Strand Algebras for DNA Computing

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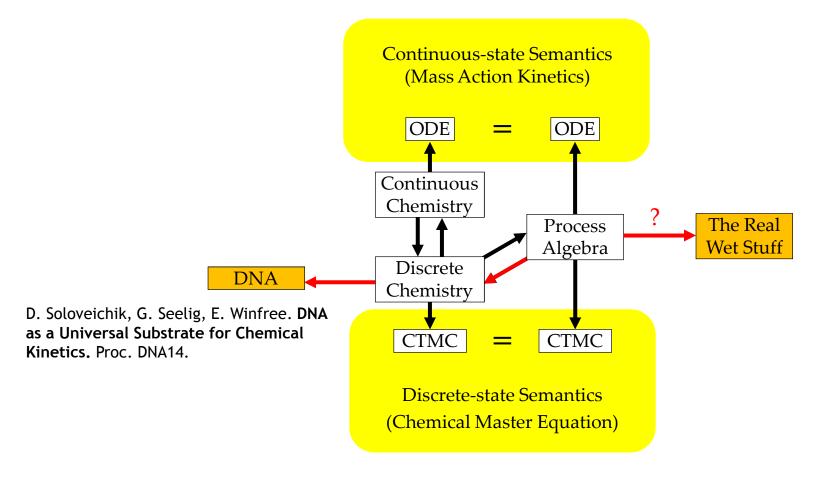
http://lucacardelli.name

How Process Algebra fits in DNA Computing

• Electronics has *electrons*

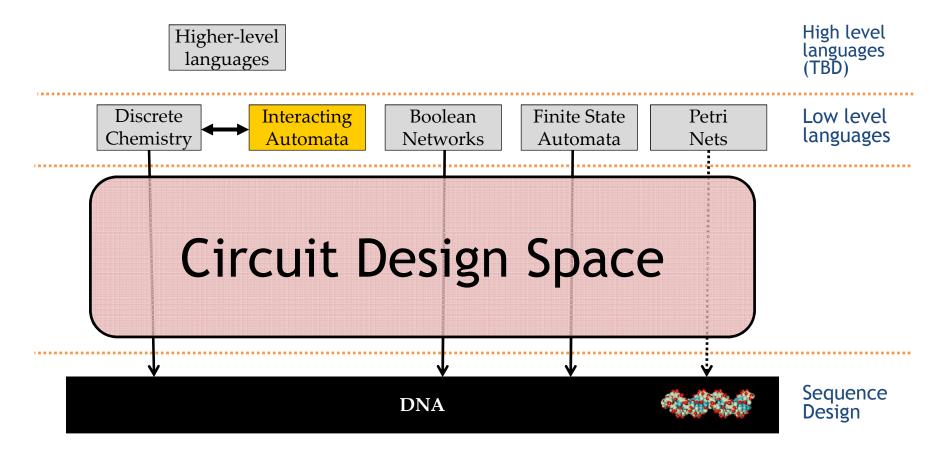
- \circ All electrons are the same
- All you can do is see if you have *few* ('False') or *lots* ('True') of electrons
- \circ Hence Boolean logic is at the basis of digital circuit design
- Symbolic and numeric computation has to be encoded above that
- \circ But mostly we want to compute with symbols and numbers, not with Booleans
- DNA computing has *symbols* (DNA words)
 - $\circ~$ DNA words are not all the same
 - Symbolic computation can be done *directly*
 - We can also directly use molecular concurrency
- Process Algebra as the 'Boolean Algebra' of DNA Computing
 - What are the 'gates' of symbolic concurrent computation?
 - $\circ~$ That's what Process Algebra is about
 - (Process Algebra comes from the theory of concurrent systems)

