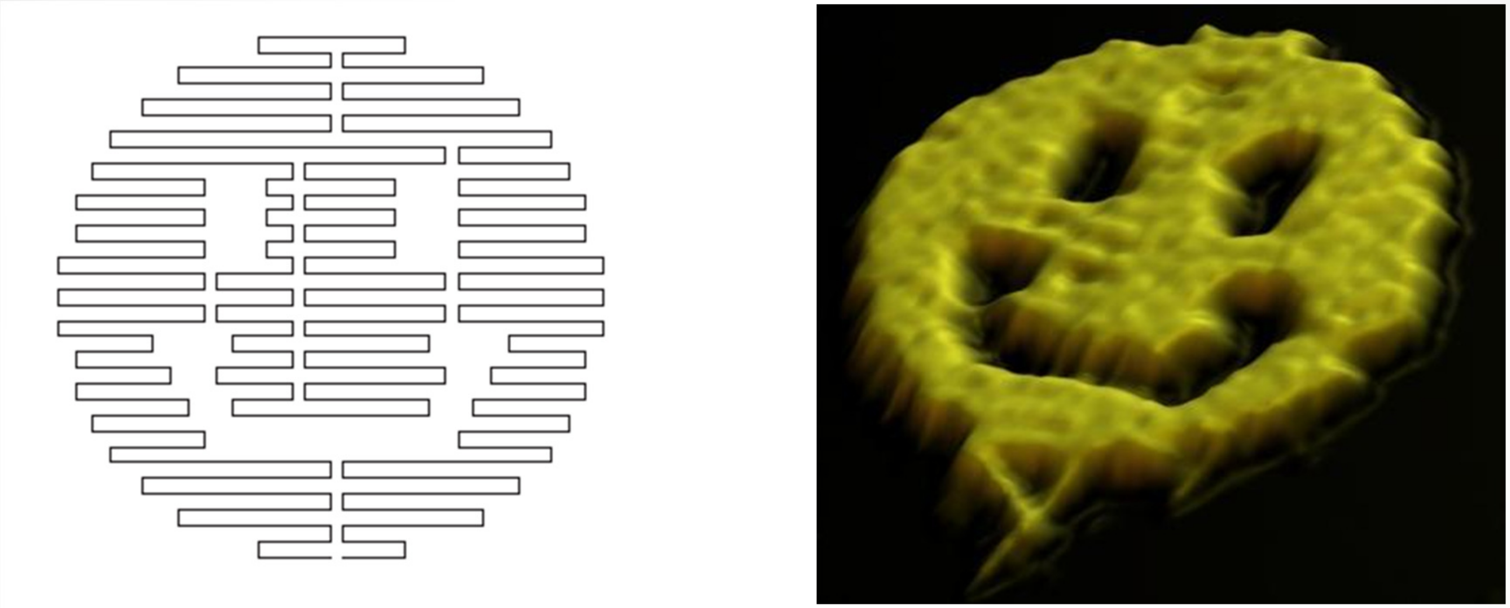


PWK Rothemund, *Nature* 440, 297 (2006)



Black: long viral strand
Color: short staple strands

DNA Origami



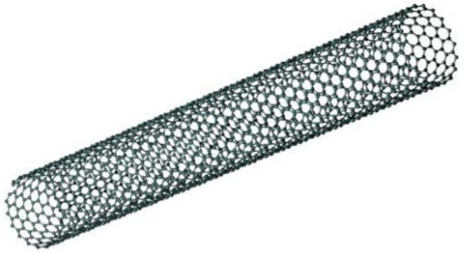
Paul Rothemund’s “Disc with three holes” (2006)

Paul W K Rothemund
California Institute of Technology

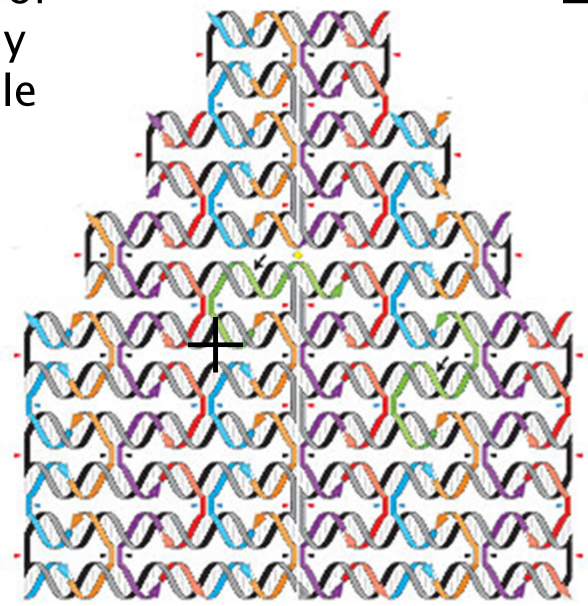
This means we can already self-assemble meso-scale structures.

DNA Circuit Boards

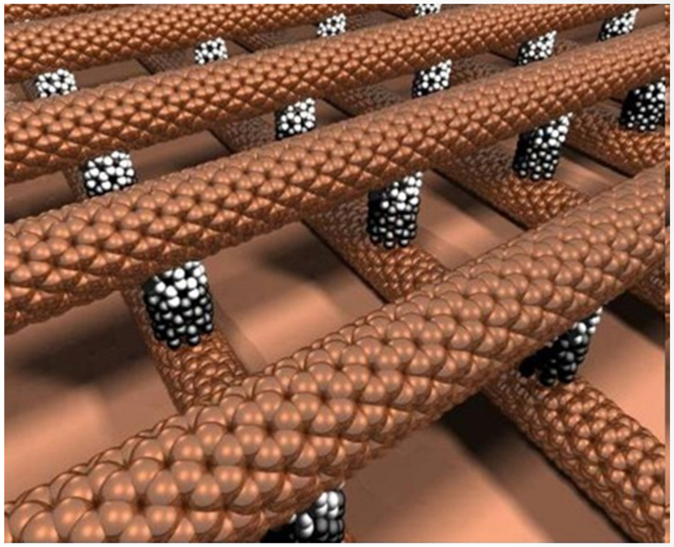
DNA-wrapped nanotubes



6 nm grid of individually addressable pixels

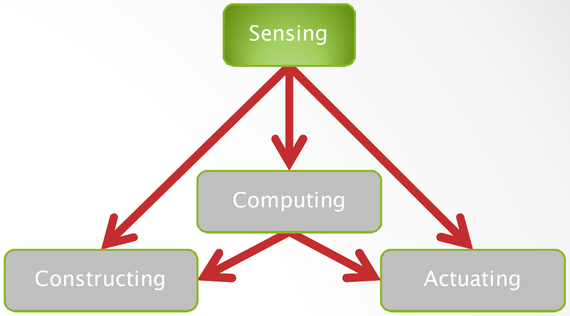


PWK Rothemund, *Nature* 440, 297 (2006)



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

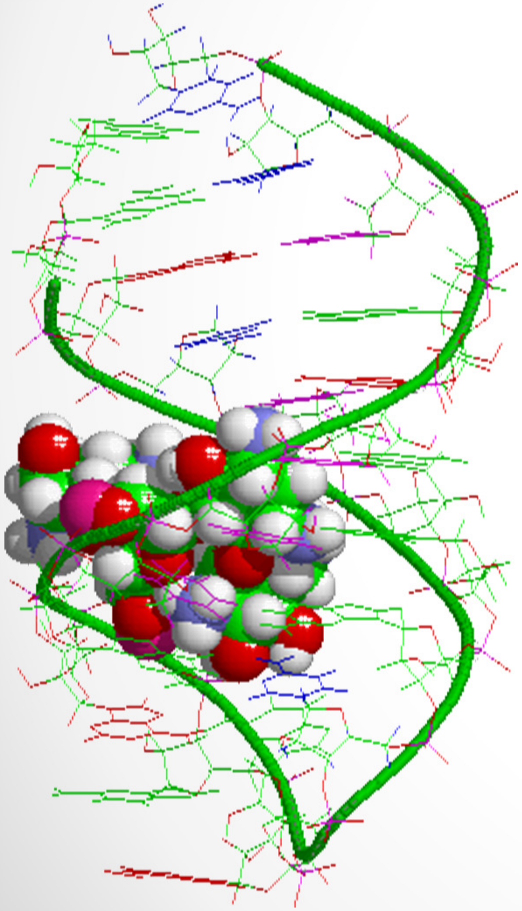


Sensing

• • •

Aptamers

- Artificially eveloved DNA molecules that stick to anything you like (highly selectively).



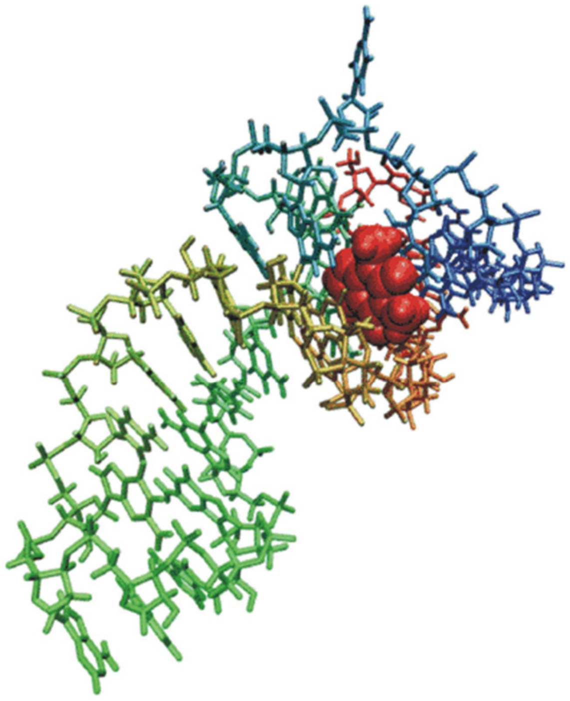
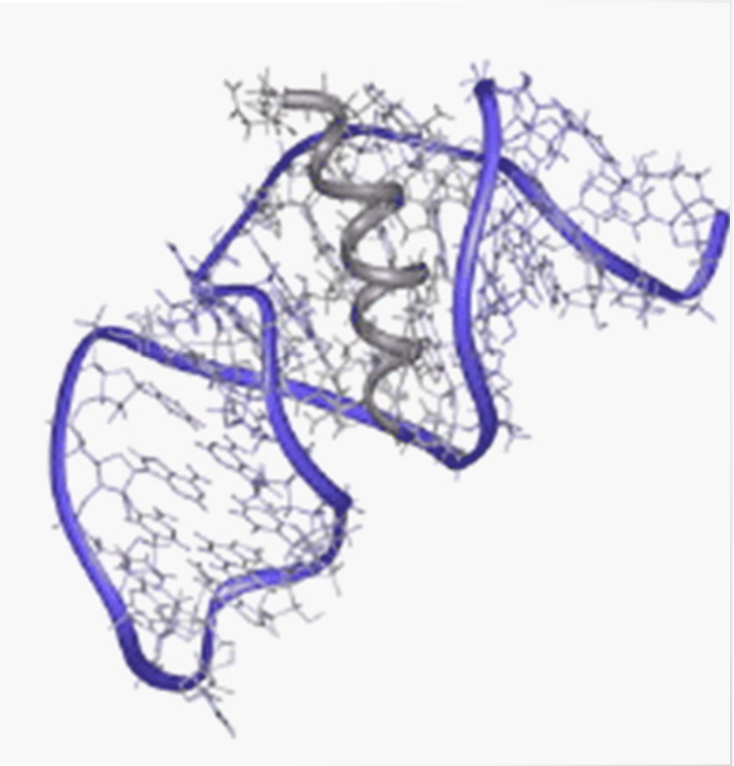


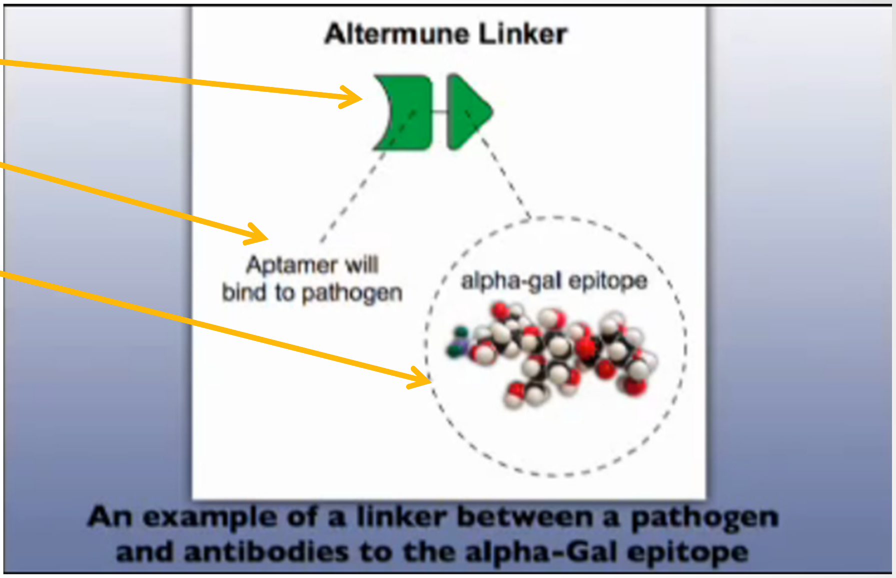
Fig.: RNA-aptamer - purine complex

PDB-ID: 1O15 generated by VMD 1.8.2



Pathogen Spotlights

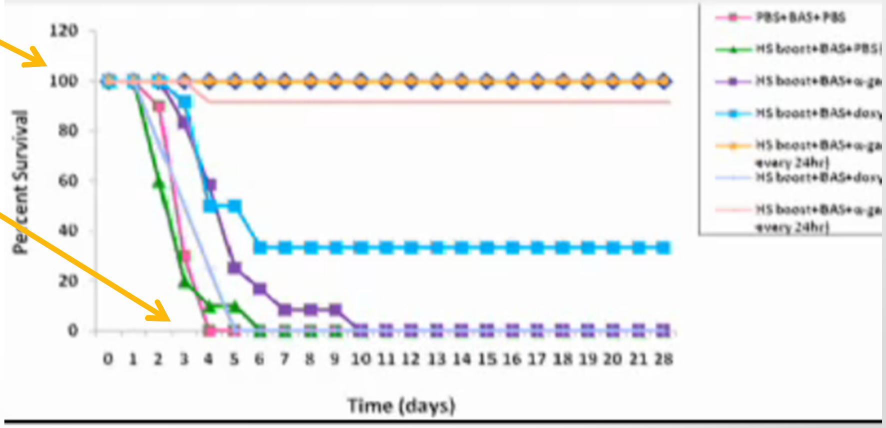
- DNA aptamer binds to:
    - A) a pathogen
    - B) a molecule our immune system already hates and immediately removes (eats) along with anything attached to it



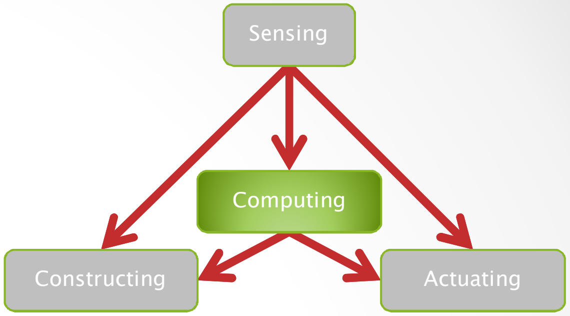
An example of a linker between a pathogen and antibodies to the alpha-Gal epitope

- Result: instant immunity
    - Mice poisoned with Anthrax plus aptamer (100% survival)
    - Mice poinsoned with Anthrax (not so good)

Survival Curve of A/J Mice Immunized with Human Serum, Challenged with BAS and Treated with α-gal PAA-12 Aptamer and Doxycycline



Kary Mullis (incidentally, also Nobel prize for inventing the Polymerase Chain Reaction)


Sensing

Computing

Constructing

Actuating

Computing

• • •

Basic Steps

Compositionality

- Sensors and Actuators at the 'edge' of the system
    - They can use disparate kinds of inputs (sensors) and outputs (actuators)
- The 'kernel' of the system computes
    - Must use uniform inputs and outputs
- Compositionality in the kernel
    - Supporting 'arbitrary' computing complexity
    - The output of each computing components must be the same kind of 'signal' as the input
- sdf
    - If the inputs are voltages, the outputs must be voltages
    - If the inputs are DNA, the outputs must be DNA
- Central design question
    - What should our signals (not components!) be?
    - Then design components that manipulate those signals.

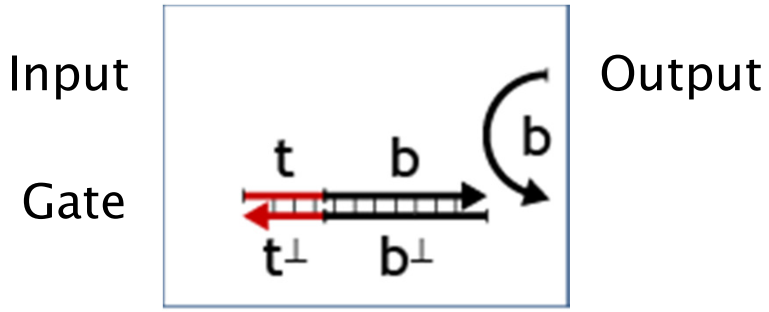
Rules of the Game

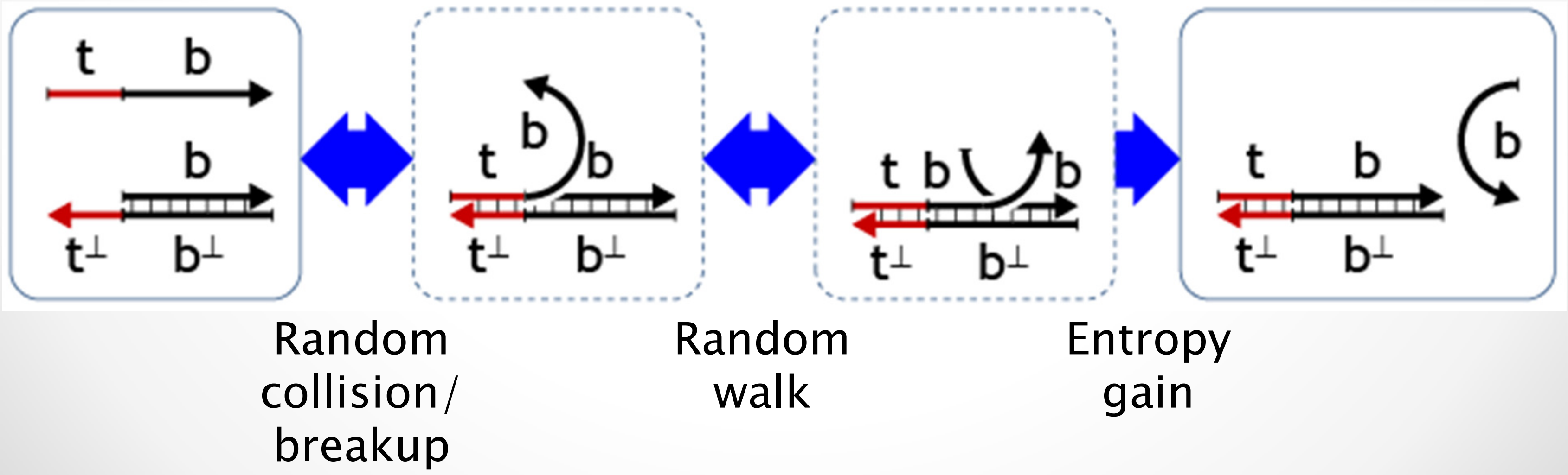
- Short complementary segments hybridize **reversibly**

- Long complementary segments hybridize **irreversibly**

DNA Strand Displacement

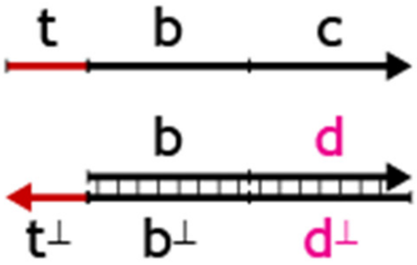
- Short strand (**toehold**): reversible binding
- Long strand (**body**): irreversible binding



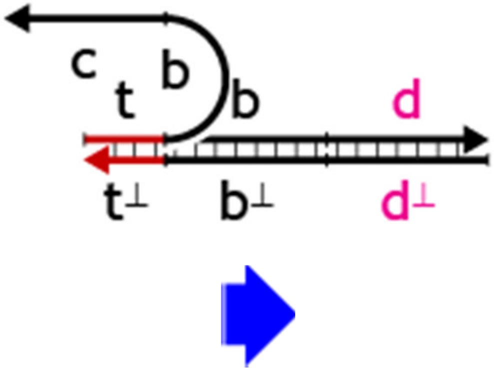


Failed Strand Displacement

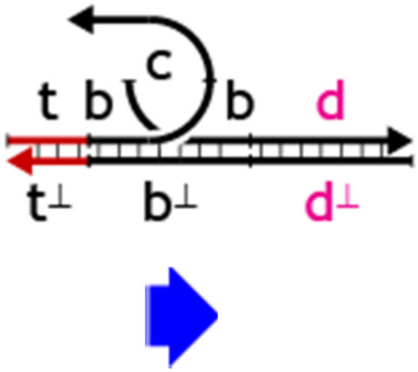
- What if the input does not match the gate?



