#### **The limits of chemical computing** Computation with chemical reaction networks

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#### 23<sup>rd</sup> International Meeting on DNA and Molecular Programming

September 2017





#### Acknowledgments

**Rachel Cummings** 

Georgia Tech

Amanda Belleville UC-Davis





Ho-Lin Chen NTU



Gr

Banff International Research Station for Mathematical Innovation and Discovery

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#### Chemical reaction networks

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Traditionally a descriptive modeling language... Let's instead use it as a prescriptive programming language Chemical caucusing

#### $X+Y \rightarrow U+U$

Chemical caucusing

 $X+Y \rightarrow U+U$ 

 $\begin{array}{l} X + U \rightarrow X + X \\ Y + U \rightarrow Y + Y \end{array}$ 



#### distributed algorithm for *"approximate majority"*: initial majority (*X* or *Y*) quickly overtakes whole population



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[Cardelli, Csikász-Nagy. The cell cycle switch computes approximate majority. *Nature Scientific Reports* 2012] [Cardelli, Morphisms of reaction networks that couple structure to function, *BMC Systems Biology* 2014]

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#### DNA strand displacement implementing $A+B \rightarrow C$



### Experimental implementations of synthetic chemical reaction networks with DNA



#### Theoretical Computer Science Approach





What computation is possible and what is not? (Computability theory)

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What computation is possible and what is not? (Computability theory)



What computations necessarily take a long time and what can be done quickly? (Computational complexity theory)

#### Outline

- Formal definition of chemical reaction networks
- What do we mean by "computation" with chemical reactions?
- What do we mean by "efficient computation" with chemical reactions?
- What is known
- What is not yet known

#### Chemical Reaction Networks (formal definition)

- finite set of *d* species  $\Lambda = \{A, B, C, D, ...\}$
- finite set of reactions: e.g.  $A+B \xrightarrow{k_1} A+C$  $C \xrightarrow{k_2} A+A$  $C+B \xrightarrow{k_3} C$
- configuration  $\mathbf{x} \in \mathbb{N}^d$ : molecular counts of each species

#### What is **possible**: Example reaction sequence

- $\alpha: \qquad A+B \rightarrow A+C \qquad A \quad B \quad C$
- β: C→A+A x = (2, 2, 0)



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- $\alpha: \qquad A+B \rightarrow A+C$  $\beta: \qquad C \rightarrow A+A$
- A A B

x = (2, 2, 0) $\alpha \downarrow$ (2, 1, 1)

A B C









#### What is **probable**:

Stochastic kinetic model of chemical reaction networks

Solution volume v

reaction typerate $A \xrightarrow{k} \dots$  $k \cdot \#A$  $A+B \xrightarrow{k} \dots$  $k \cdot \#A \cdot \#B / v$ 

[McQuarrie 1967, van Kampen, Gillespie 1977]

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expected time until next reaction is 1 / (sum of all reaction rates)

#### Relationship to distributed computing

**population protocol** = list of *transitions* such as

 $x, y \rightarrow x, x$   $a, b \rightarrow c, d$   $a, a \rightarrow a, a$  (null transition)

• Repeatedly, two *agents* (molecules) are picked at random to *interact* (react) and change *state* (species).
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population protocols  $\subsetneq$  chemical reactions, but "most" ideas that apply to one model also apply to the other

### Time complexity in population protocols

- pair of agents picked uniformly at random to interact (possibly null interaction)
- *parallel time* = number of interactions / *n*

i.e., each agent has O(1) interactions per "unit time"

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initial configuration

i











(assuming finite set of reachable configurations) equivalent to: The system <u>will</u> reach a correct stable configuration with probability 1.

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Like any respectable computer scientist...

as a function of input size *n* (how required time grows with *n*)
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*n* = total molecular count

volume v = O(n)

*i.e.*, <u>require bounded concentration</u> (finite density constraint)

*n* molecules volume v = O(n)



*n* molecules volume v = O(n)



 $A + B \rightarrow Y + B$ 

propensity:  $#A \cdot #B / v = O(1/n)$ 

expected time to produce *Y*:

O(n)

*n* molecules volume v = O(n)

produce *Y*:




#### An exponential time difference

*n* molecules volume *v* = *O*(*n*)



expected time to

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  - $\psi(\mathbf{o}) = Y$  (configuration  $\mathbf{o}$  outputs "yes") if vote is unanimously yes:  $\mathbf{o}(s) > 0 \Leftrightarrow s \in \Lambda_{Y}$
  - $\psi(\mathbf{o}) = N$  (configuration  $\mathbf{o}$  outputs "no") if vote is unanimously no:  $\mathbf{o}(s) > 0 \Leftrightarrow s \in \Lambda_N$
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- **o** is stable if  $\psi(\mathbf{o}) = \psi(\mathbf{o'})$  for all **o'** reachable from **o**