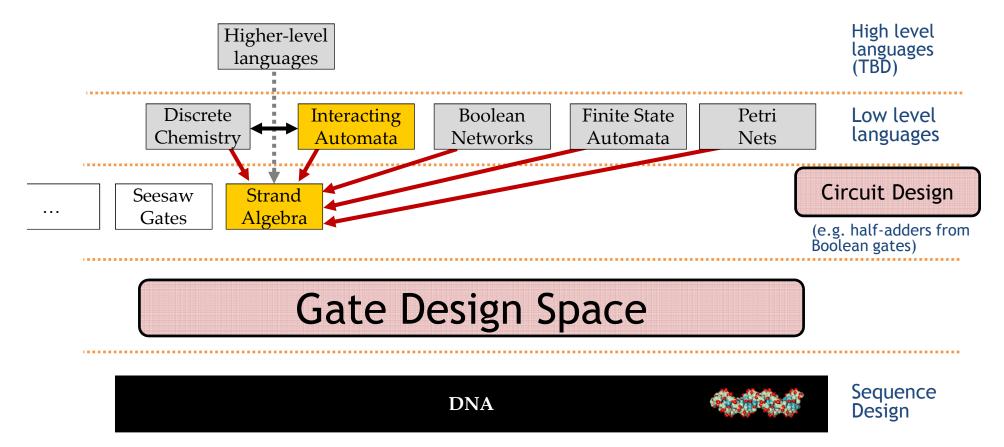
Molecules as Automata (DNA14 Invited Talk)

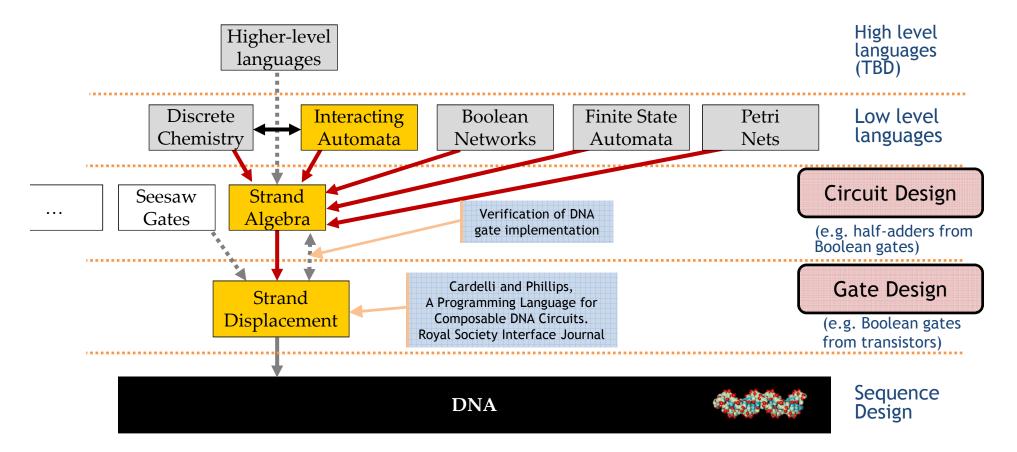


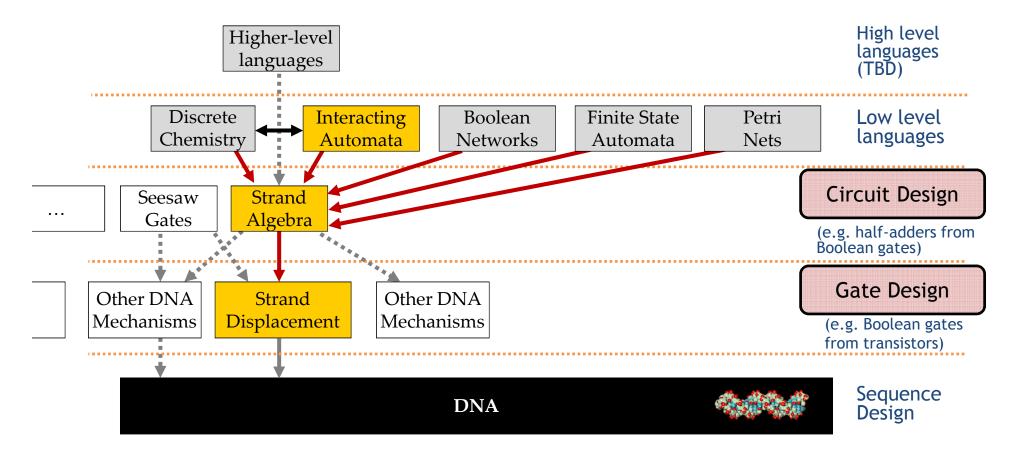
L. Cardelli: "On Process Rate Semantics" (TCS)