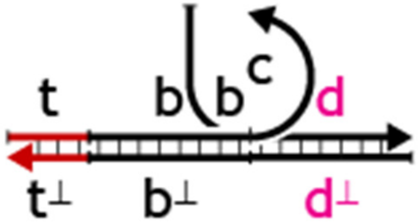
Failed Strand Displacement



Failed Strand Displacement



Failed Strand Displacement



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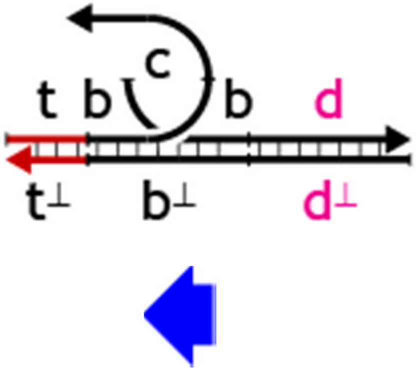
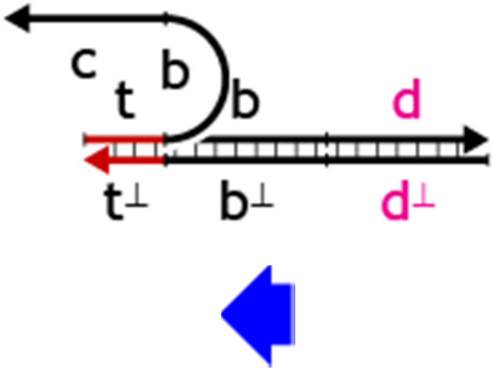
Failed Strand Displacement

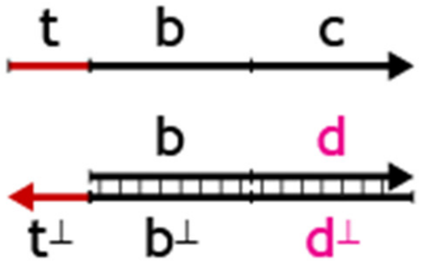


Failed Strand Displacement

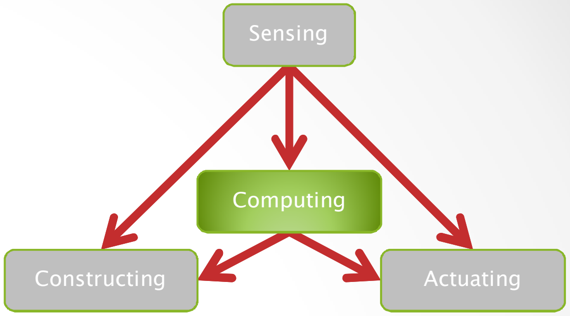


Failed Strand Displacement

- Hence an incorrect binding will undo
  - That’s why toeholds must bind reversibly



- Matching depends on the long segment only
  - Strand displacement succeeds iff the whole long segment matches
  - The address space is determined by the size of the long segment, which is unbounded (not by the size of the toehold)
  - The toehold is just a ‘cache’ of the address



Computing

•••

Implementing "Arbitrary" Computing Functions

What does DNA Compute?

- Electronics has *electrons*
  - All electrons are the same: you can only count them
  - *Few* electrons = False; *lots* of electrons = True
  - But Boolean Logic is only a necessary evil to build symbolic computation

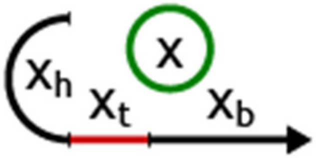
- DNA computing has *symbols* (DNA words)
  - DNA words are not all the same
  - Symbolic computation on abstract signals can be done *directly*
  - Signals are presented concurrently (in a soup)
  - No requirement to do Boolean Logic

- Then, what are our 'gates' (if not Boolean?)
  - Theory of Concurrency
  - Process Algebra as the "Boolean Algebra" of DNA Computing

Signals

- A signal is the representation of an abstract event
    - E.g. generated by a sensor
    - E.g. accepted by an effector
    - We are not limited to true/false

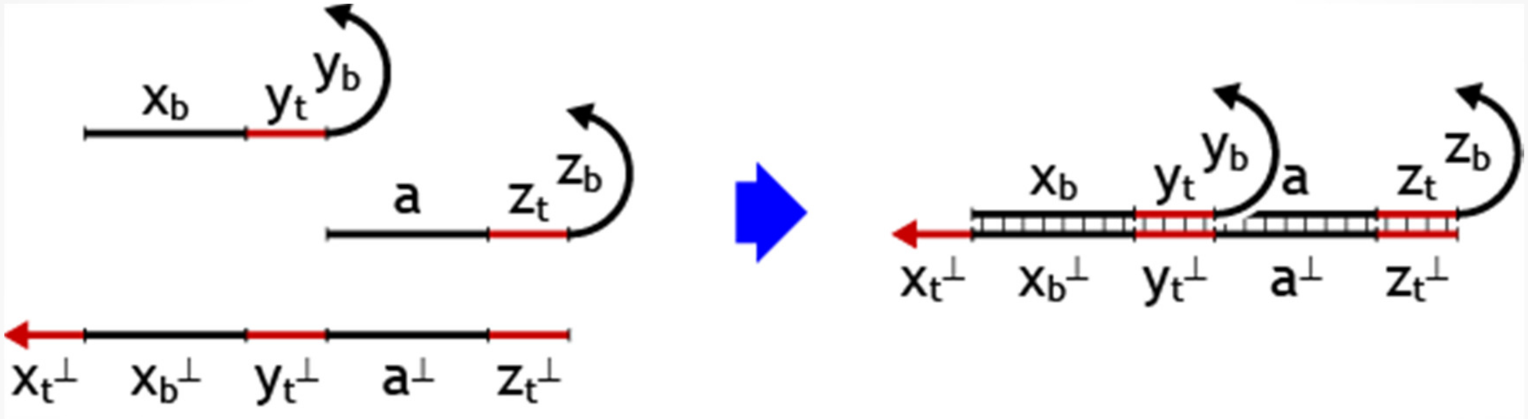
- 3-domain signals
    - x_h: hystory (ignore)
    - x_t: toehold (binding)
    - x_b: body (recognition)



- Signals (single stranded DNA) are prepared by (artificial) DNA synthesis

Gates

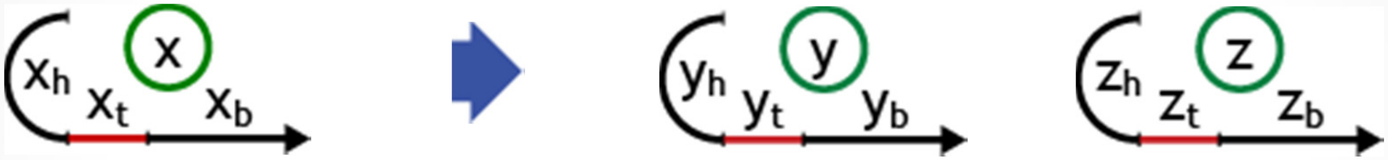
- Double-stranded structures with free toeholds



- Gates are prepared by **self-assembly** from single-stranded DNA that is synthesized

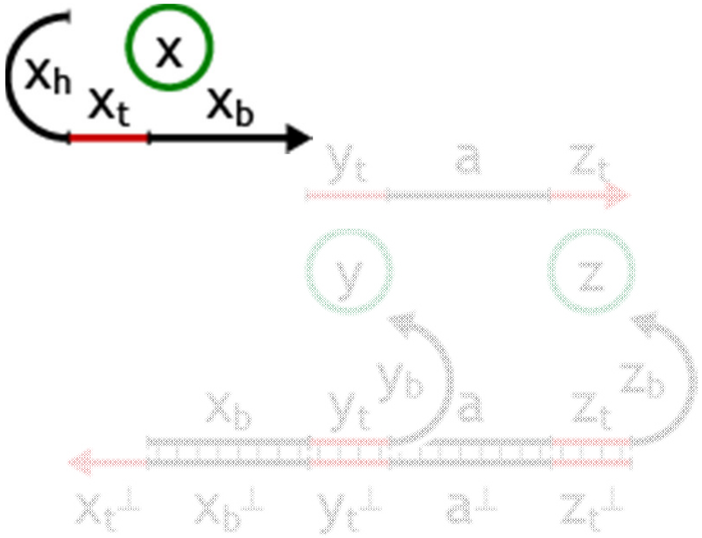
Fork Gate

- $x \rightarrow y + z$



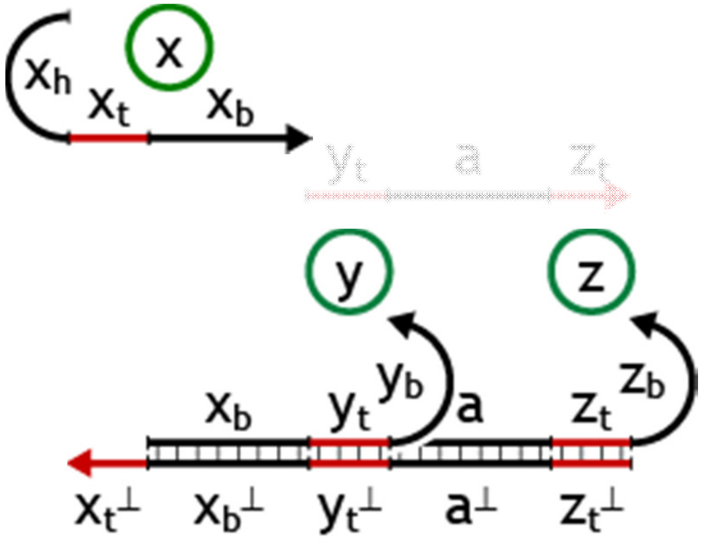
- $x \rightarrow y + 0$ transform x to y (transducer)
- $x \rightarrow x + y$ linear production of y (catalyst)
- $x \rightarrow x + x$ exponential production of x (amplifier)

Fork Gate



This is the Fork Gate structure

Fork Gate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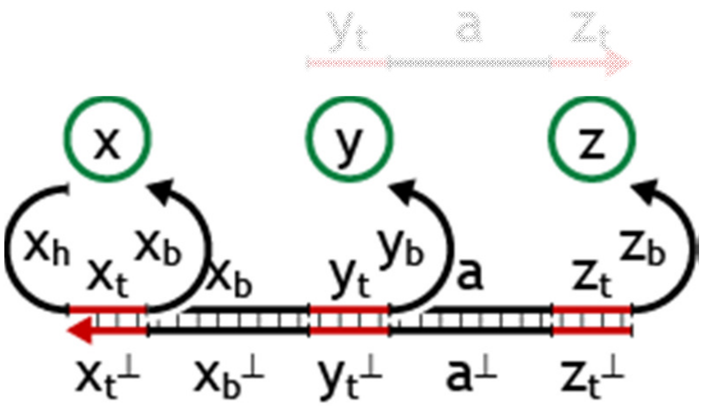
Fork Gate



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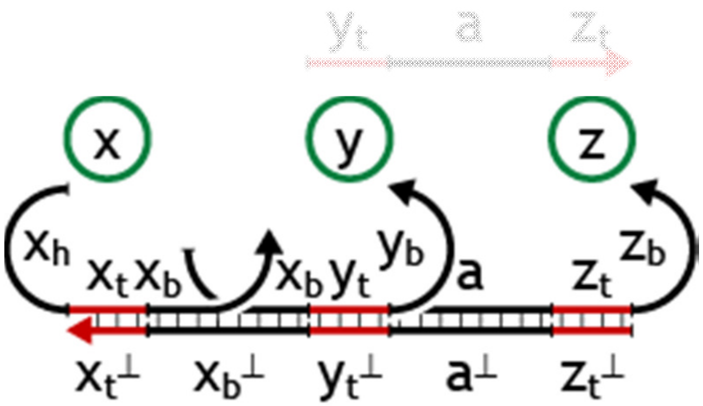
Fork Gate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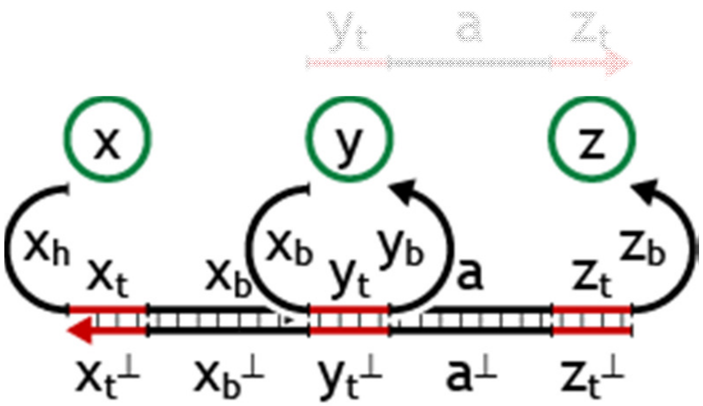
Fork Gate



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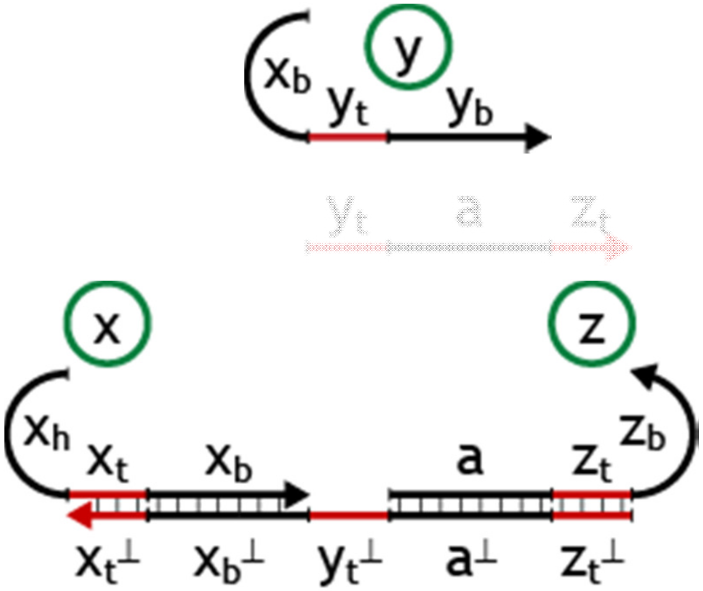
Fork Gate



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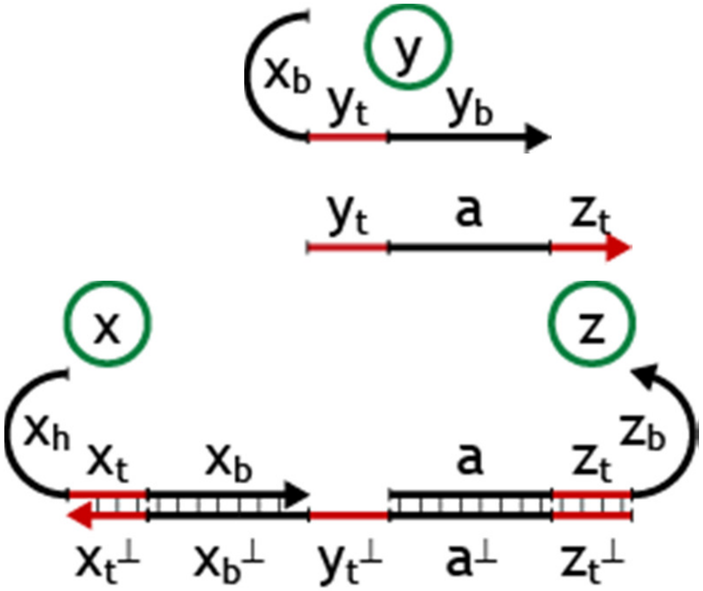
Fork Gate



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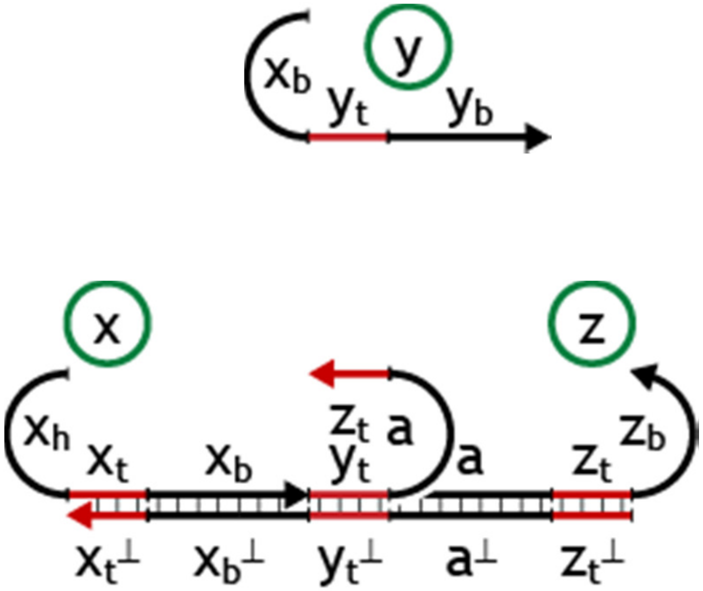
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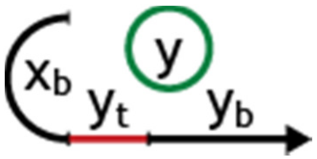
Fork Gate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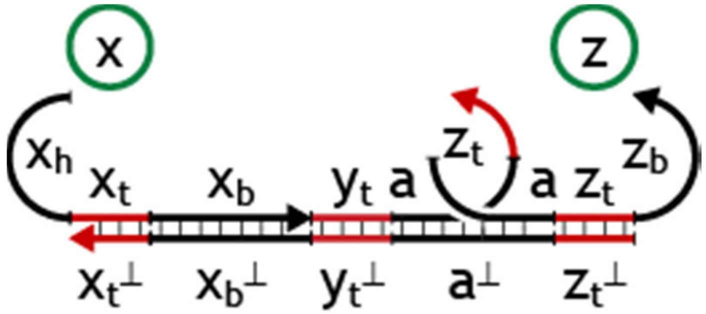
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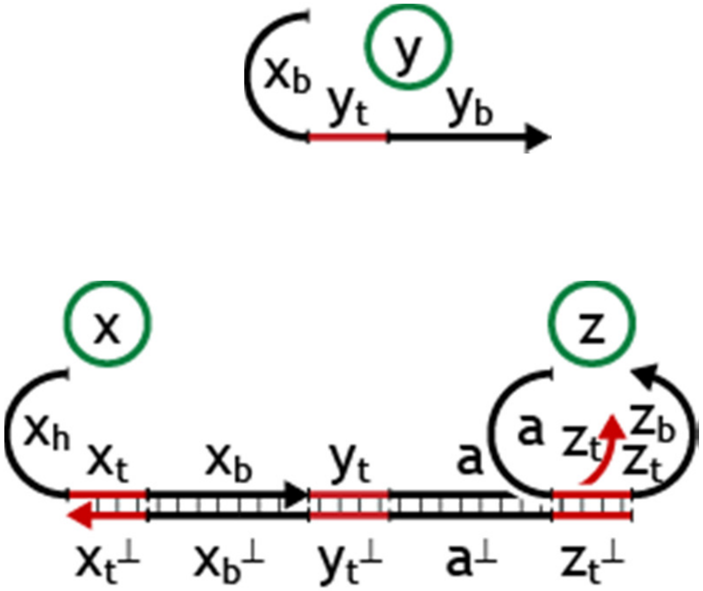
Fork Gate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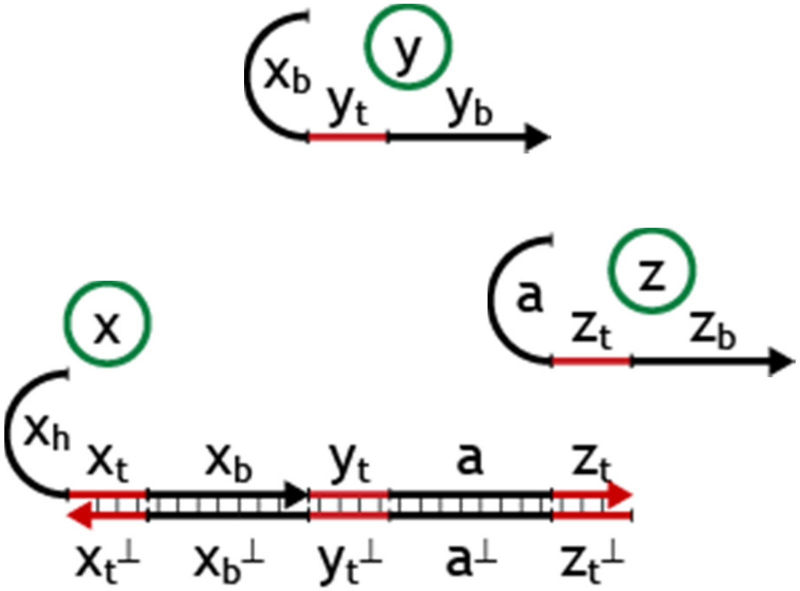
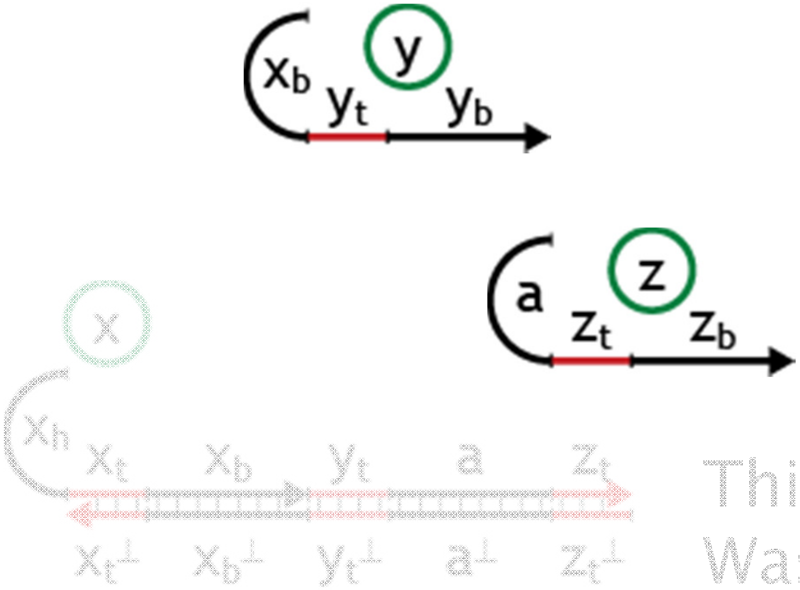
Fork Gate