**Detection:**  $\varphi(a,b) = Y \Leftrightarrow b > 0$ 



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a votes no; b votes yes
E[time] = O(log n)



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Counting:  $\varphi(a,b) = Y \Leftrightarrow b > 1$   $b+b \rightarrow y+y \quad O(n)$  time  $y+b \rightarrow y+y \quad O(\log n)$  time  $y+a \rightarrow y+y \quad O(\log n)$  time

a,b vote no; y votes yes E[time] = O(n)



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 $A+B \rightarrow a+b$  (both become "followers" but <u>preserve difference</u> between A's and B's)

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O(n) time if a - b = O(1)

#### $O(\log n)$ time if a - b > 0.01n

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two leaders XOR their parity, and one becomes follower

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#### $O(n \log n)$ time

O(n) bottleneck transition before leader reaches count 1, then  $O(n \log n)$  coupon collector for leader to encounter each follower

#### possible to optimize to O(n)

[Angluin, Aspnes, Eisenstat, DISC 2006]

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- recall: o is stable if o(y) = o'(y) for all o' reachable from o

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 $a \rightarrow y$  $b \rightarrow y$ 

 $E[time] = O(\log n)$ 

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 $a \rightarrow y$  $b \rightarrow y$  subtraction: f(a, b) = a - b

 $a \rightarrow y$ b+y  $\rightarrow$ 

 $E[time] = O(\log n)$ 

E[time] = O(n) if a - b = O(1) initially (last transition is bottleneck)

subtract constant: f(a) = a - 1

subtract constant: f(a) = a-1

 $a+a \rightarrow a+y$ E[time] = O(n)

subtract constant: f(a) = a-1 $a+a \rightarrow a+y$ E[time] = O(n)

**minimum:** *f*(*a*,*b*) = min(*a*,*b*)

subtract constant: f(a) = a-1 $a+a \rightarrow a+y$ E[time] = O(n)

subtract constant: f(a) = a-1 $a+a \rightarrow a+y$ E[time] = O(n) **maximum:** f(a,b) = max(a,b) = a+b-min(a,b)

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maximum: 
$$f(a,b) = \max(a,b) = a+b-\min(a,b)$$
  
 $a \rightarrow y+a_2$   
 $b \rightarrow y+b_2$   
addition

subtract constant: f(a) = a-1 $a+a \rightarrow a+y$ E[time] = O(n)

**maximum:** 
$$f(a,b) = max(a,b) = a+b-min(a,b)$$

 $\begin{array}{l}
a \rightarrow \mathbf{y} + a_2 \\
b \rightarrow \mathbf{y} + b_2
\end{array}$ addition

$$a_2 + b_2 \rightarrow k$$
 minimum

**maximum:** f(a,b) = max(a,b) = a+b - min(a,b)subtract constant: f(a) = a-1 $a+a \rightarrow a+y$  $a \rightarrow y + a_2$  $b \rightarrow y + b_2$ addition E[time] = O(n) $a_2 + b_2 \rightarrow k$ minimum **minimum:** f(a,b) = min(a,b)subtraction  $k+y \rightarrow$  $a+b \rightarrow y$ E[time] = O(n) if a - b = O(1) initially

E[time] = O(n) (uses minimum and subtraction as "subroutines")

**constant:** *f*(*a*) = 1

constant: f(a) = 1  $a \rightarrow y$   $y+y \rightarrow y$ E[time] = O(n)

**constant:** *f*(*a*) = 1

a.k.a. "leader election"

E[time] = O(n)

 $a \rightarrow y$ 

 $y+y \rightarrow y$ 

#### Predicates

•  $\varphi$  is stably computable if and only if  $\varphi$  is *semilinear*.

[Angluin, Aspnes, Diamadi, Fischer, Peralta, Computation in networks of passively mobile finite-state sensors, *PODC* 2004] [Angluin, Aspnes, Eisenstat, Stably computable predicates are semilinear, *PODC* 2006]

#### Predicates

- φ is stably computable if and only if φ is semilinear.
- semilinear = Boolean combination of <u>threshold</u> and <u>mod</u> predicates: take weighted sum s = w<sub>1</sub>·a<sub>1</sub> + ... w<sub>k</sub>·a<sub>k</sub> of inputs and ask if s > constant c?

```
s \equiv c \mod m for constants c,m?
```



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a>b?	a=b?	<i>a</i> is odd?	a>07	? а	>1?
NOT	a=b²?	<i>a</i> is a power of 2	?	<i>a</i> is pr	ime?