L. Cardelli: "A Process Algebra Master Equation" (QEST'07)

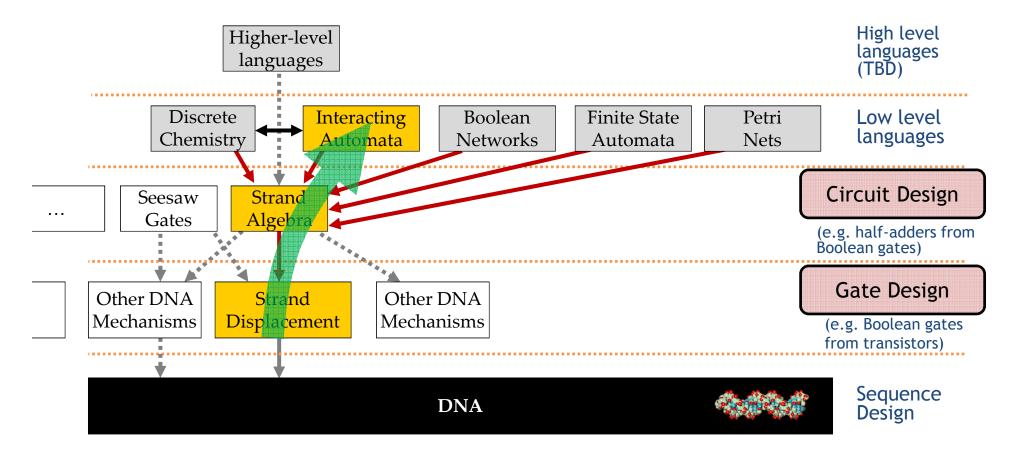






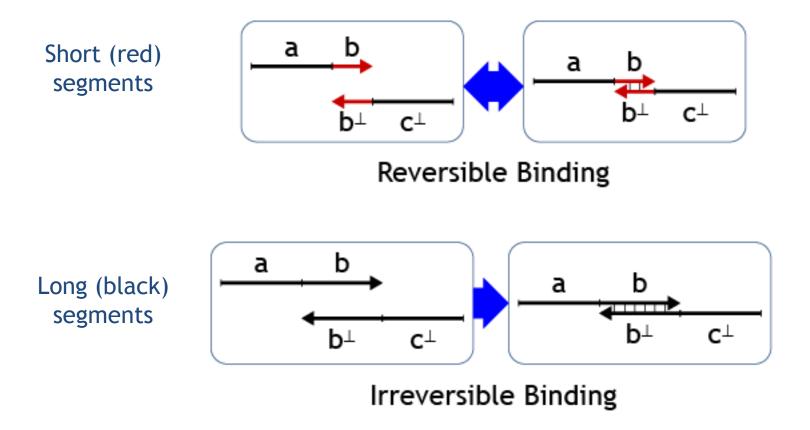


Separating Circuit Design from Gate Design

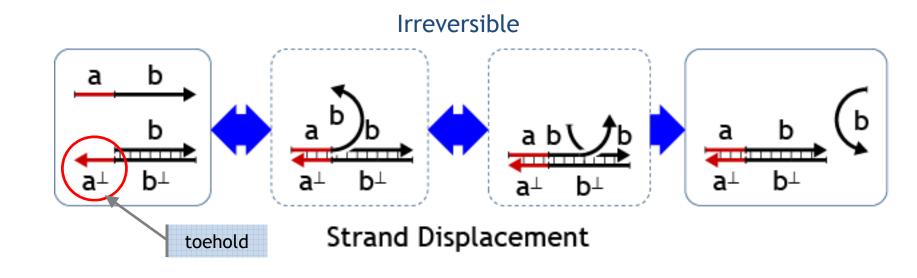


Rest of the talk: bottom up

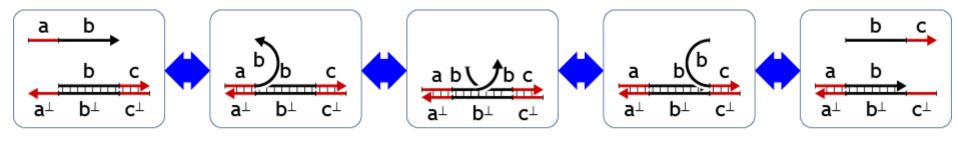
Gate Elements: Short and Long DNA Segments