Fork Gate

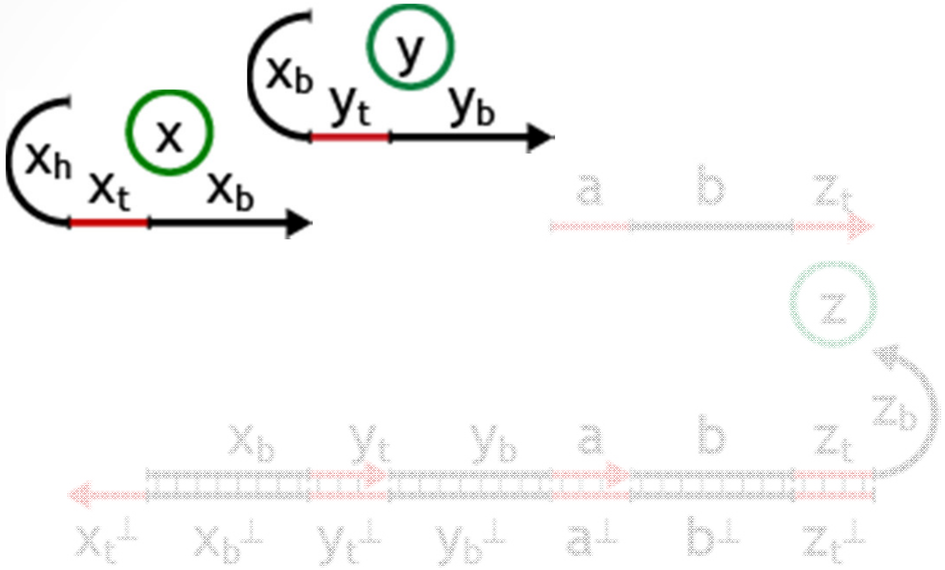


This is Waste

Join Gate

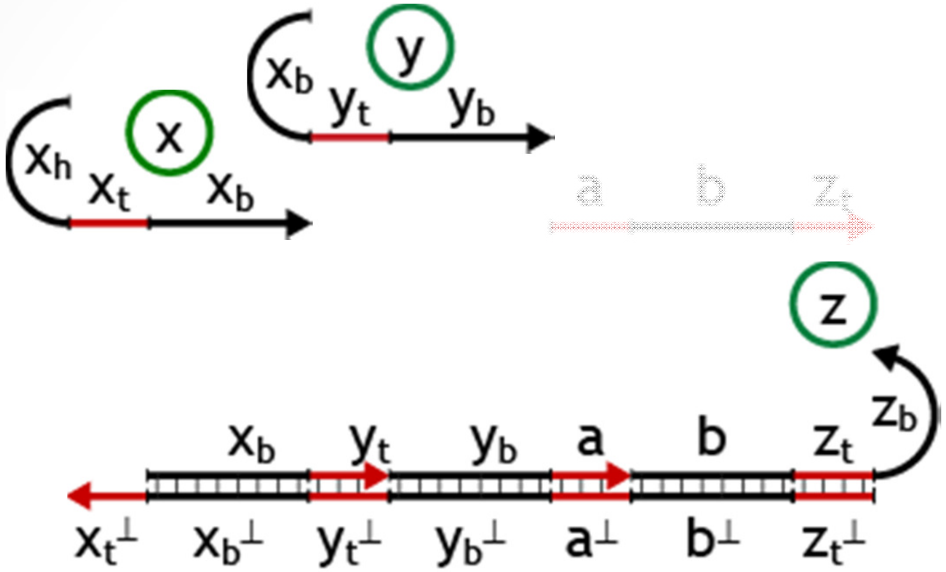
- $x + y \rightarrow z$

Join Gate



This is the Join Gate structure

Join Gate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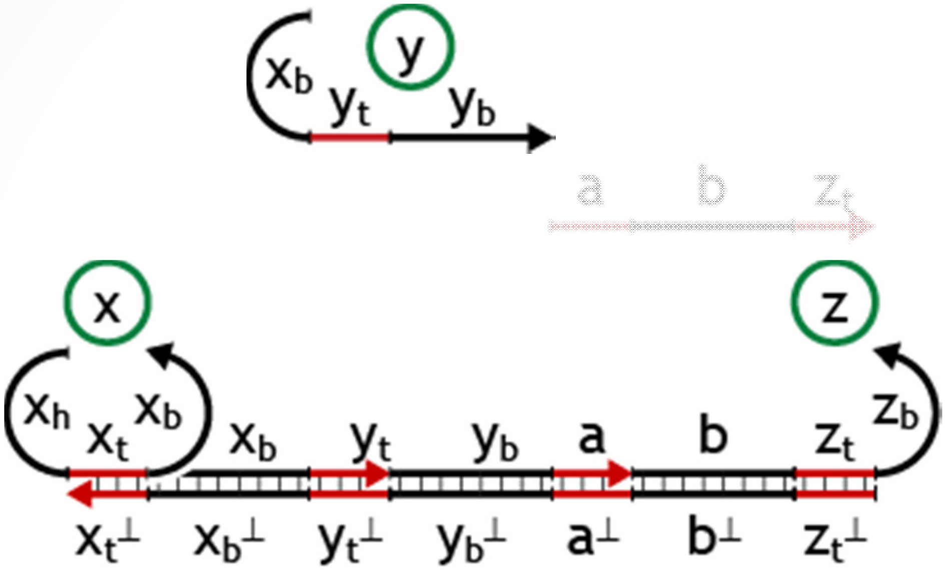
Join Gate



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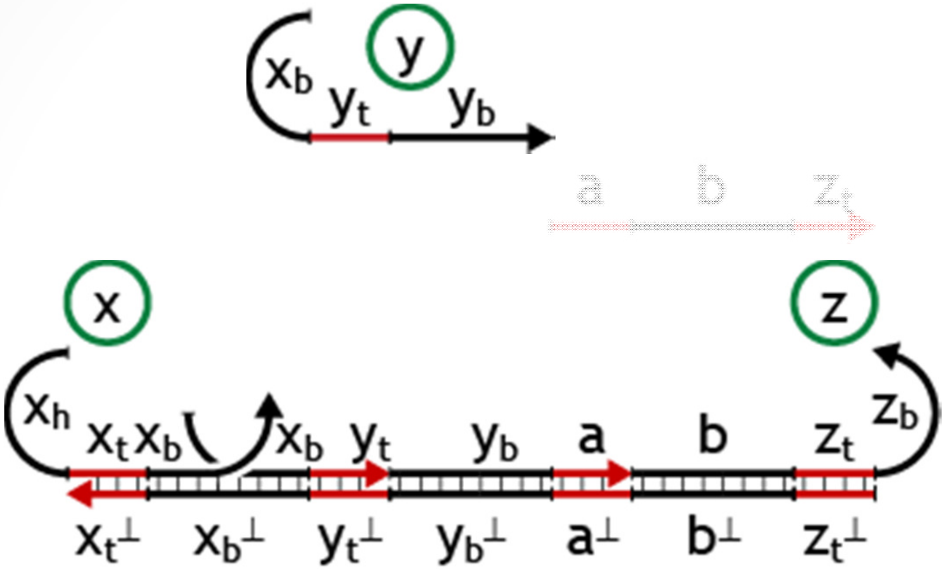
Join Gate



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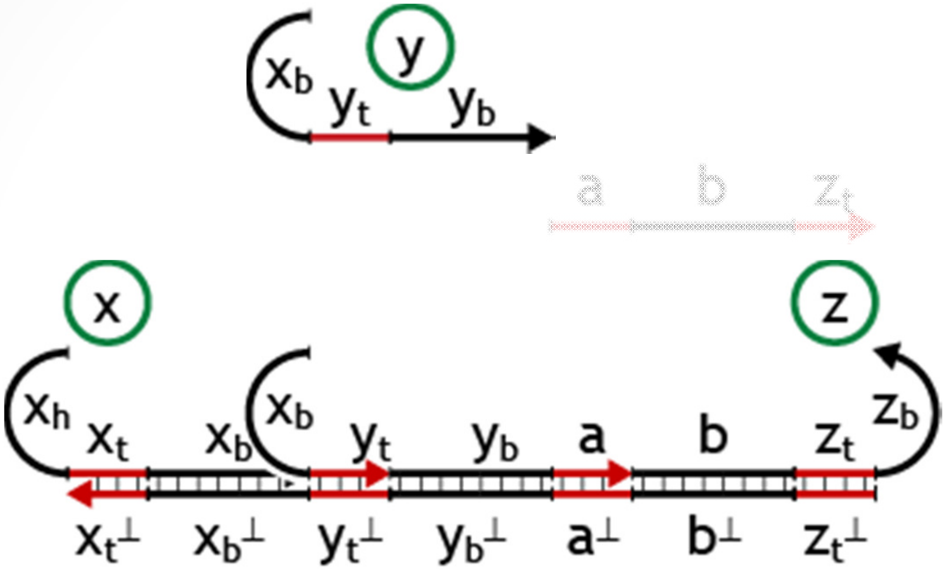

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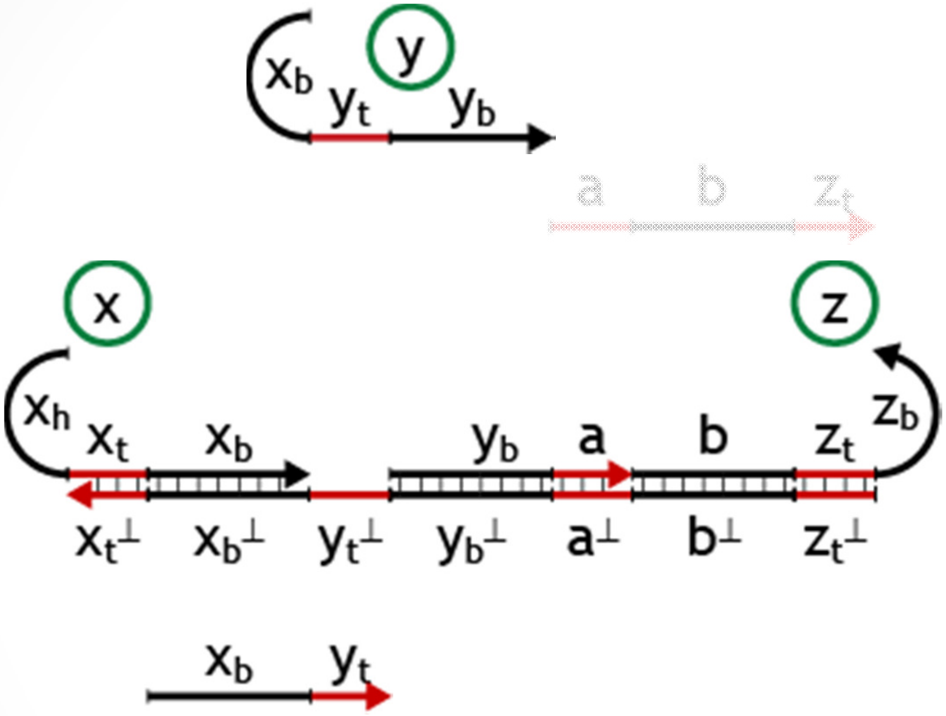
Join Gate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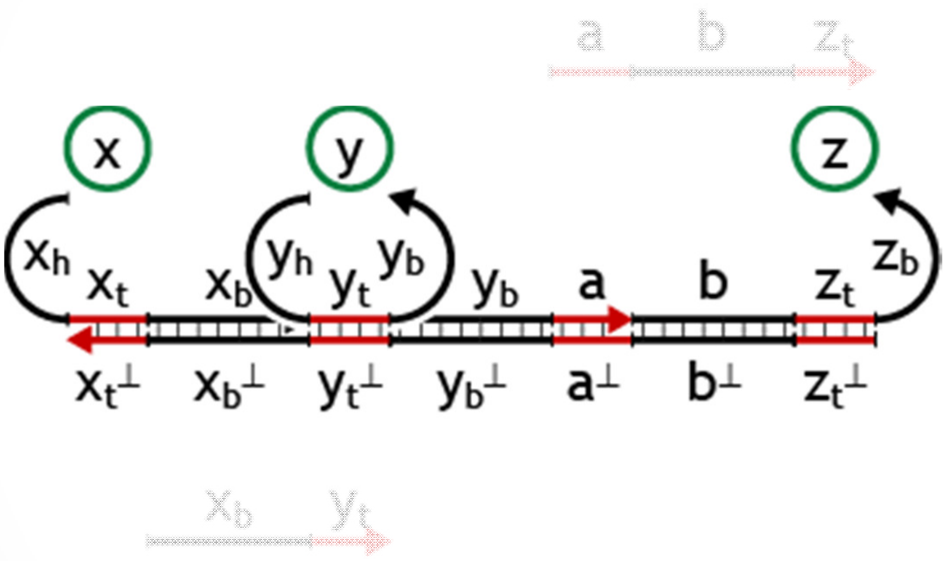
Join Gate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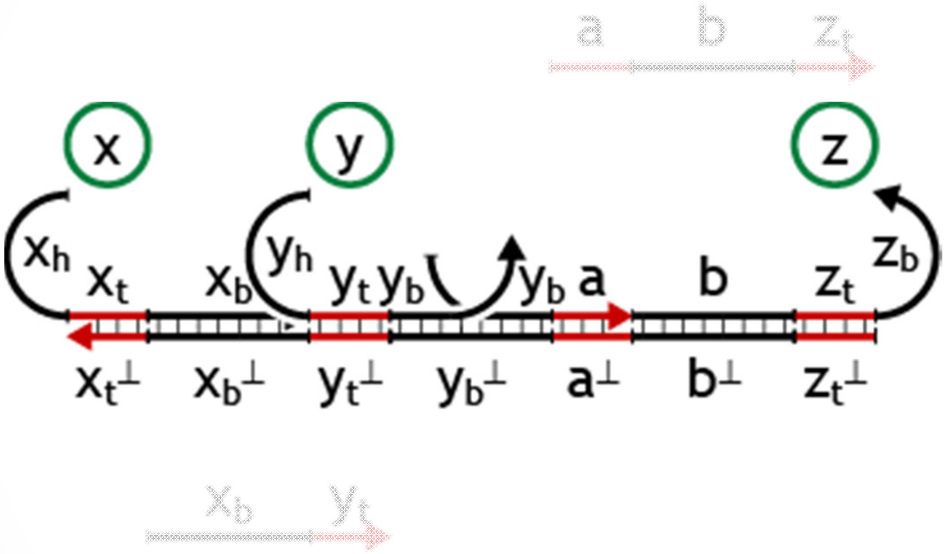

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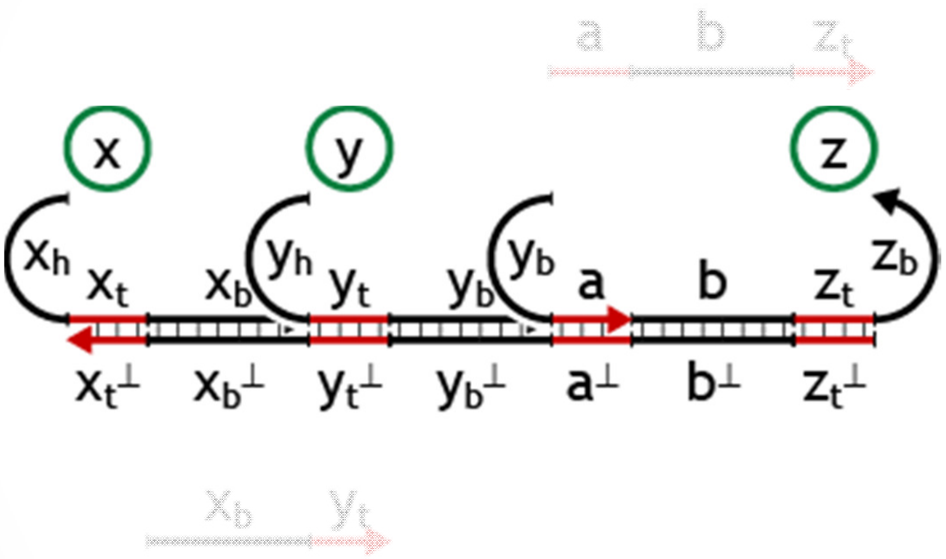
Join Gate



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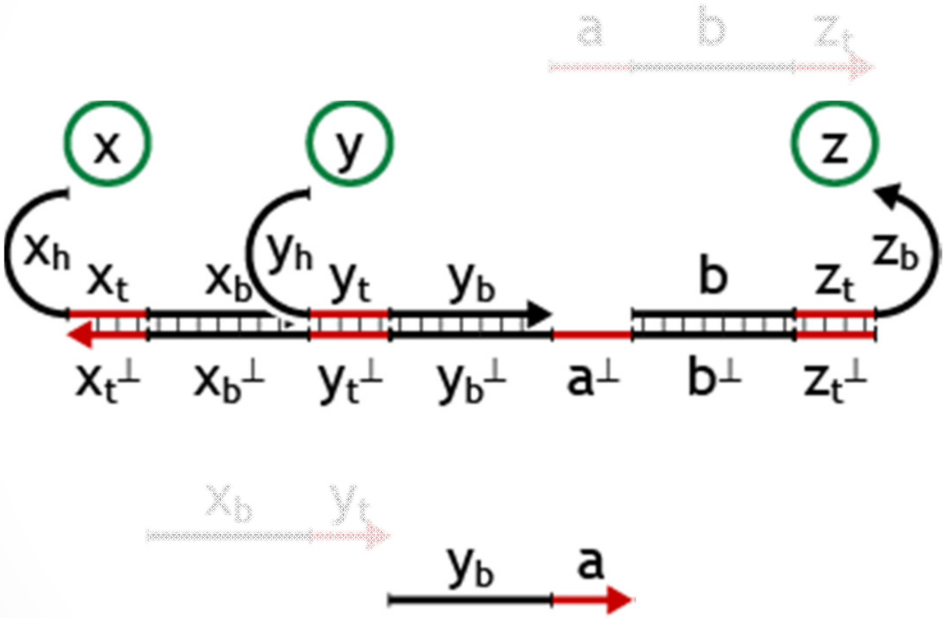
Join Gate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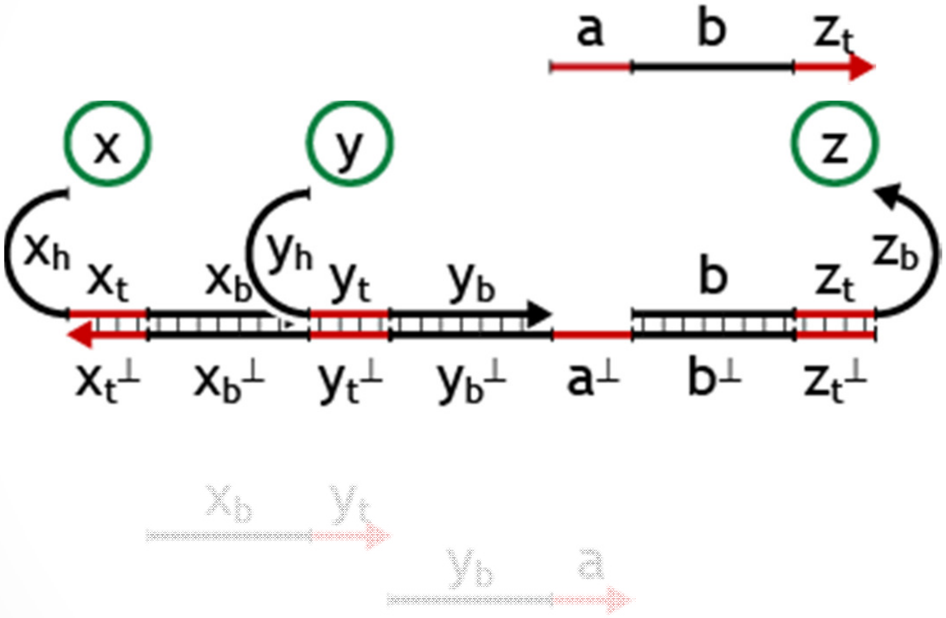
Join Gate



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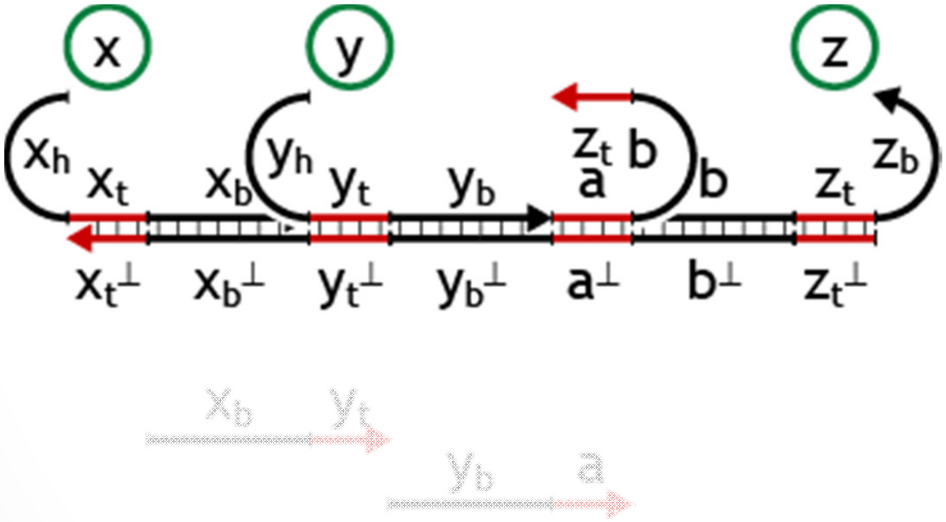
Join Gate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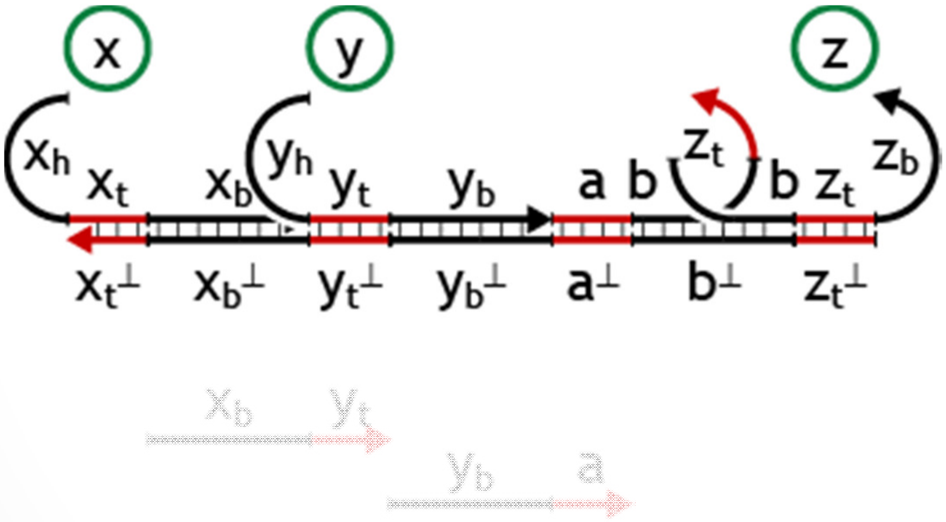
Join Gate