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#### Functions

- f is stably computable if and only if graph(f) = { (a,y) | f(a)=y } is semilinear.
- <u>piecewise linear</u>, with semilinear predicate to determine which piece.

a+b	a–b	2a	a/2	min( <i>a,b</i> )	a+1	<i>a</i> –1
f(a) =	2 <i>a</i> -b/3 i	if <i>a+b</i>	is odd,	else $f(a) = a$	/4+5b	

NOT	<b>a</b> <sup>2</sup>	2 <sup>a</sup>	2 <i>a</i> if <i>a</i> is prime, else 3 <i>a</i>
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#### Functions

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- <u>piecewise linear</u>, with semilinear predicate to determine which piece.

a+b a-b 2a a/2 min(a,b) a+1 a-1 f(a) = 2a-b/3 if a+b is odd, else f(a) = a/4+5b

**NOT**  $a^2$   $2^a$  2a if a is prime, else 3a

# All semilinear predicates/functions are known to be computable in O(n) time.

[Chen, Doty, Soloveichik, Deterministic function computation with chemical reaction networks, *DNA* 2012] [Doty, Hajiaghayi, Leaderless deterministic chemical reaction networks, *DNA* 2013]

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Boolean combination of detection predicates

"detection" means  $\varphi(a) = a > 0$ ?"

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*φ*(*a*,*b*,*c*) = *a*>0 OR (*b*>0 AND *c*=0)

i.e., constant except when a variable changes from 0 to positive

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 $\mathbb{N}$ -linear functions (coefficients are nonnegative integers)

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#### **Functions**

 $\mathbb{N}$ -linear functions (coefficients are nonnegative integers)

e.g., f(a,b) = 2a + 3b $a \rightarrow y+y$  $b \rightarrow y+y+y$ 

[Angluin, Aspnes, Eisenstat, Fast computation by population protocols with a leader, *DISC* 2006] [Chen, Doty, Soloveichik, Deterministic function computation with chemical reaction networks, *DNA* 2012]

#### Known time lower bounds: "most" predicates/functions

 <u>Informal</u>: "most" semilinear predicates and functions not known to be computable in o(n) time, actually require at least O(n) time to compute

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- <u>Definition</u>:  $f: \mathbb{N}^k \to \mathbb{N}$  is eventually N-linear if there is  $m \in \mathbb{N}$  so that f(a) is N-linear for all a with all components  $\geq m$ 
  - Both definitions allow exceptions "near a face of  $\mathbb{N}^{k''}$

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  - Both definitions allow exceptions "near a face of  $\mathbb{N}^{k''}$
- <u>Formal theorem</u>: Every predicate that is not eventually constant, and every function that is not eventually  $\mathbb{N}$ -linear, requires at least time O(n) to compute.
  - They're all computable in at most O(n) time, so this settles their time complexity.

[Doty, Soloveichik, Stable leader election in[Belleville, Doty, Soloveichik, Hardness of computing and approximatingpopulation protocols requires linear time, DISC 2015]predicates and functions with leaderless population protocols, ICALP 2017]

	Predicates	Functions
computable in O(log n) time	<u>detection</u> <i>a</i> >0 <b>AND</b> ( <i>b</i> >0 <b>OR</b> <i>c</i> =0)	$\frac{\mathbb{N}-\text{linear}}{3a+b+2c}$
not computable in less than O(n) time	non-eventually constant a>b? a=b? a is odd?	$\begin{array}{llllllllllllllllllllllllllllllllllll$
unknown (best known protocol is <i>O</i> ( <i>n</i> ) time)	eventually constant but not constant on positive values a>1?	eventually N-linear but not N-linear $f(a) = \begin{cases} a \text{ if } a > 1, \\ 0 \text{ otherwise} \end{cases} \begin{cases} f(a) 5 \\ 4 \\ 3 \\ 2 \\ 1 \\ 0 \end{cases}$

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not computable in less than O(n) time	non-eventually constant a>b? a=b? a is odd?	$\begin{array}{ll} \underline{non-eventually \mathbb{N}-linear} \\ a/2 & a-b & a+1 & a-1 & 1 \\ \min(a,b) & \max(a,b) \\ \max(a,\min(b+3,2c)) - c - 1 \end{array}$
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## Other modeling choices?

#### Modeling choices in formalizing "Computing with chemistry"

- **integer** counts ("stochastic") or **real** concentrations ("mass-action")?
- what is the object being "computed"?
  - yes/no decision problem? "number of A's > number of B's?"
  - numerical function?
- "make Y become double the amount of X"
- first part of talk
- guaranteed to get correct answer? or allow small probability of error?
  - if Pr[error] = 0, system works *no matter the reaction rates*
- to represent an input  $n_1, ..., n_k$ , what is the initial configuration?
  - only input species present
  - auxiliary species can be present?
- when is the computation finished? when...
  - the output stops changing? (convergence)
  - the output becomes unable to change? (stabilization)
  - a certain species T is first produced? (termination)
- require exact numerical answer? or allow an approximation?