Gate Elements: Basic Mechanisms



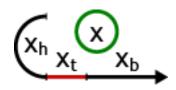
Reversible



Toehold Exchange

Gate Elements: Signals and Gates

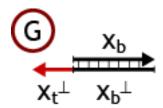
• Signals "x" are single-stranded and 'positive'



x_h = history x_t = toehold x_b = binding

$$x_t, x_b = signal identity for x$$

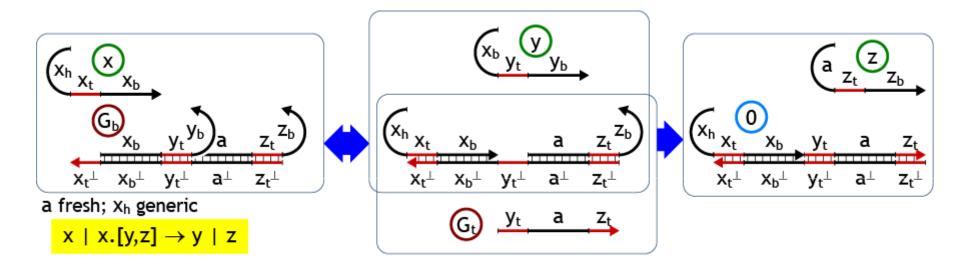
- This 3-segment signal representation is original to this work, it is based on the 4-segment signals of D. Soloveichik, G. Seelig, E. Winfree. Proc. DNA14, but leads to simpler and more regular gate structures
- Gate backbones are double-stranded, except for 'negative' toeholds.



• Separation of strands and gates helps the DNA realization, as one can use 3-letter alphabets (ATC/ATG) for each strand, minimizing secondary structure and entanglement.

Circuit Elements: X.[y,z] Fork Gate

• A Fork signal-processing gate takes a signal x and produces two signals y, z according to the reaction $x \mid x.[y,z] \rightarrow y \mid z$



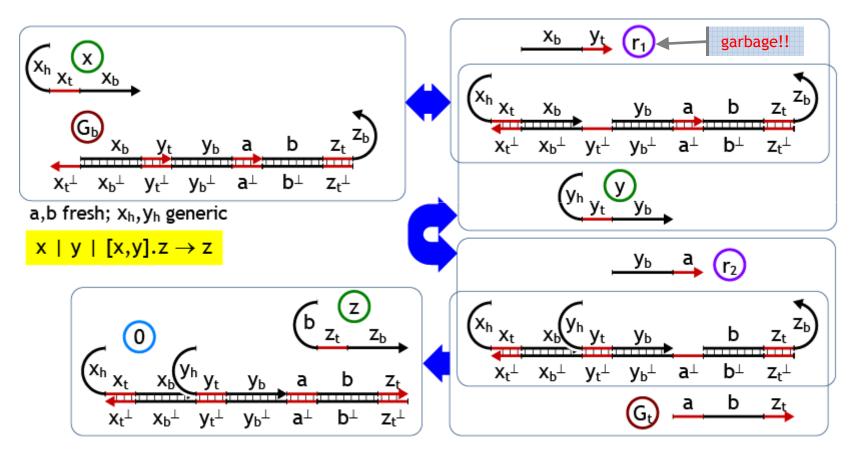
 G_b, G_t (gate backbone and trigger) form the gate.

Any history segment that is not determined by the gate structure is said to be 'generic' (can be anything).

Any gate segment that is not a non-history segment of an input or output signal is taken to be 'fresh' (globally unique for the gate), to avoid possible interferences.

Circuit Elements: [X,y].Z Join Gate (function)

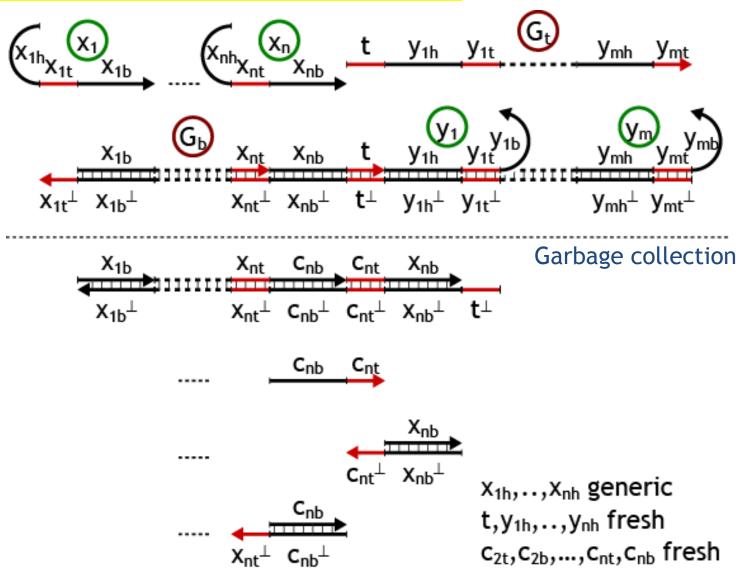
• A Join signal-processing gate takes both signals x, y and produces a signal z according to the reaction $x | y | [x,y].z \rightarrow z$



The garbage r_1 and r_2 must be collected (*after* the gate has fired) to avoid accumulation. This can be achieved by a similar scheme taking r_1 , r_2 as input signals.