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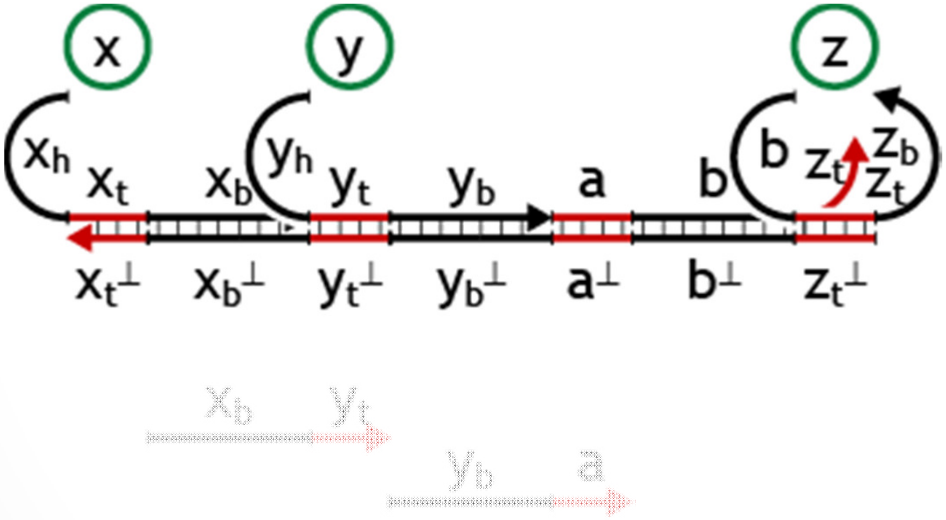
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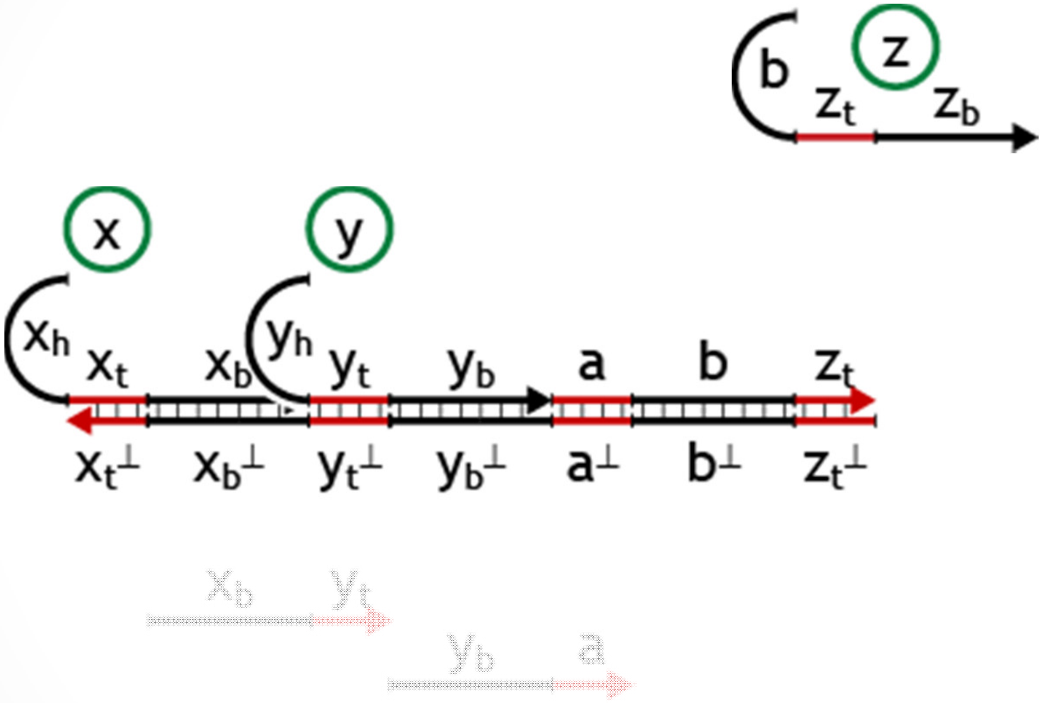
Join Gate



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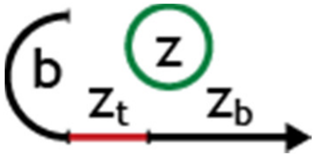
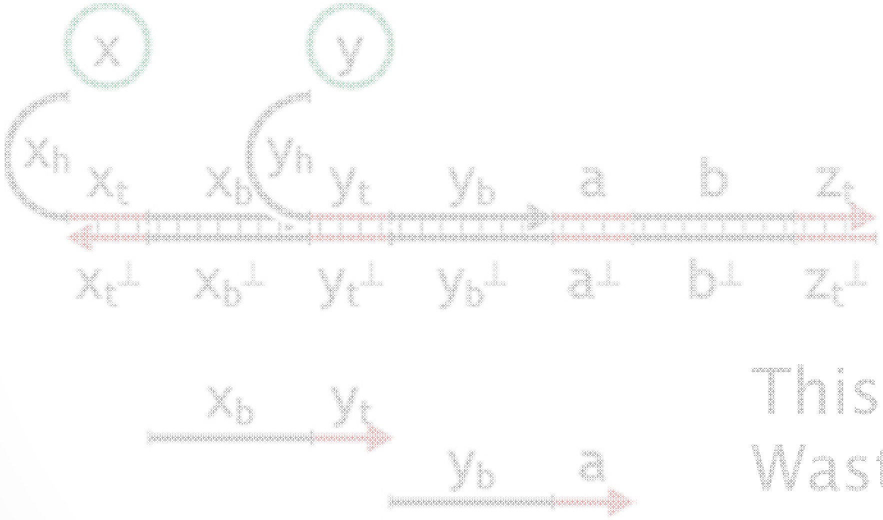
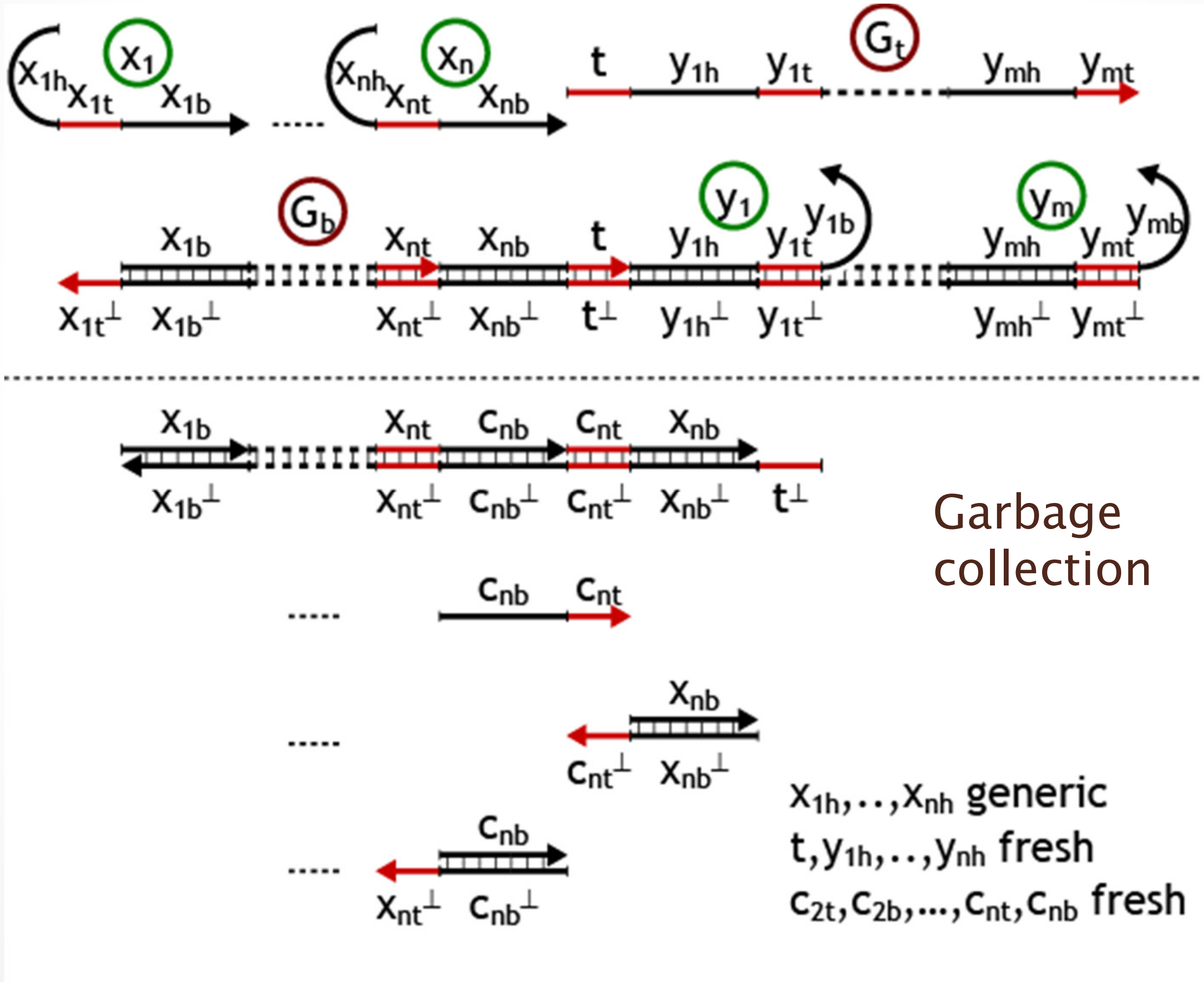




This is Waste

General n-Join/m-Fork Gate



Garbage collection

$x_{1h},..,x_{nh}$ generic

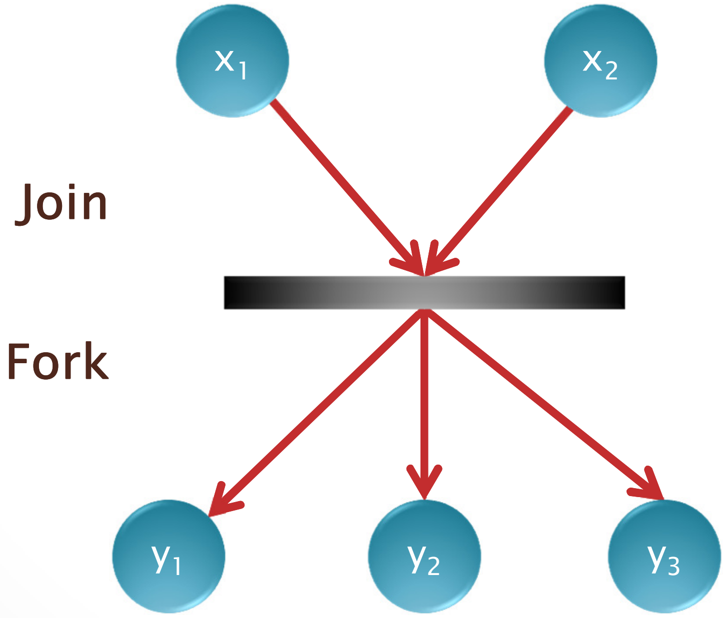
$t,y_{1h},..,y_{nh}$ fresh

$c_{2t},c_{2b},...,c_{nt},c_{nb}$ fresh

Strand Algebra

$$x_1 \mid .. \mid x_n \mid [x_1,..,x_n].[y_1,..,y_m] \rightarrow y_1 \mid .. \mid y_m$$

- Join + Fork + Populations = (Stochastic) Petri Nets

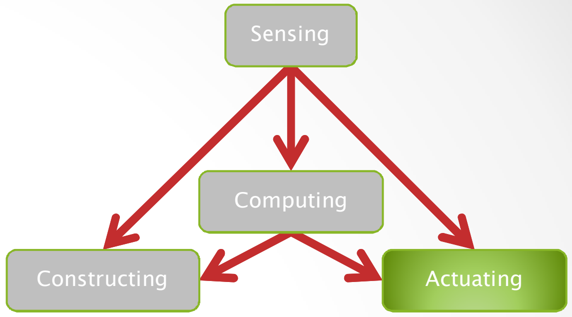


Gate Design Verification

- Active garbage
    - The active join residuals slow down the performance of following joins.
    - → Add a garbage collector to remove the active residuals.

- Interference between gates
    - The join garbage collector interferes with the fork gate.
    - → Modify the fork gate to remove the interference.

- What else could go wrong?
    - Endless possibilities.
    - → Prove that the fork/join gate structures correctly implement fork/join in all larger circuits.



Sensing

Computing

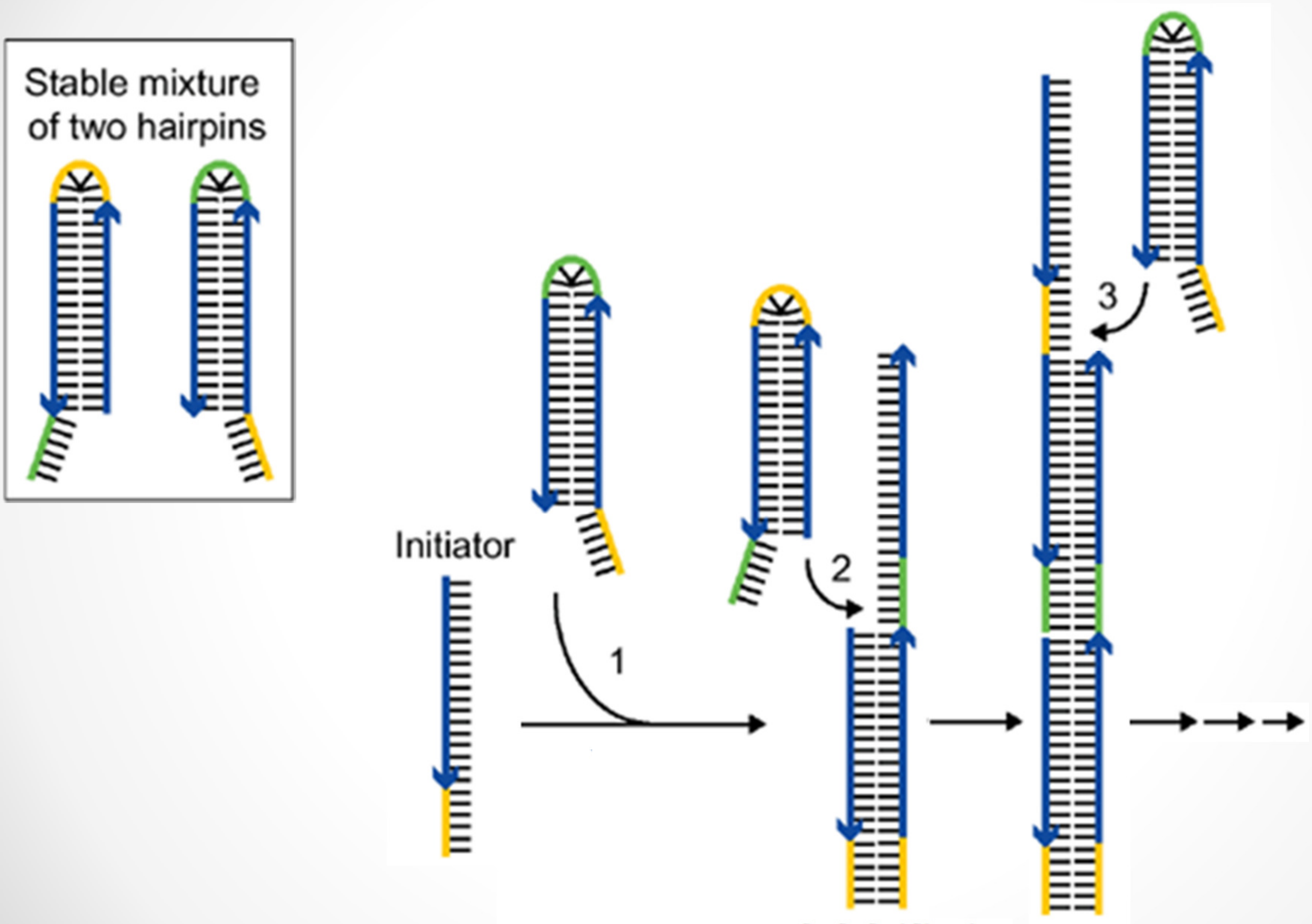
Constructing

Actuating

Actuating

• • •

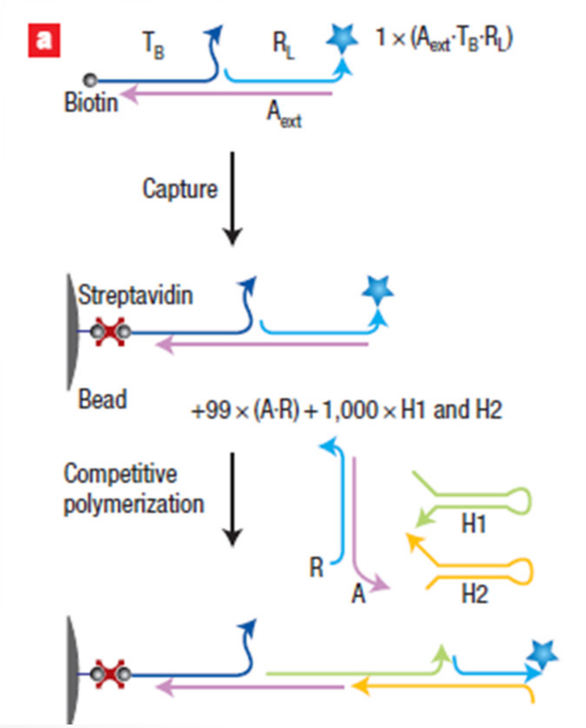
Hybridization Chain Reaction



n by hybridization
chain reaction

Robert M. Dirks† and Niles A. Pierce‡,§

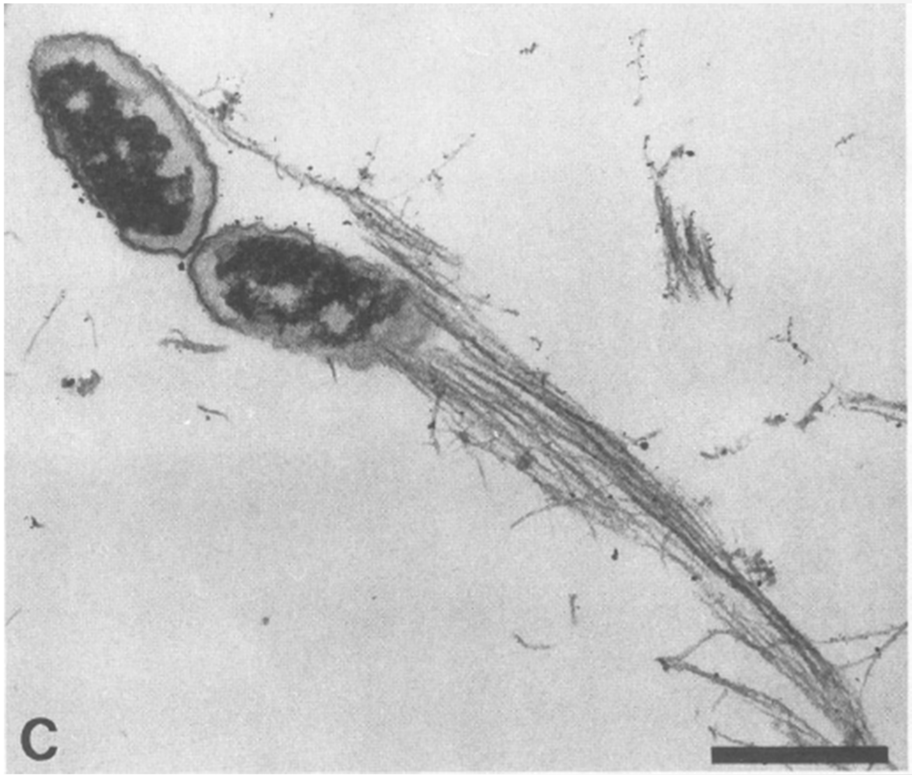
Polymerization Motor



An autonomous polymerization motor powered by DNA hybridization

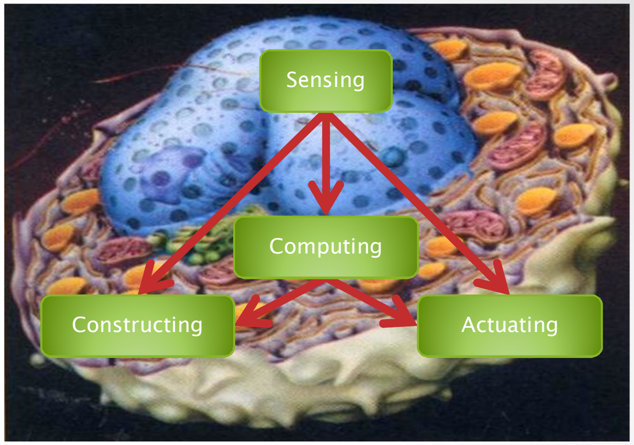
SUVIR VENKATARAMAN[1], ROBERT M. DIRKS[1], PAUL W. K. ROTHEMUND[2,3], ERIK WINFREE[2,3] AND NILES A. PIERCE[1,4]*