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summarized in next few slides

some predicates/functions get "easier" (i.e., it's easy to think of the reactions)

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$$\begin{array}{lll} \underline{\text{without}} & A_{0}+A_{0} \rightarrow A_{e}+a_{e} \\ a \text{ leader} & A_{e}+A_{e} \rightarrow A_{e}+a_{e} \\ A_{0}+A_{e} \rightarrow A_{0}+a_{0} \\ A_{0}+a_{e} \rightarrow A_{0}+a_{0} \\ A_{0}+a_{e} \rightarrow A_{0}+a_{0} \\ A_{e}+a_{0} \rightarrow A_{e}+a_{e} \end{array}$$

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But *fundamental computability* doesn't change: exactly the semilinear predicates/functions can be computed (same as without a leader).

[Angluin, Aspnes, Diamadi, Fischer, Peralta, *PODC* 2004] [Angluin, Aspnes, Eisenstat, *PODC* 2006] [Chen, Doty, Soloveichik, *DNA* 2012] [Doty, Hajiaghayi, *DNA* 2013]

#### <u>Convergence vs stabilization</u> and <u>leader vs anarchy</u>

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**Theorem**: Without a leader, all non-eventually constant predicates and non-eventually- $\mathbb{N}$ -linear functions require at least O(n) stabilization time. [Belleville, Doty, Soloveichik, *ICALP* 2017]



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**Previous work**: With a leader, all semilinear predicates/functions can be computed in at most  $O(\log^5 n)$  convergence time. [Angluin, Aspnes, Eisenstat, *DISC* 2006]



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**Conjecture**: With a leader, all non-detection predicates and non- $\mathbb{N}$ -linear functions require at least O(n) stabilization time.

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**Theorem**: A function is stably computable by a real-valued chemical reaction network if and only if it is *continuous* and piecewise linear.



[Chen, Doty, Soloveichik, ITCS 2014]

**Theorem**: A function is computable with probability of error < 1% by an integer-valued chemical reaction network if and only if it is computable by <u>any algorithm whatsoever</u>...

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Furthermore, computation doesn't merely converge to the correct answer eventually, but can be made *"terminating"*: producing a molecule *T* **signaling when the computation is done**. (provably impossible when Pr[error] = 0)

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**Conjecture**: *Even without a leader,* any computable function can be efficiently computed with high probability.

# What if we use real-valued concentrations... **and** allow reaction rates to influence outcome??

## **Theorem**: A function is computable by a real-valued chemical reaction network using mass-action kinetics if and only if it is computable by <u>any algorithm whatsoever</u>.

[Fages, Le Guludec, Bournez, Pouly. Strong Turing completeness of continuous chemical reaction networks and compilation of mixed analog-digital programs. *Computational Methods in Systems Biology – CMSB* 2017]

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mass-action kinetics:  $\begin{bmatrix} \bullet \\ V \end{bmatrix} = \begin{bmatrix} V \end{bmatrix}$ 

Y

$$[X] = -k_1[X] + k_2[Y][Z]$$

$$X \xrightarrow{k_1} Y + Y \qquad [\mathring{Y}] = 2k_1[X] - k_2[Y][Z]$$

$$Y + Z \xrightarrow{k_2} X \qquad [\mathring{Z}] = -k_2[Y][Z]$$

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## ... with only a polynomial-time slowdown.

[Bournez, Graça, Pouly. Polynomial time corresponds to solutions of polynomial ordinary differential equations of polynomial length. *Journal of the ACM* 2017]

### Fast approximate division by 2

initial configuration:
{ n X, εn A, εn B }

 $\begin{array}{c} X + A \rightarrow B + Y \\ X + B \rightarrow A \end{array}$ 

<u>guaranteed</u> to get  $Y = n/2 \pm \varepsilon n$ E[time] = O(log n) /  $\varepsilon$ 

[Belleville, Doty, Soloveichik, Hardness of computing and approximating predicates and functions with leaderless population protocols, *ICALP* 2017]

### Fast approximate division by 2

 $n = 100 \quad \varepsilon = 0.1$ 

![](_page_177_Figure_2.jpeg)

[Belleville, Doty, Soloveichik, Hardness of computing and approximating predicates and functions with leaderless population protocols, *ICALP* 2017]

## Thank you!

**Questions?** 

Proofs of conjectures?

#### Criticism of model?

*suggestions*: 1) lack of reverse reactions (energy dissipated =  $\infty$ ), 2) assumption of single initial copy of leader, 3) reactions aren't mass-conserving, 4) what about leak reactions?, 5) no discussion of diffusion rates, 6) this has nothing to do with how biological cells compute