[x₁,..,x_n].[y₁,..,y_m] General Join/Fork Gate

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



Strand Algebra

P ::= $x \in [x_1,, x_n]$	x _n].[y ₁ ,,y _m]	: 0 : P P	: P*	n≥1, m≥0
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X	is a signal
$[x_1,, x_n] \cdot [y_1,, y_m]$	is a <i>gate</i>
0	is an <i>inert solution</i>
P P	is <i>parallel composition</i> of signals and gates
P*	is a <i>population</i> (multiset) of signals and gates

Reaction Rule

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

Auxiliary rules (axioms of diluted well-mixed solutions)

 $\begin{array}{cccc} P \rightarrow P' & \Rightarrow & P \mid P'' \rightarrow P' \mid P'' & & \text{Dilution} \\ P \equiv P_1, P_1 \rightarrow P_2, P_2 \equiv P' & \Rightarrow & P \rightarrow P' & & \text{Well Mixing} \end{array}$

Where \equiv is a congruence relation (syntactical 'chemical mixing') with $P^* \equiv P \mid P^*$ for unbounded populations.

Compiling Strand Algebra to DNA

P ::= x : $[x_1,..,x_n]$. $[y_1,..,y_m]$: 0 : P|P : P* n≥1, m≥0

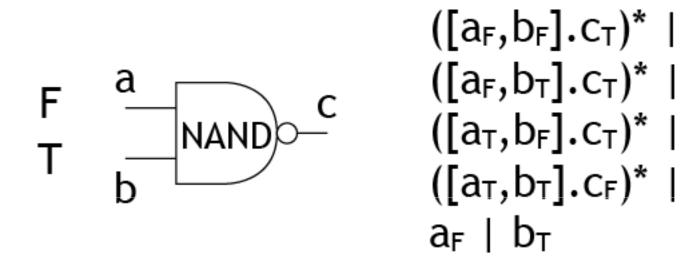
- compile(x) = $(x_h x_t x_b)$
- compile([x₁,..,x_n].[y₁,..,y_m]) =

$$= \underbrace{\begin{array}{c} t \\ x_{1b} \\ x_{1t^{\perp}} \\ x_{1t^{$$

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

Boolean Networks

Boolean Networks to Strand Algebra



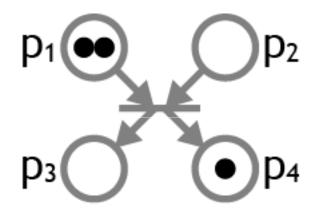
This encoding is *compositional*, and can encode *any* Boolean network:

- multi-stage networks can be assembled (combinatorial logic)
- network loops are allowed (sequential logic)