Rickettsia (spotted fever)



Directional Actin Polymerization Associated with Spotted Fever Group Rickettsia Infection of Vero Cells

ROBERT A. HEINZEN, STANLEY F. HAYES, MARIUS G. PEACOCK, AND TED HACKSTADT*



Curing

• • •

A Doctor in Each Cell

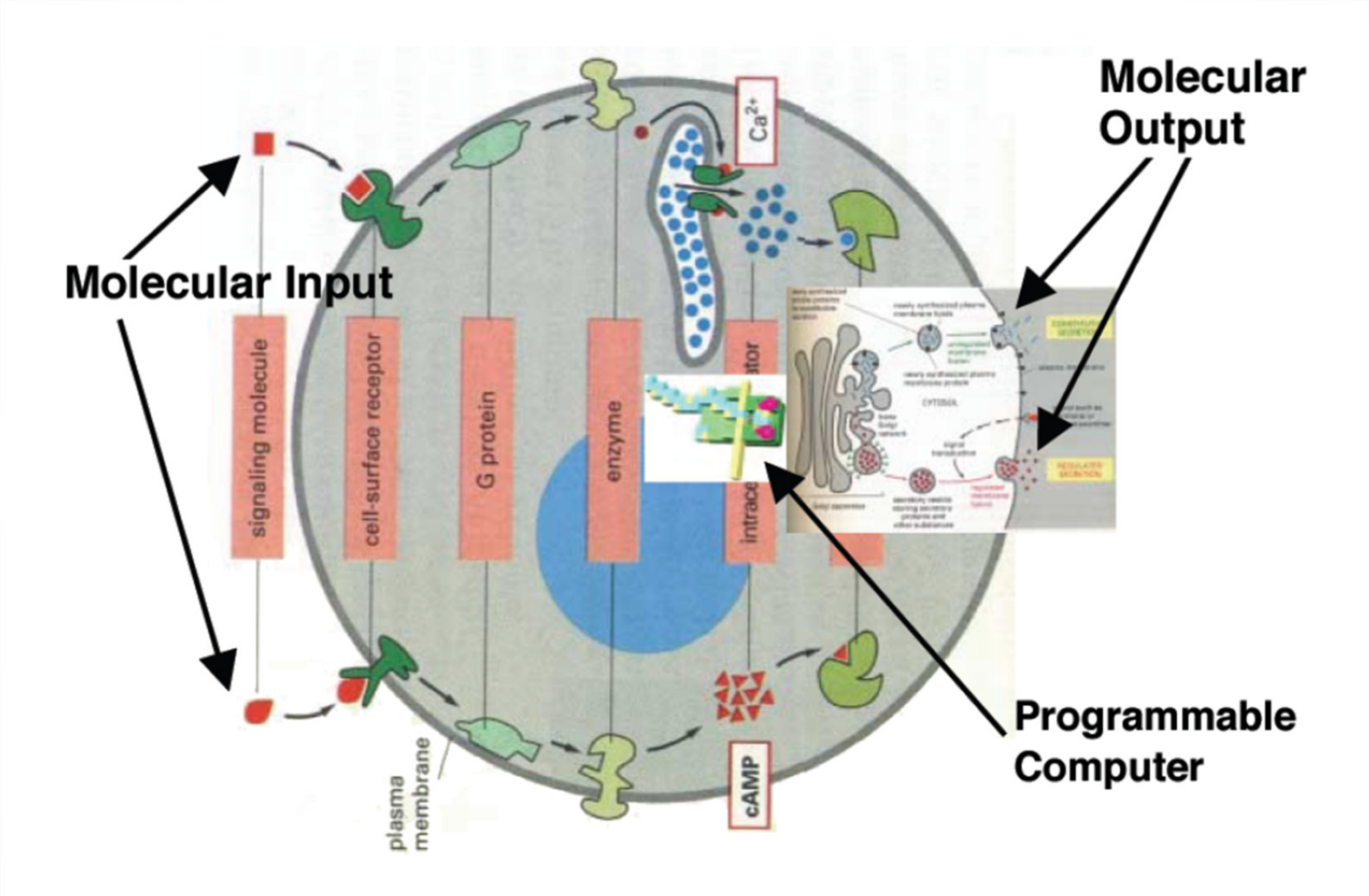


Fig. 1 Medicine in 2050: "Doctor in a Cell"

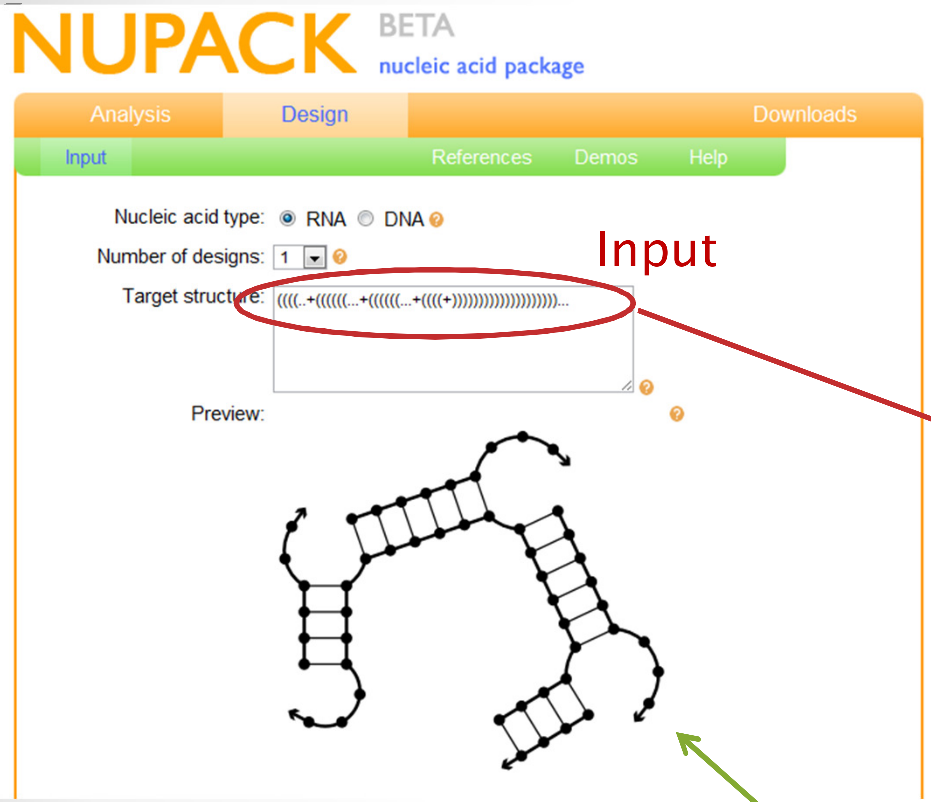
Ehud Shapiro

Rivka Adar
Kobi Benenson
Gregory Linshitz
Aviv Regev
William Silverman

Molecules and computation

Tools

Sequence Design



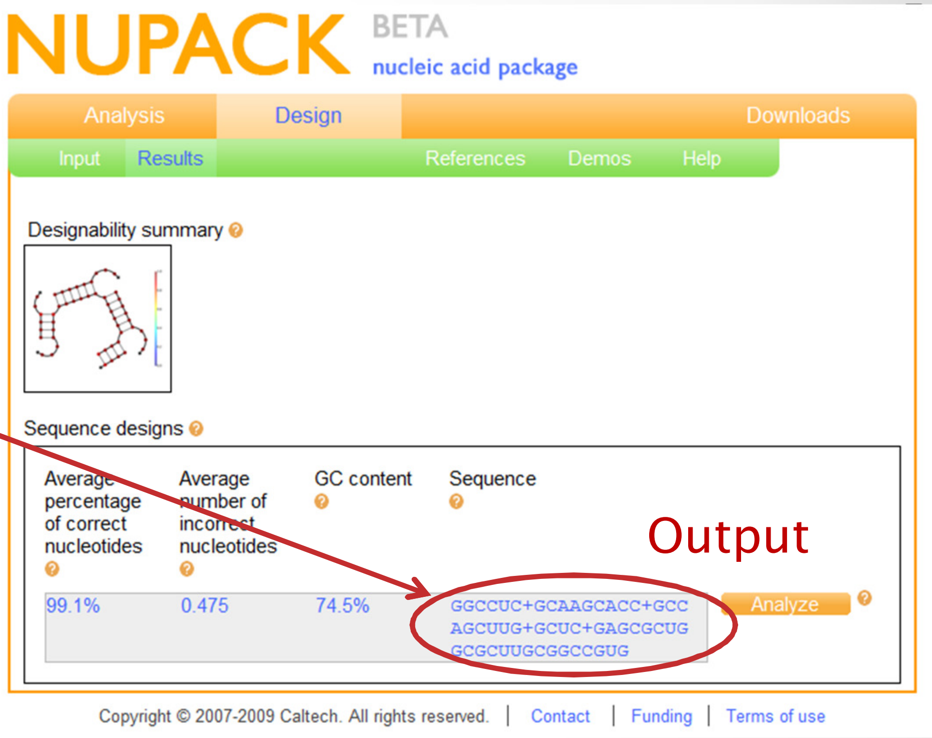
Nucleic acid type: ● RNA ○ DNA

Number of designs: 1

Target structure: ((((..+((((((...+((((((...+((((+))))))))))))))))))))...

Preview:

Input



Sequence designs

Average percentage of correct nucleotides	Average number of incorrect nucleotides	GC content	Sequence
99.1%	0.475	74.5%	GGCCUC+GCAAGCACC+GCCAGCUUG+GCUC+GAGCGCUGGCGCUUGCGGCCGUG

Output

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So we can in principle work at this level.

Visual DSD

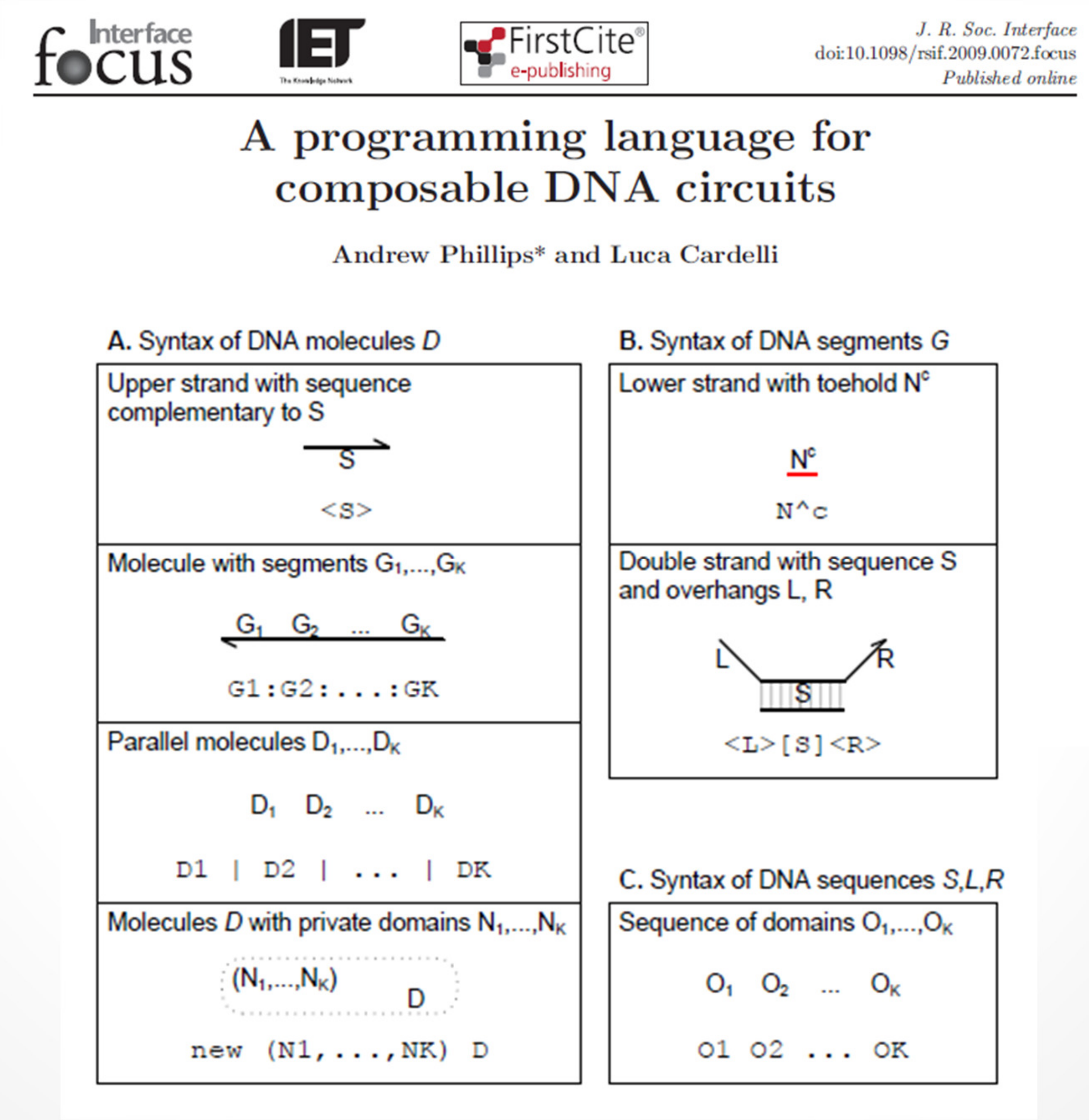
A Strand Displacement Simulator

• • •

Matthew Lakin, Simon Youssef, Andrew Phillips

http://lepton.research.microsoft.com/webdna/

Syntax



Interface focus
IET
FirstCite® e-publishing
J. R. Soc. Interface
doi:10.1098/rsif.2009.0072.focus

A programming language for composable DNA circuits

Andrew Phillips* and Luca Cardelli

A. Syntax of DNA molecules *D*

Upper strand with sequence complementary to S

S

`<S>`

Molecule with segments $G_1,\ldots,G_K$

G_1 G_2 ... G_K

`G1:G2:...:GK`

Parallel molecules $D_1,\ldots,D_K$

D_1 D_2 ... D_K

`D1 | D2 | ... | DK`

Molecules *D* with private domains $N_1,\ldots,N_K$

$(N_1,\ldots,N_K)$ D

`new (N1,...,NK) D`

B. Syntax of DNA segments *G*

Lower strand with toehold N^c

N^c

`N^c`

Double strand with sequence S and overhangs L, R

L R S

`<L>[S]<R>`

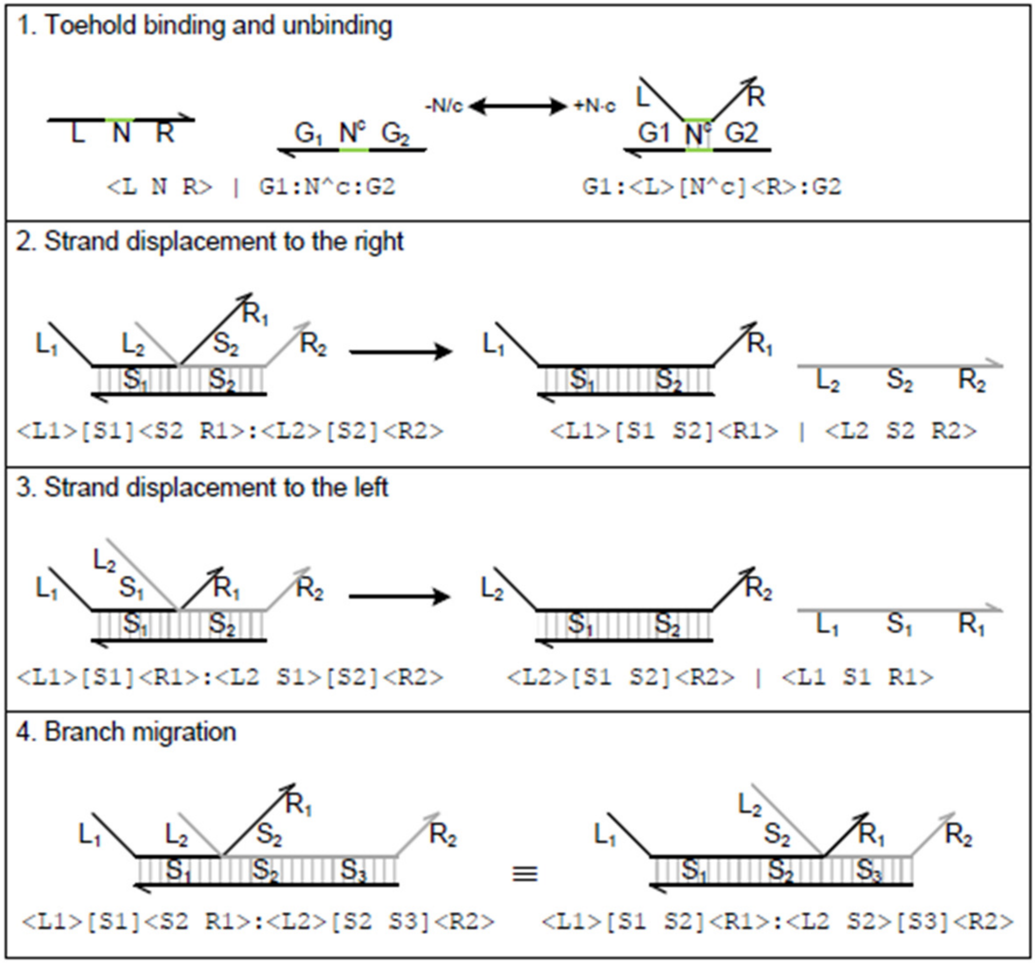
C. Syntax of DNA sequences *S*,*L*,*R*

Sequence of domains $O_1,\ldots,O_K$

O_1 O_2 ... O_K

`O1 O2 ... OK`

Dynamics


1. Toehold binding and unbinding

```
<L N R> | G1:N^c:G2
G1:<L>[N^c]<R>:G2
```

2. Strand displacement to the right

```
<L1>[S1]<S2 R1>:<L2>[S2]<R2>
<L1>[S1 S2]<R1> | <L2 S2 R2>
```

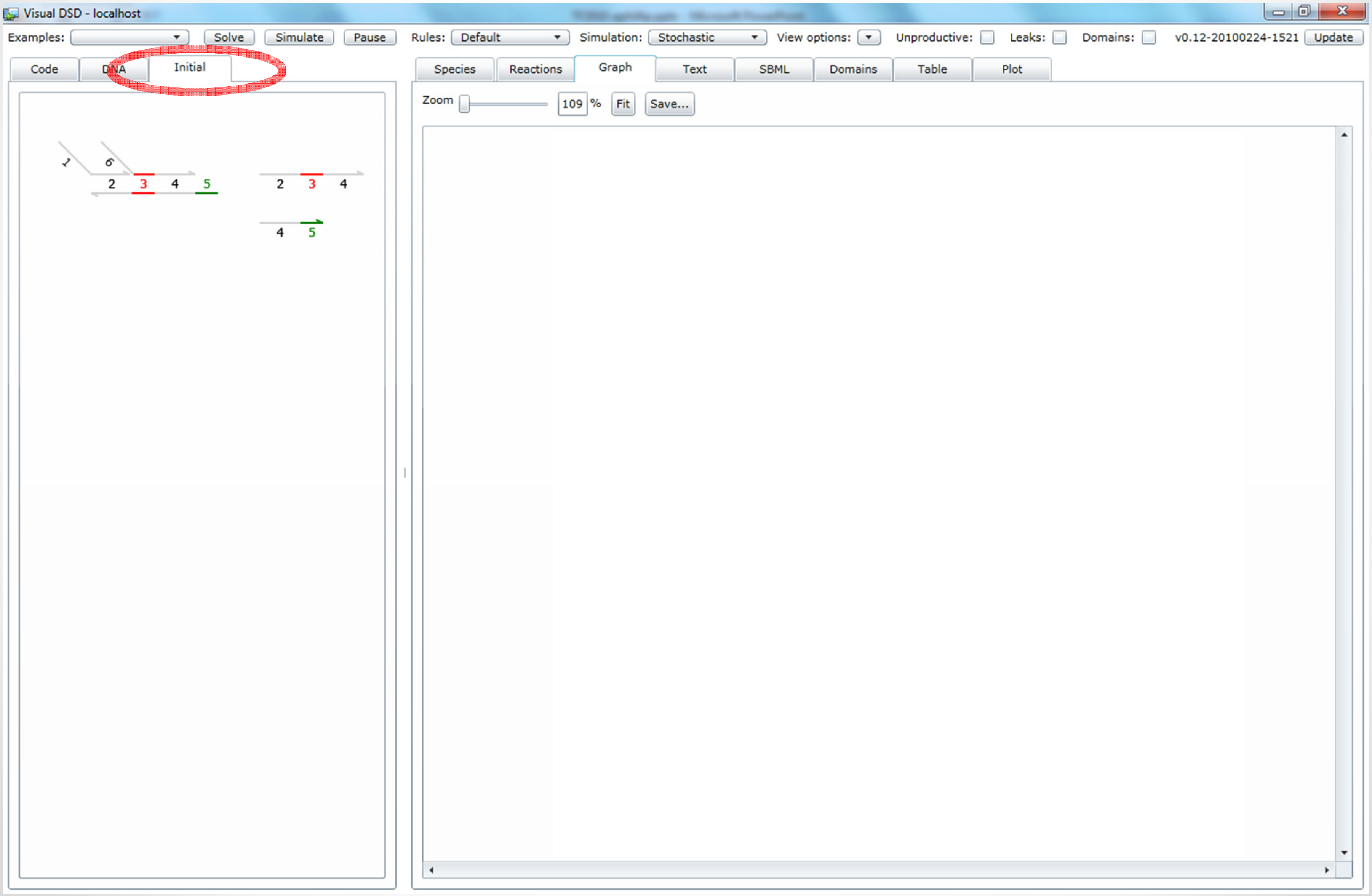
3. Strand displacement to the left

```
<L1>[S1]<R1>:<L2 S1>[S2]<R2>
<L2>[S1 S2]<R2> | <L1 S1 R1>
```

4. Branch migration

```
<L1>[S1]<S2 R1>:<L2>[S2 S3]<R2>
<L1>[S1 S2]<R1>:<L2 S2>[S3]<R2>
```

Initial Species



Visual DSD - localhost

Examples:

Rules: Default

Simulation: Stochastic

Unproductive: ☐

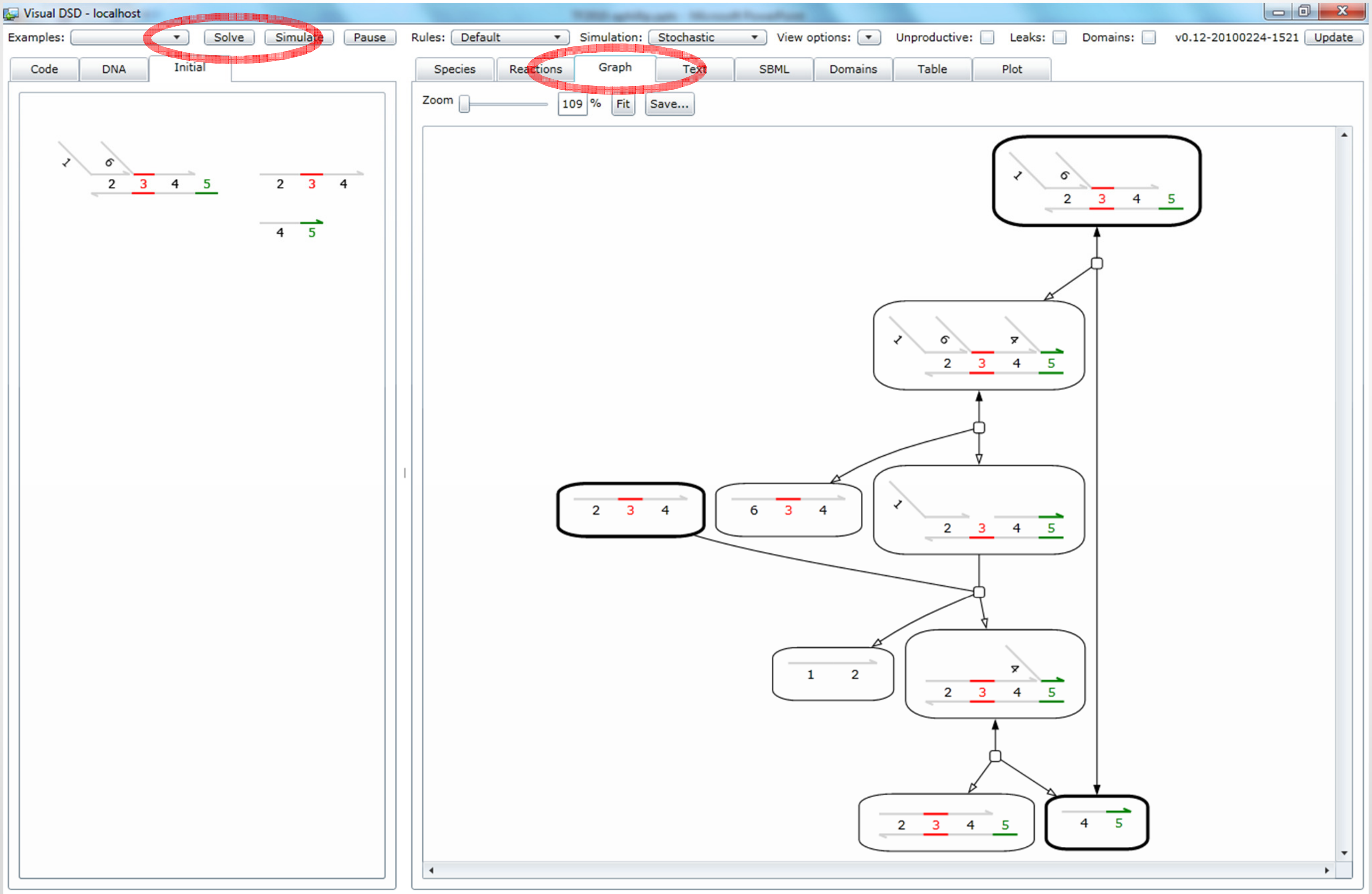
Leaks: ☐

Domains: ☐

v0.12-20100224-1521

Zoom 109 %

Reaction Graph



Visual DSD - localhost

Examples:

Rules: Default

Simulation: Stochastic

View options:

Unproductive: ☐

Leaks: ☐

Domains: ☐

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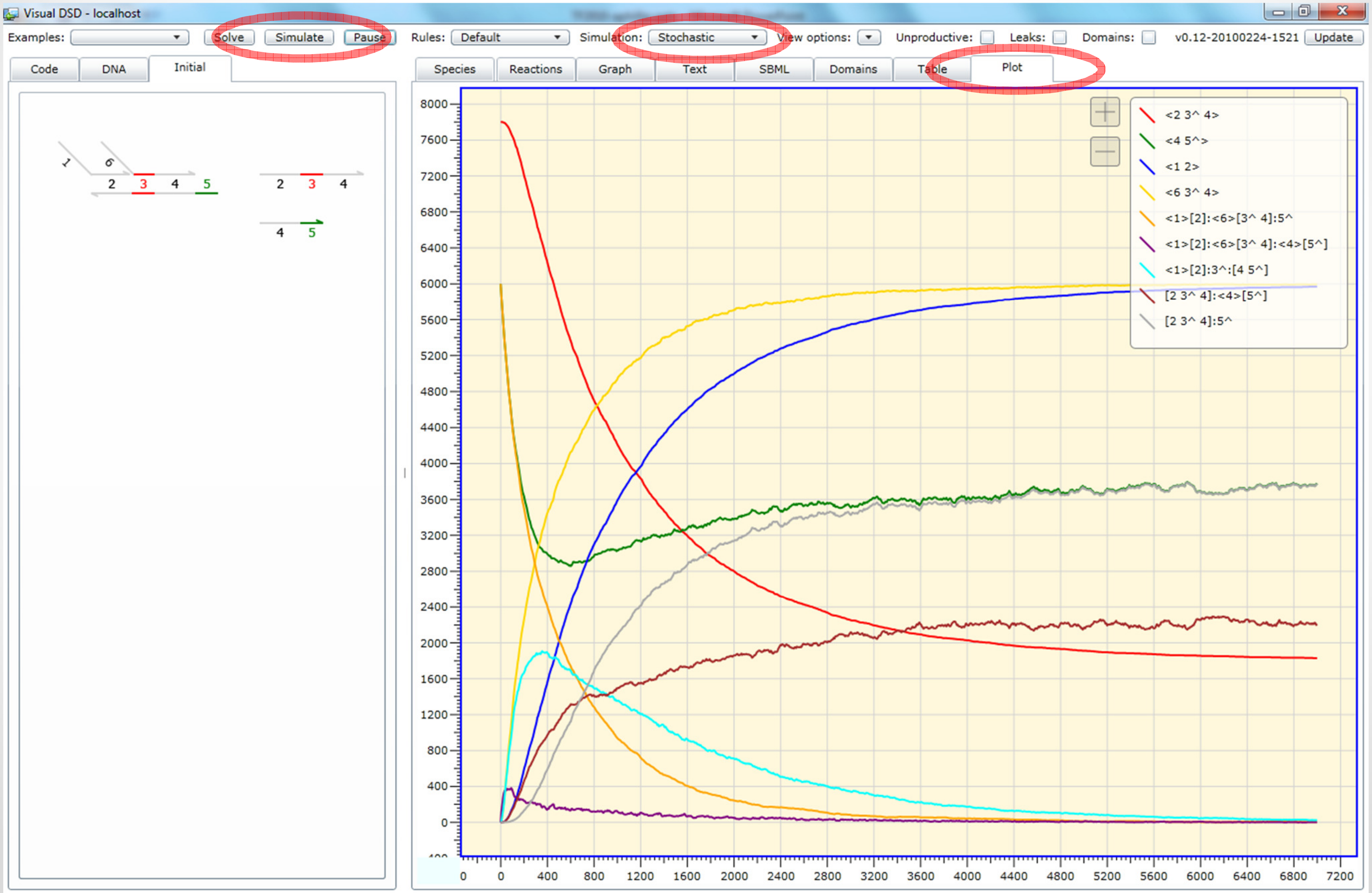
Zoom 109 %

Simulation



Visual DSD - localhost

Rules: Default

Simulation: Stochastic

Unproductive: ☐ Leaks: ☐ Domains: ☐

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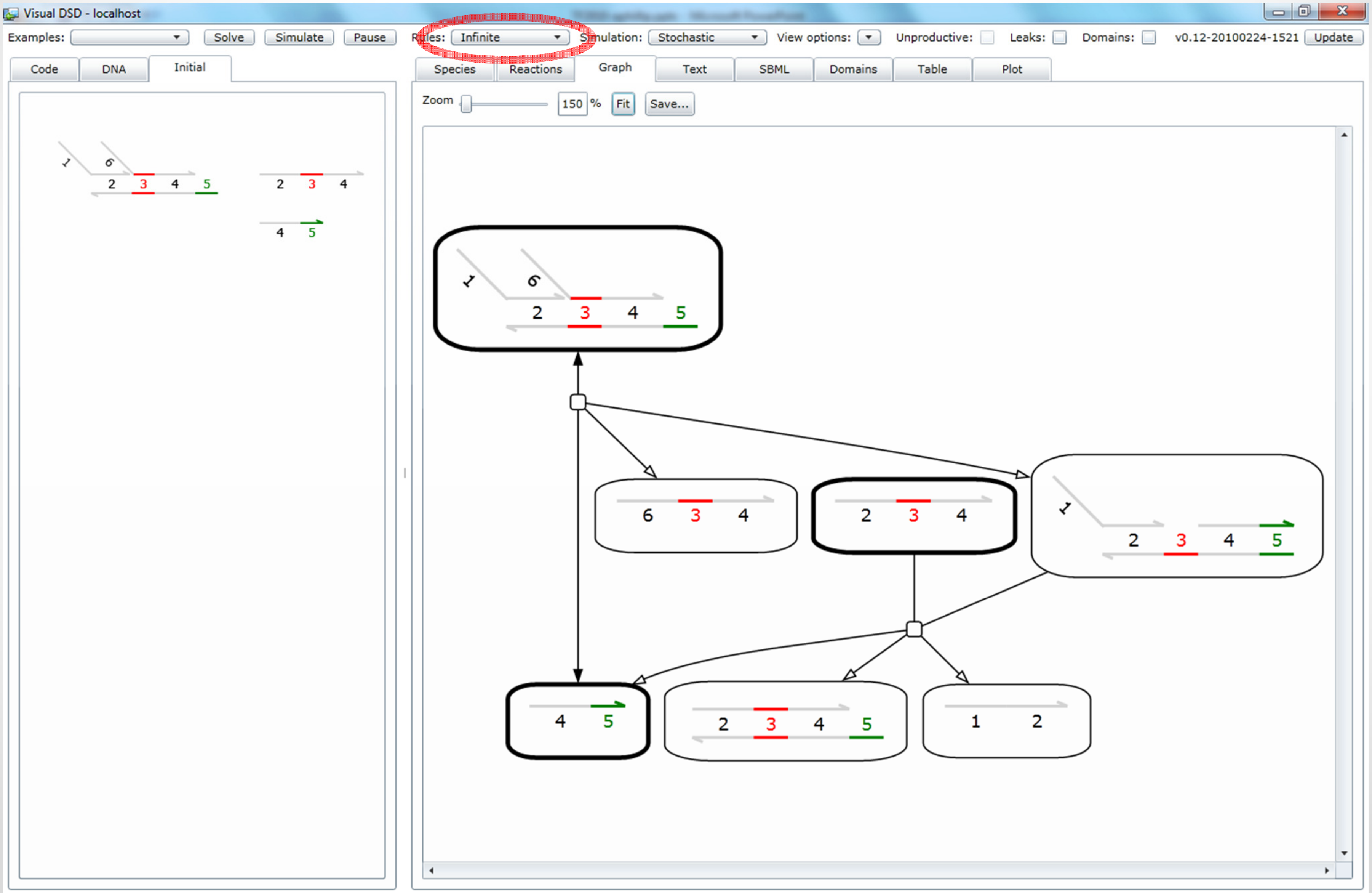
Abstract Reactions



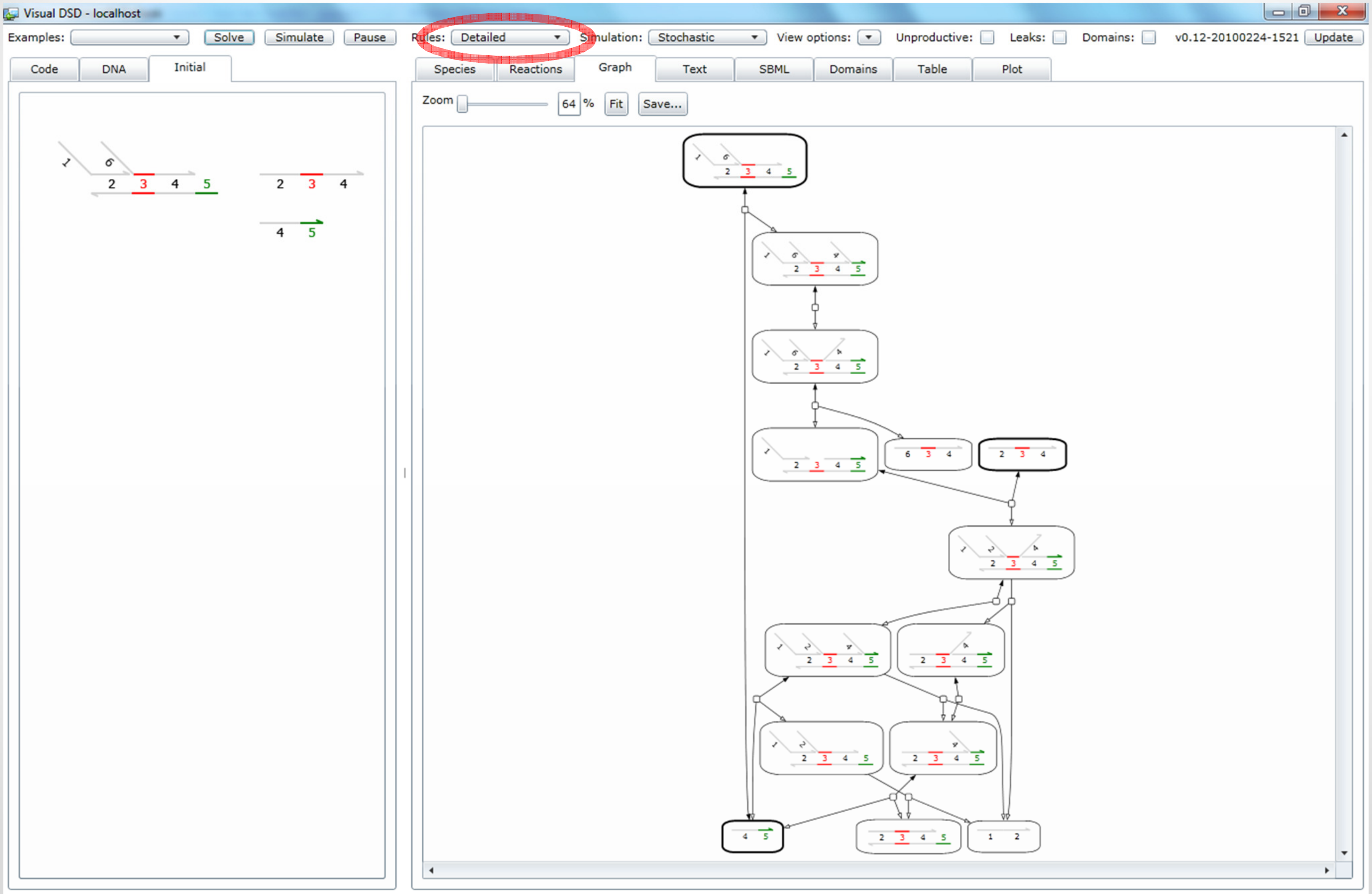
Rules: Infinite

Simulation: Stochastic

Zoom 150 %

v0.12-20100224-1521

Detailed Reactions



Visual DSD - localhost

Examples:

Rules: Detailed

Simulation: Stochastic

View options:

Unproductive: ☐

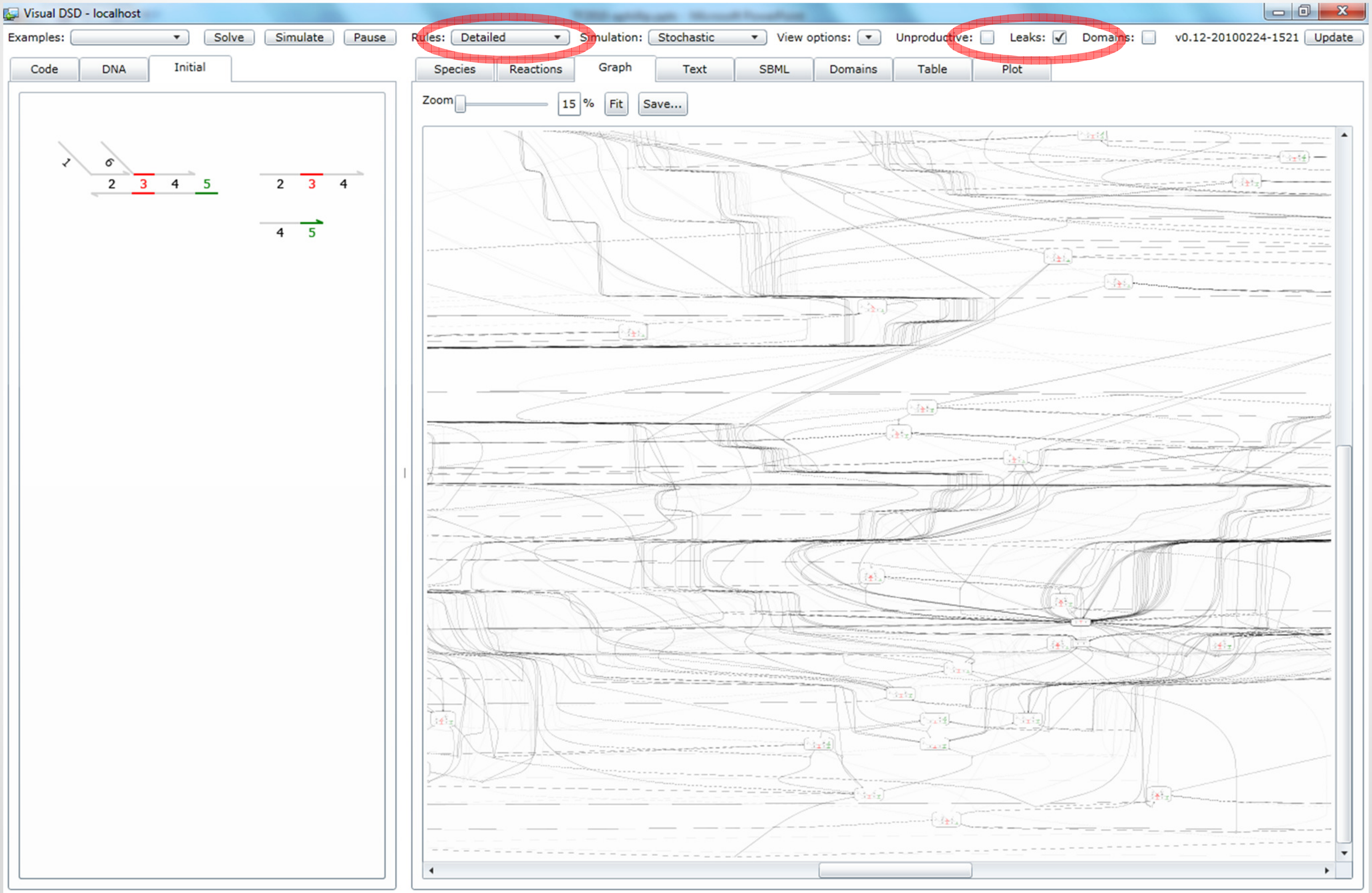
Leaks: ☐

Domains: ☐

v0.12-20100224-1521

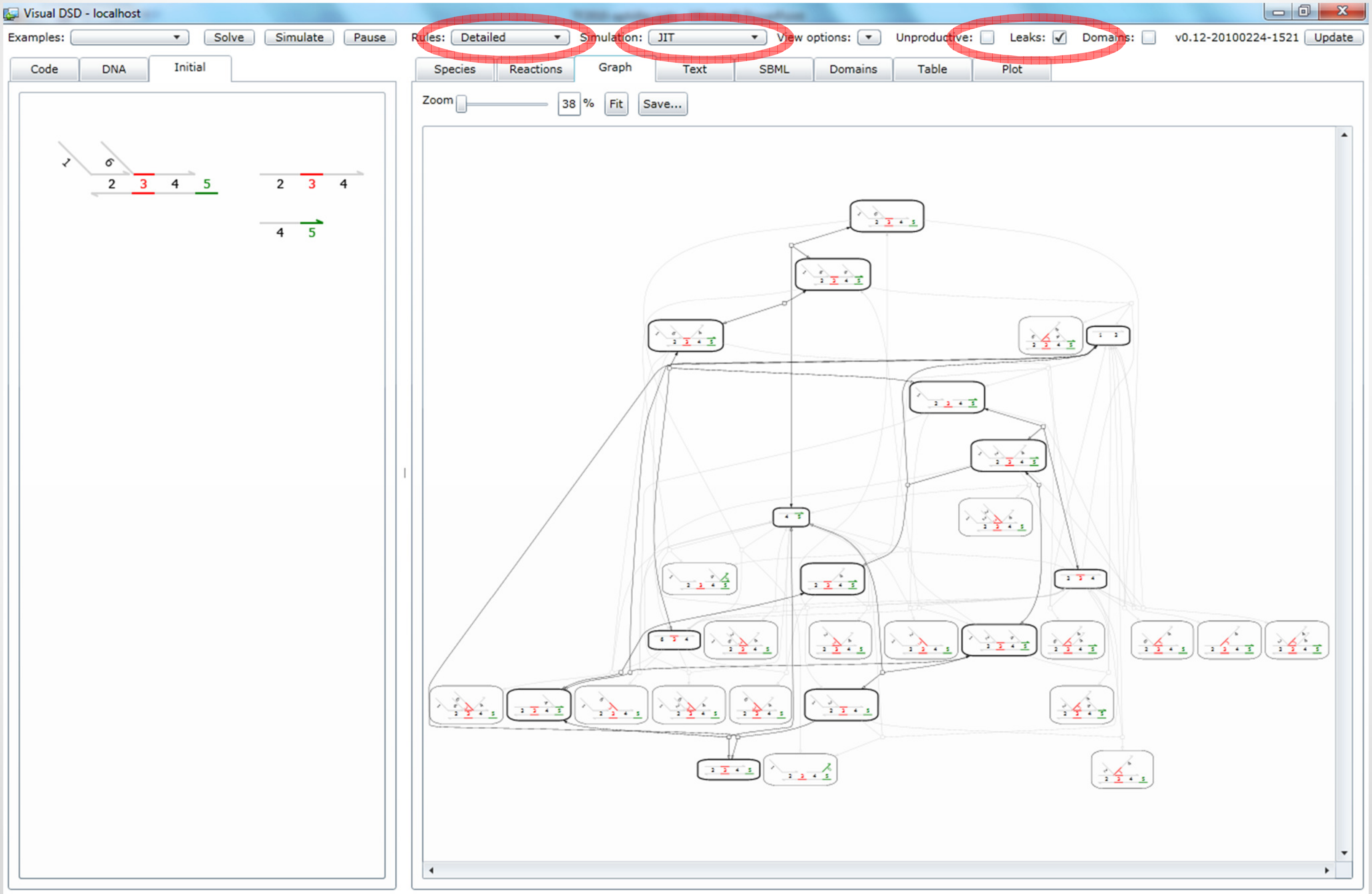
Zoom 64 %

Detailed Leak Reactions!