Petri Nets

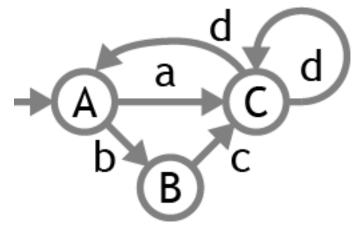
Petri Nets to Strand Algebra

Transitions as Gates Place markings as Signals



Finite State Automata

FSA to Strand Algebra

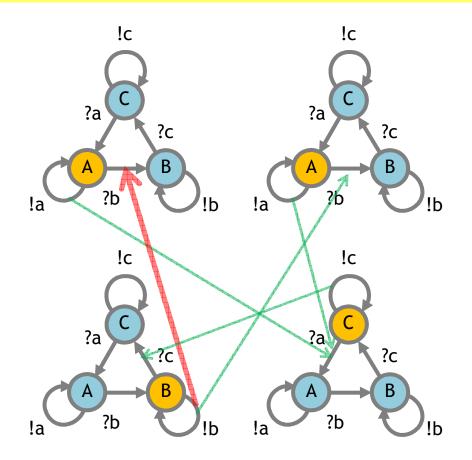


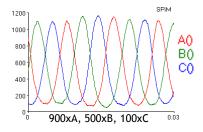
Input strings

a,b,c,d

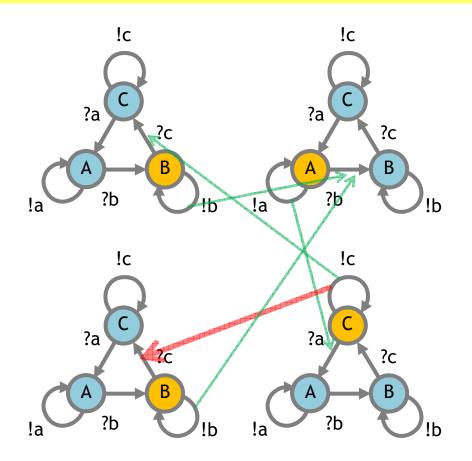
([A,a].[C,τ])* | ([A,b].[B,τ])* | ([B,c].[C,τ])* | ([C,d].[C,τ])* | ([C,d].[A,τ])* | ΑΙτ τ.[**a**,σ₁]|

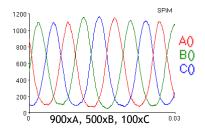
 $[\sigma_1, \tau]. [b, \sigma_2]|$ $[\sigma_2, \tau]. [c, \sigma_3]|$ $[\sigma_3, \tau]. d$



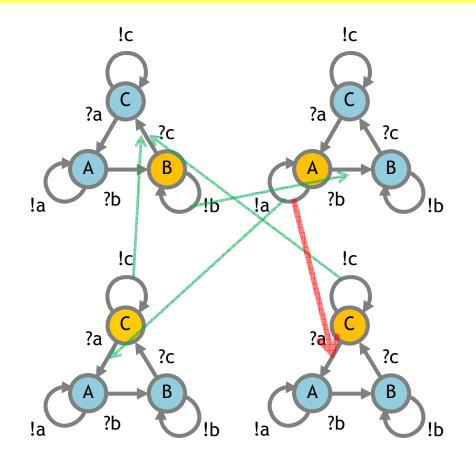


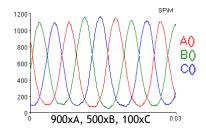
([A,B].[B,B])* | ([B,C].[C,C])* | ([C,A].[A,A])* | A | A | B | C



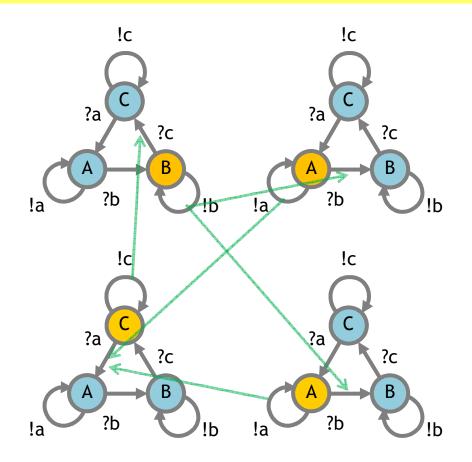


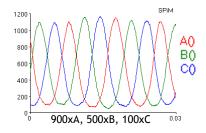
([A,B].[B,B])* | ([B,C].[C,C])* | ([C,A].[A,A])* | A | B | B | C





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





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

More in the Paper

• Stochastic strand algebra

- $\circ~$ Matches the stochastic semantics of interacting automata
- Uses a technique for implementing constant buffered populations, to replace P* with finite populations
- Nested strand algebra
 - \circ An higher-level language (with nested expressions)
 - $\circ~$ A compilation algorithm into the basic strand algebra

Conclusions

• Strand algebra is an intermediate language for DNA compilation

- $\circ~$ It has its own abstract kinetics
- Supports the compilation of multiple higher-level languages
 - Boolean Networks
 - Finite State Automata
 - Petri Nets
 - Interacting Automata
 - Etc.?
- \circ Into (possibly) multiple lower-level DNA architectures
 - Strand displacement
 - Etc.?

• Acknowledgments

- \circ The DNA 14 organizers for inviting me and providing stimulus for this work.
- Extensive discussions with Lulu Qian, David Soloveichik and Erik Winfree on possible gate designs (about 15 of them!).
- John Reif and Urmi Majumder for working on the problem.