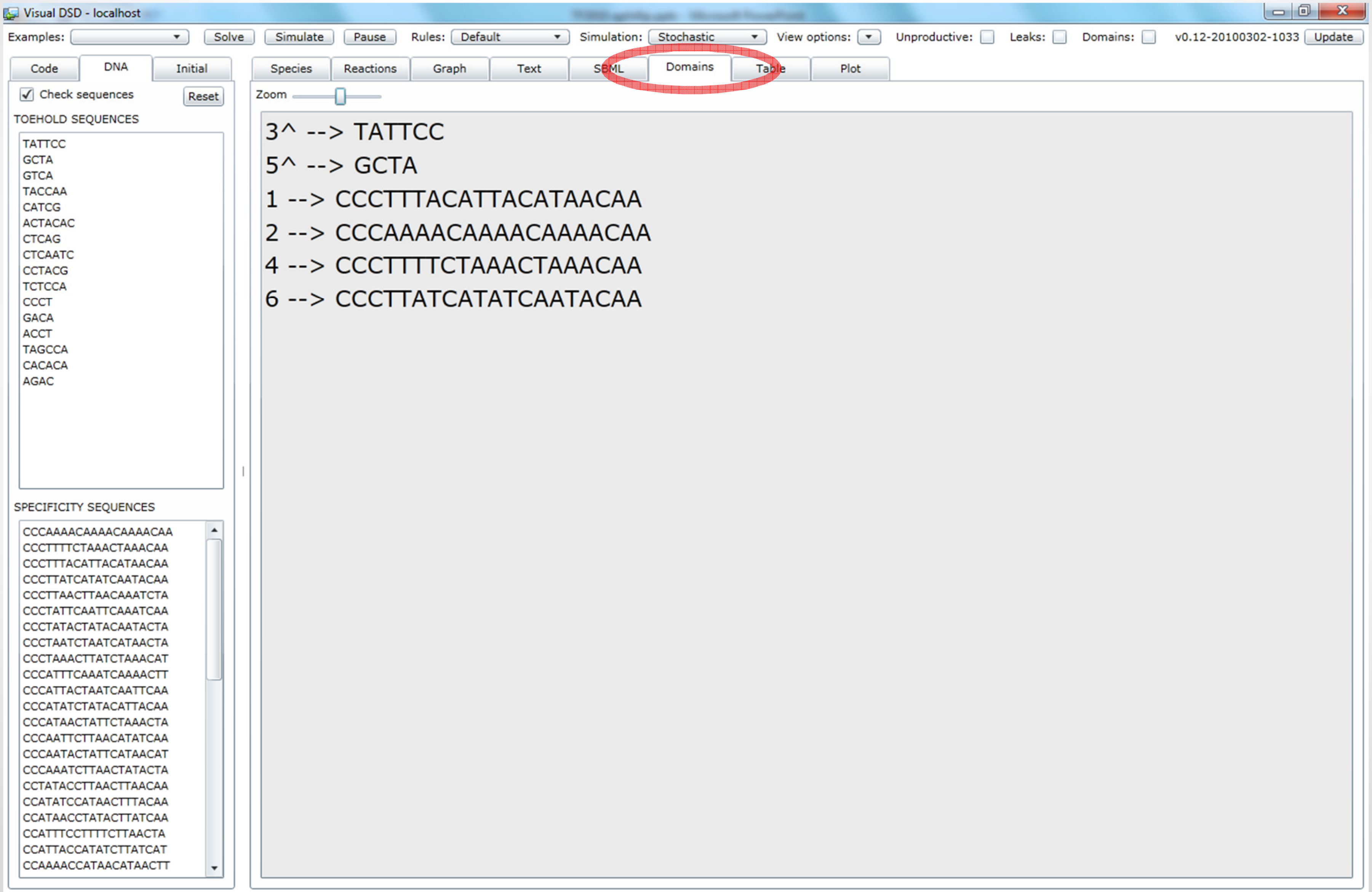
Rules: Detailed
Simulation: Stochastic
Unproductive: ☐
Leaks: ☑
Domains: ☐
v0.12-20100224-1521

Just-in-Time Simulation



Rules: Detailed
Simulation: JIT
Unproductive: ☐
Leaks: ☑
Domains: ☐
v0.12-20100224-1521
Zoom 38 %

DNA Sequences



Examples:
Rules: Default
Simulation: Stochastic
View options:
Unproductive: ☐
Leaks: ☐
Domains: ☐
v0.12-20100302-1033

☑ Check sequences

TOEHOLD SEQUENCES

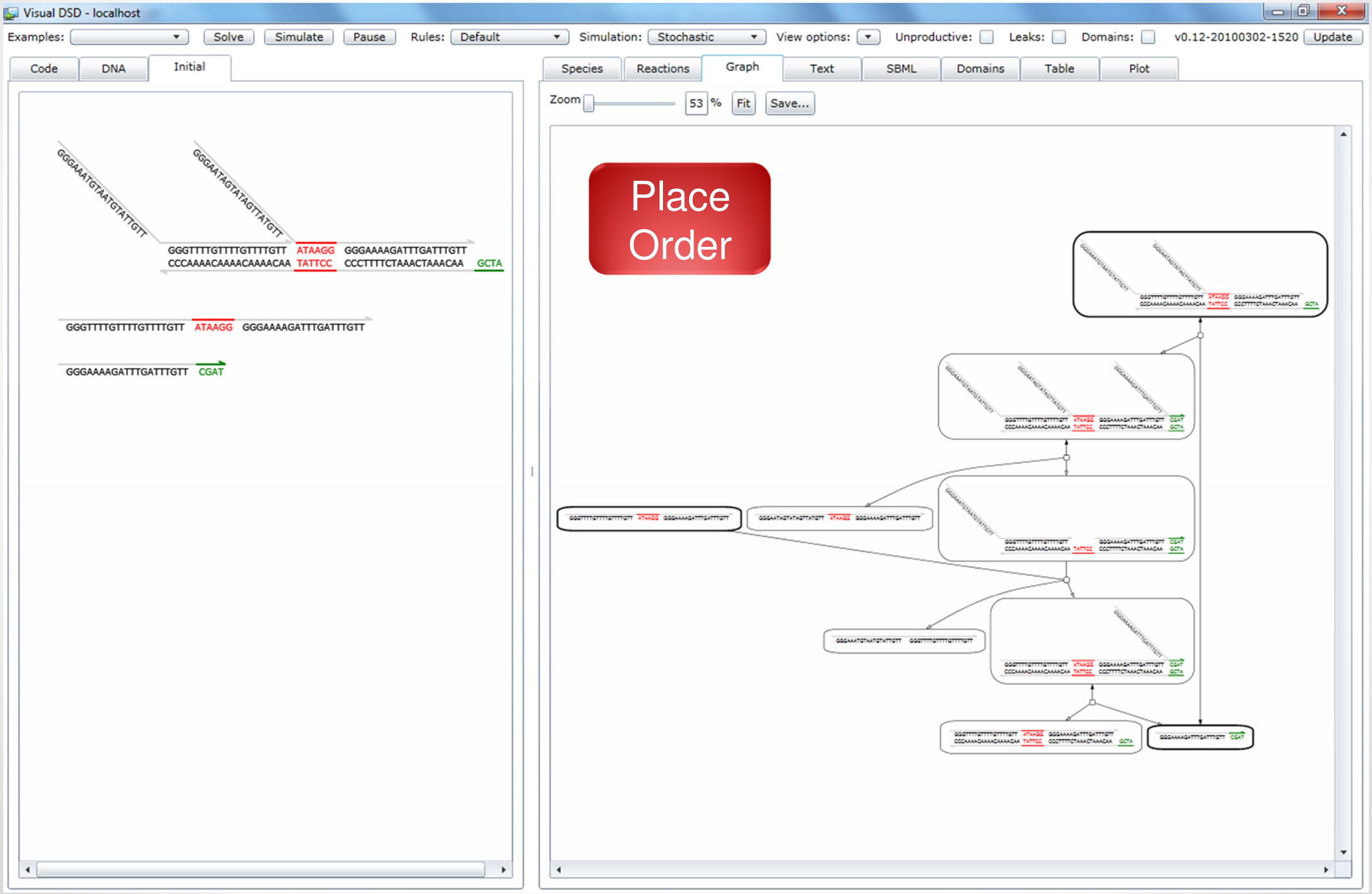
```
TATTCC
GCTA
GTCA
TACCAA
CATCG
ACTACAC
CTCAG
CTCAATC
CCTACG
TCTCCA
CCCT
GACA
ACCT
TAGCCA
CACACA
AGAC
```

SPECIFICITY SEQUENCES

```
CCCAAAACAAAACAAAACAA
CCCTTTTCTAAACTAAACAA
CCCTTTACATTACATAACAA
CCCTTATCATATCAATACAA
CCCTTAACTTAACAAATCTA
CCCTATTCAATTCAAATCAA
CCCTATACTATACAATACTA
CCCTAATCTAATCATAACTA
CCCTAAACTTATCTAAACAT
CCCATTTCAAATCAAAACTT
CCCATTACTAATCAATTCAA
CCCATATCTATACATTACAA
CCCATAACTATTCTAAACTA
CCCAATTCTTAACATATCAA
CCCAATACTATTCATAACAT
CCCAAATCTTAACTATACTA
CCTATACCTTAACTTAACAA
CCATATCCATAACTTTACAA
CCATAACCTATACTTATCAA
CCATTTCCTTTTCTTAACTA
CCATTACCATATCTTATCAT
CCAAAACCATAACATAACTT
```

```
3^ --> TATTCC
5^ --> GCTA
1 --> CCCTTTACATTACATAACAA
2 --> CCCAAAACAAAACAAAACAA
4 --> CCCTTTTCTAAACTAAACAA
6 --> CCCTTATCATATCAATACAA
```

Final DNA Circuit



Visual DSD - localhost

Examples:

Rules: Default

Simulation: Stochastic

View options:

Unproductive: ☐

Leaks: ☐

Domains: ☐

v0.12-20100302-1520

Zoom 53 %

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Unmodified

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Change Form: 1 Expand to this many items ☐ Duplex ☐ Paste Go

25 nmole DNA Oligo = 15-60 bases	100 nmole DNA oligo = 10-90 bases	250 nmole DNA oligo = 5-100 bases
1 µmole DNA oligo = 5- 0 bases	5 µmole DNA oligo = 5-50 bases	10 µmole DNA oligo = 5-50 bases
25 nmole Ultramer DNA Oligo=6 0 bases	4 nmole Ultramer DNA Oligo=60-200 bases	PAGE Ultramer DNA Oligo=60-200 bases

urification: Standard Desalting

25 nmole DNA oligo

Sequence Name

\# Bases: 21

5'- ACT GCA CCA TAA GCA ACT TTT -3'

tes: Enter your tes here se do t enter modifications

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IDT
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Innovation and Precision in Nucleic Acid Synthesis

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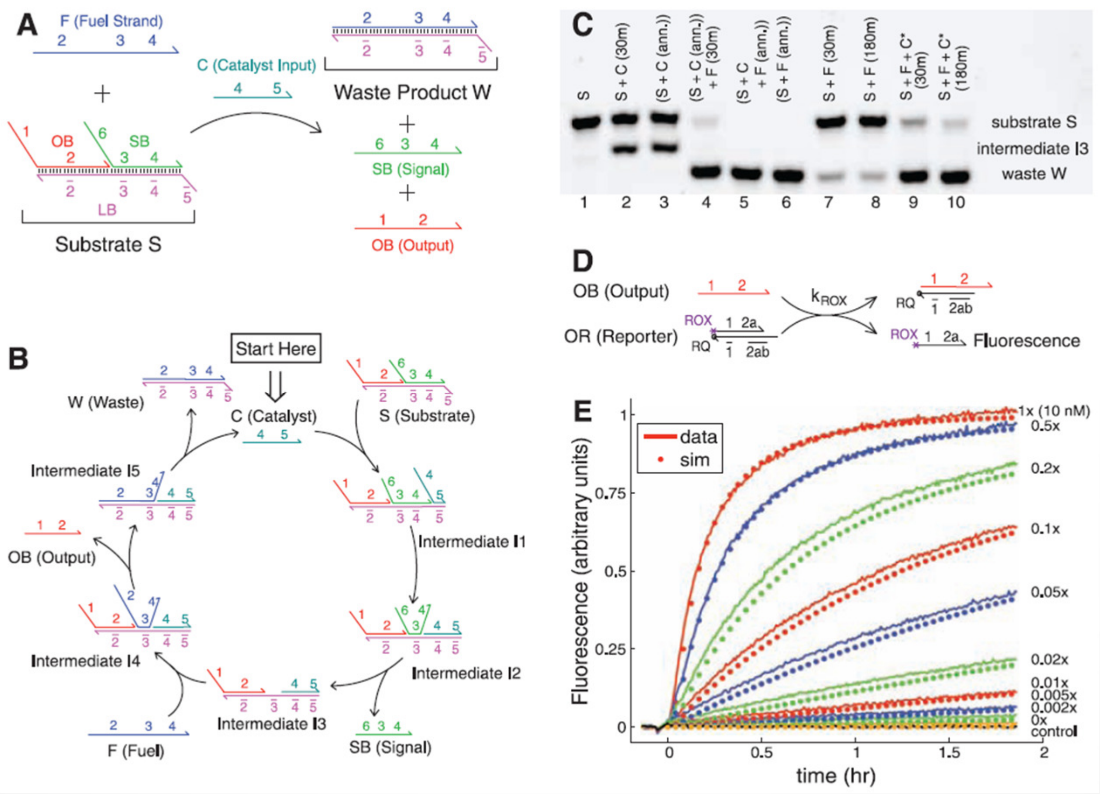
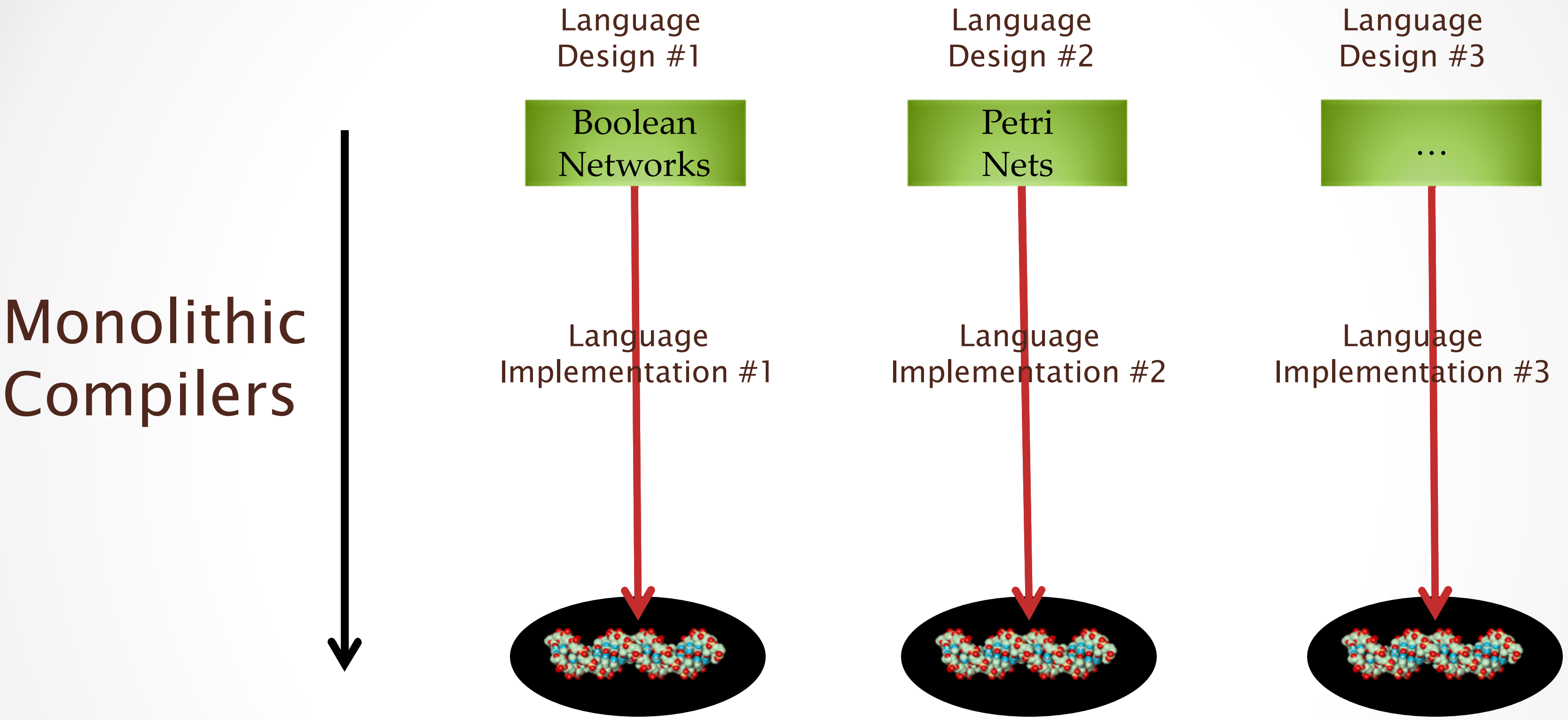
- (Nothing to do with us.)

Engineering Entropy-Driven Reactions and Networks Catalyzed by DNA
David Yu Zhang, *et al.*
Science **318**, 1121 (2007);
DOI: 10.1126/science.1148532



DNA Compilation

Compilers



Monolithic Compilers

Language Design #1

Boolean Networks

Language Implementation #1

Language Design #2

Petri Nets

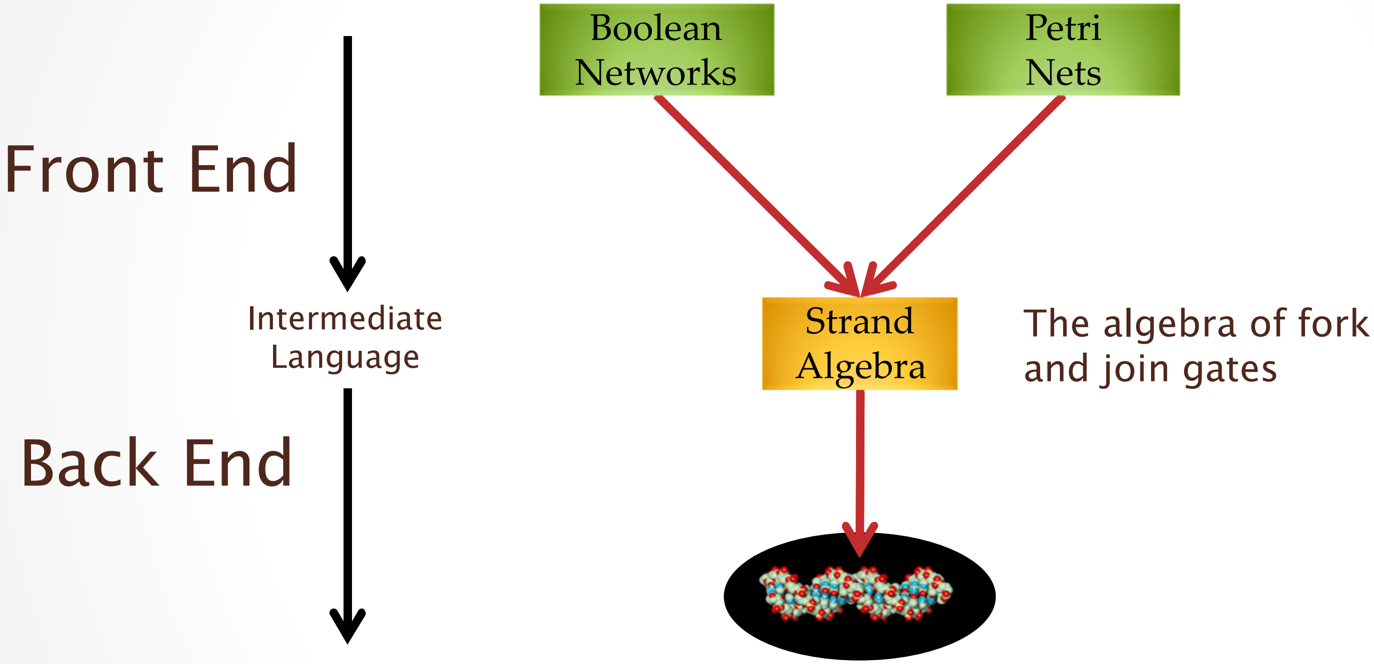
Language Implementation #2

Language Design #3

…

Language Implementation #3

Intermediate Languages



Front End

Intermediate
Language

Back End

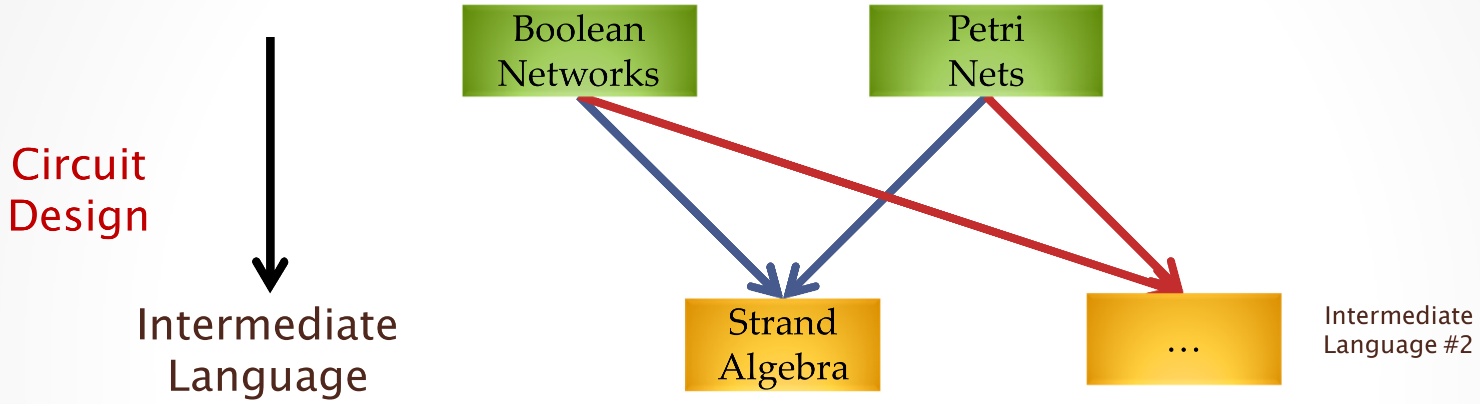
Boolean Networks

Petri Nets

Strand Algebra

The algebra of fork
and join gates

Front Ends



Circuit Design

Intermediate Language

Boolean Networks

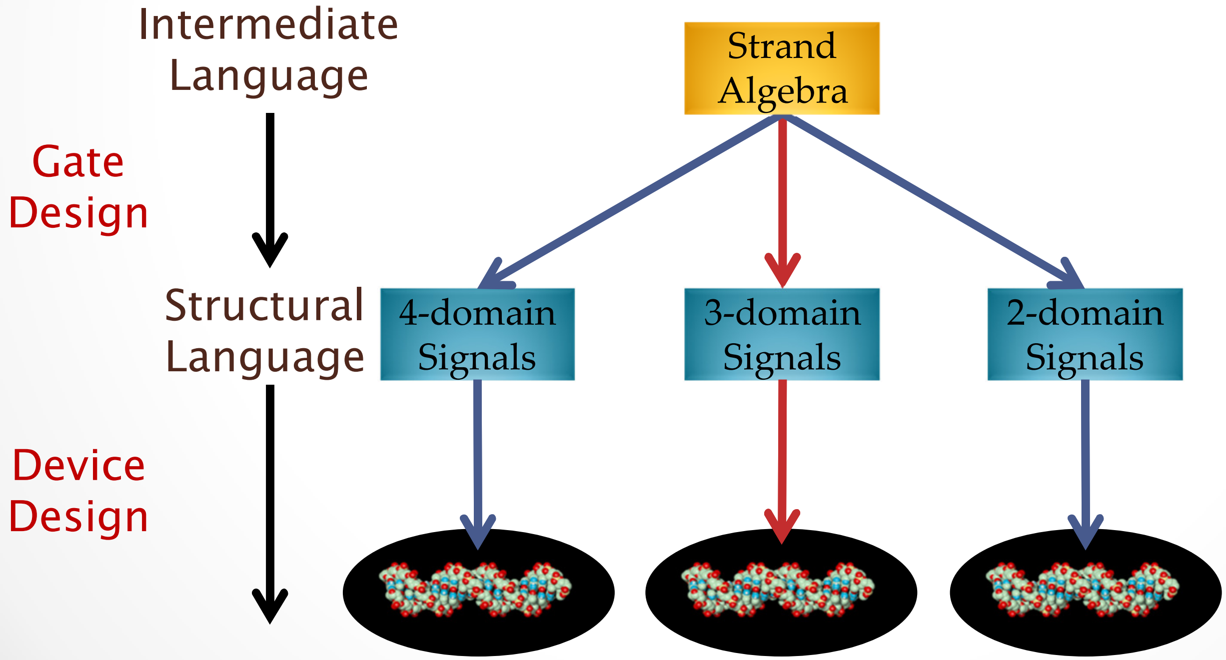
Petri Nets

Strand Algebra

…

Intermediate Language #2

Back Ends



Intermediate Language

Gate Design

Structural Language

Device Design

Strand Algebra

4-domain Signals

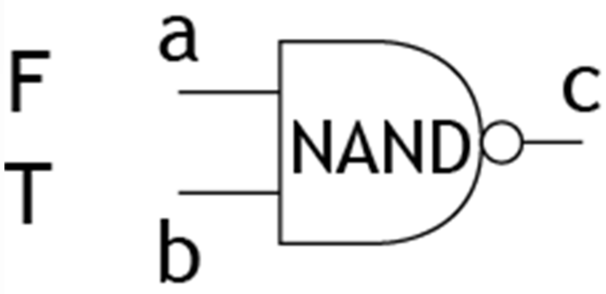
3-domain Signals

2-domain Signals

Compiling Abstract Machines

Boolean Networks

Boolean Networks to Strand Algebra



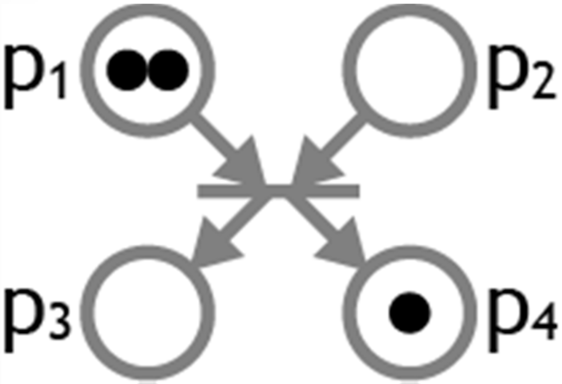
$$([a_F,b_F].c_T)^* \mid$$
$$([a_F,b_T].c_T)^* \mid$$
$$([a_T,b_F].c_T)^* \mid$$
$$([a_T,b_T].c_F)^* \mid$$
$$a_F \mid b_T$$

This encoding is *compositional*, and can encode *any* Boolean network:
- multi-stage networks can be assembled (combinatorial logic)
- network loops are allowed (sequential logic)

Petri Nets

Petri Nets to Strand Algebra

Transitions as Gates
Place markings as Signals



$$([p_1,p_2].[p_3,p_4])^* \mid p_1 \mid p_1 \mid p_4$$

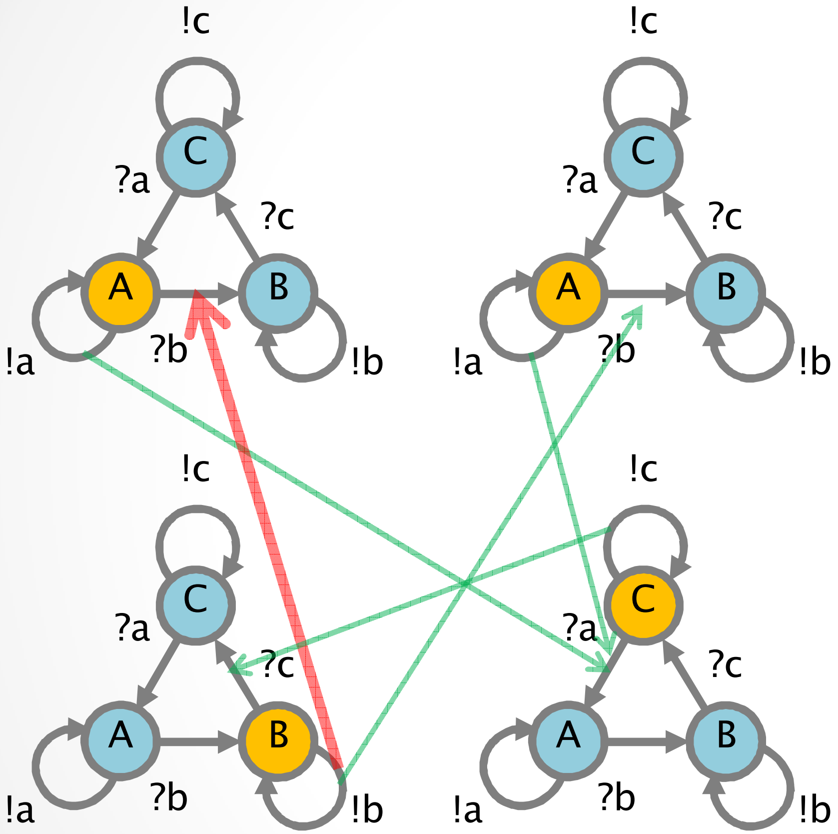
Chemical Reaction Networks

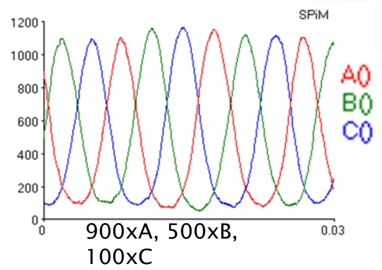
Implementing an arbitrary finite chemical system in
DNA with asymptotically correct kinetics
Soloveichick & al. DNA 15

Species become signals
Reactions become gates

$$A + B \to C + D \qquad \Rightarrow \qquad [A,B].[C,D]$$

Interacting Automata

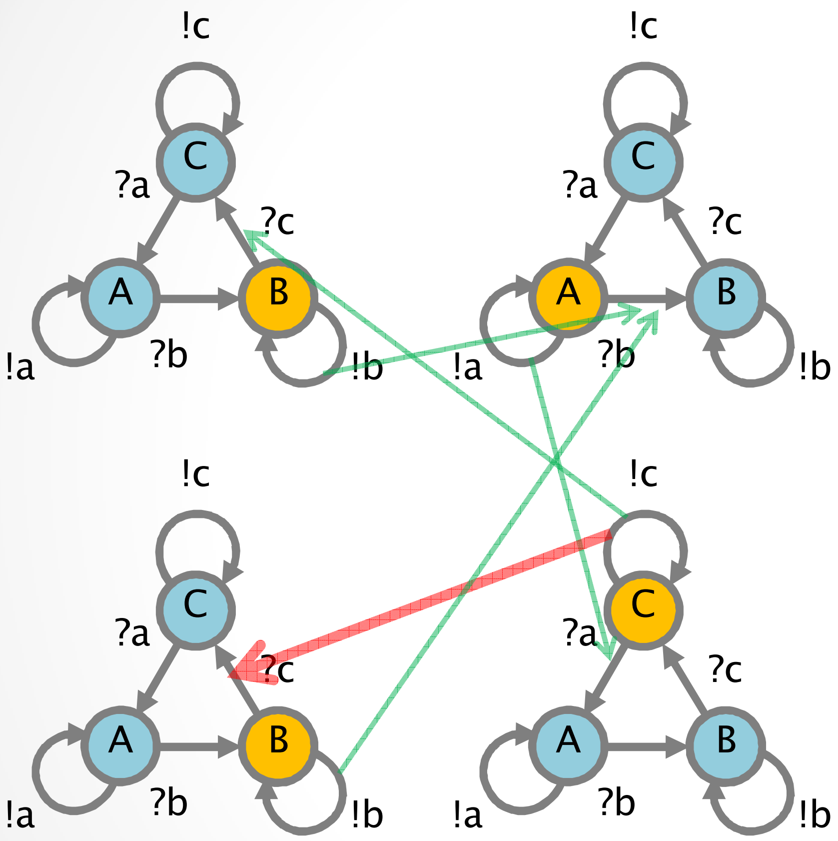


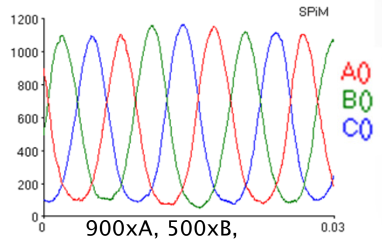


([A,B].[B,B])* |
([B,C].[C,C])* |
([C,A].[A,A])* |
A | A | B | C

This is a uniform population of identical automata,
but heterogeneous populations of interacting automata can be similarly handled.

Interacting Automata



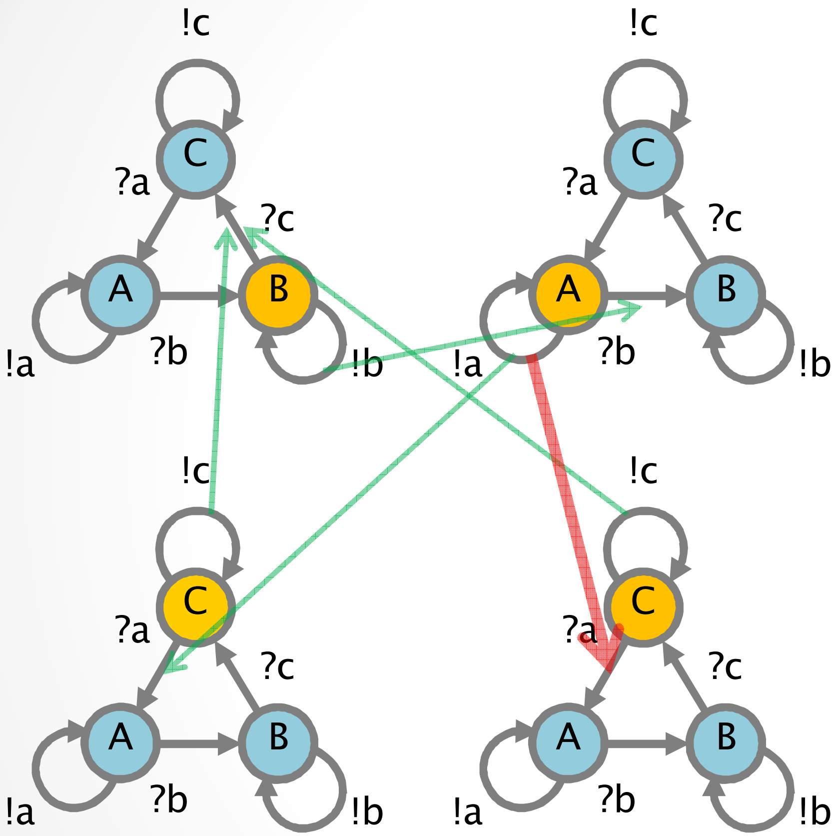


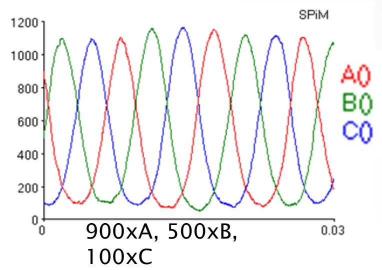
900xA, 500xB,
100xC

([A,B].[B,B])* |
([B,C].[C,C])* |
([C,A].[A,A])* |
A | B | B | C

This is a uniform population of identical automata,
but heterogeneous populations of interacting automata can be similarly handled.

Interacting Automata





([A,B].[B,B])* |
([B,C].[C,C])* |
([C,A].[A,A])* |
A | B | C | C

This is a uniform population of identical automata,
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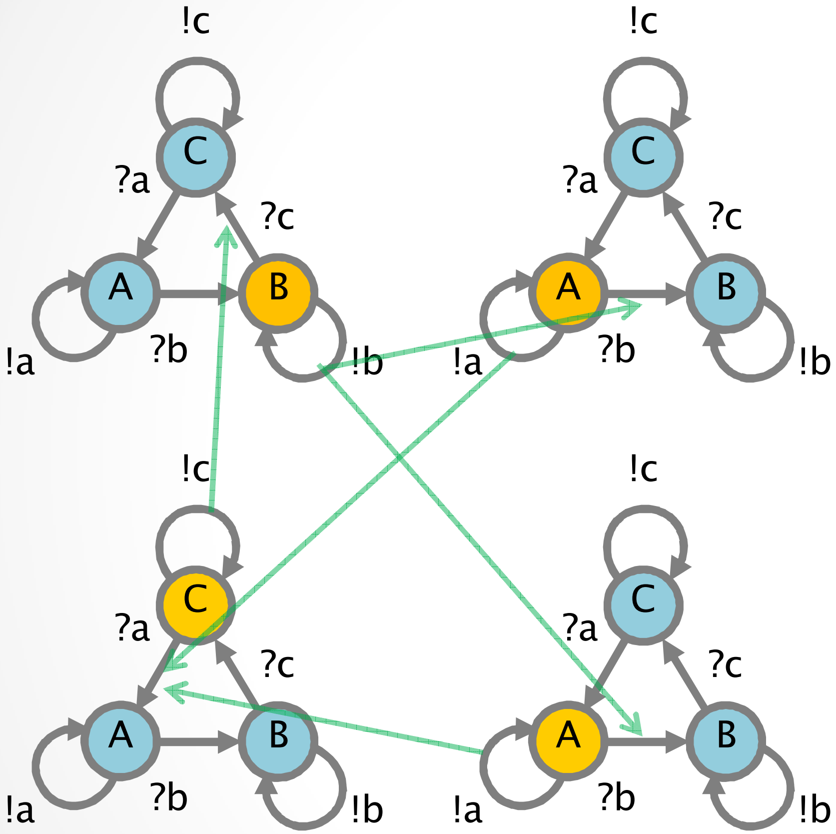
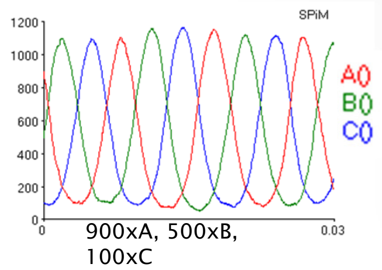
Interacting Automata





900xA, 500xB, 100xC

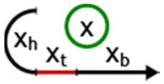
([A,B].[B,B])* |
([B,C].[C,C])* |
([C,A].[A,A])* |
A | A | B | C

This is a uniform population of identical automata,
but heterogeneous populations of interacting automata can be similarly handled.

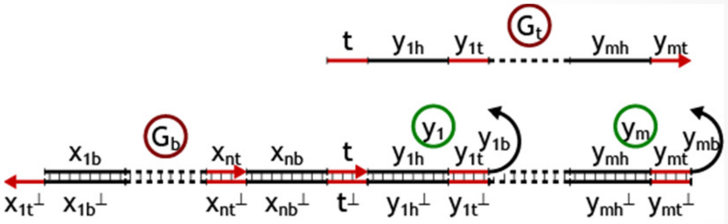
Strand Algebra to DSD

$P \ ::= \ x \ ⁝ \ [x_1,..,x_n].[y_1,..,y_m] \ ⁝ \ 0 \ ⁝ \ P|P \ ⁝ \ P^* \qquad n \geq 1,\ m \geq 0$

- compile(x) =



- compile($[x_1,..,x_n].[y_1,..,y_m]$) =



- compile(0) = empty solution
- compile(P | P’) = mix(compile(P), compile(P’))
- compile(P*) = population(compile(P))

And finally...

• • •

Summary

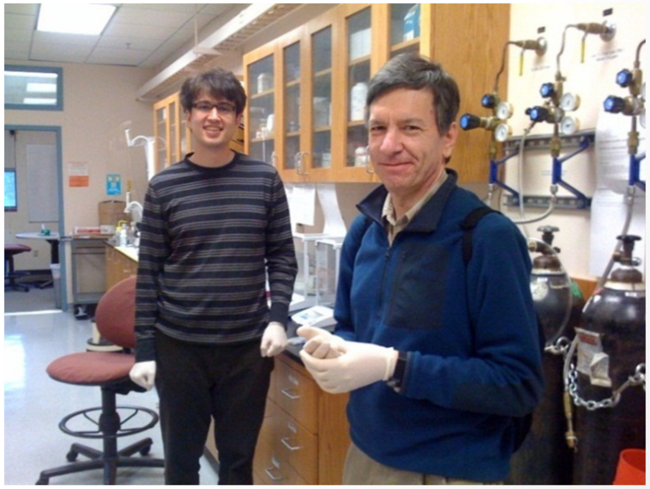
- Abstract Machines to Strand Algebra
  - Or other intermediate language
- Strand Algebra to DSD
  - Or other structural language
- Simulation, analysis, etc.
  - Iterate a lot
- DSD to Sequences
  - E.g. NuPack, or pre-build strand libraries
- Sequences to DNA
  - Web order
- DNA experiments
  - Fairly basic wet lab
- Deployable Nanotech

Conclusions

- Nucleic Acids
  - Programmable matter
- DNA Strand Displacement
  - A computational mechanism at the molecular level
- DNA as a Compilation Target for Abstract Machines
  - Abstract Machines (Boolean Networks, Petri Nets, Interacting Automata)
  - Intermediate languages (Strand Algebra, Strand Displacement Language).
  - DNA sequence generation.
- Tools
  - Thermodynamic analysis.
  - Reaction graph generation.
  - Simulation.
  - Verification (not yet).

Acknowledgments

- Illustrations
  - John Reif, Duke
  - Ned Seeman, NYU
  - Erik Winfree, Caltech
  - Bernard Yurke, Boise State
  - Wikipedia
  - YouTube
- David Soloveichik



Q?

http://lucacardelli.name