

# Models of Distributed Computing in Molecular Programming

**Nicholas Schiefer**

This is a survey, with some  
informal statements.

Stop me at any time.

Prelude

Perspective on  
molecular programming

# Molecular programming is...

## computing with molecules

what do we mean by  
“computing”?

what kinds of problems  
can we solve?

what are “molecules”?

how do they interact with  
each other?

# Three perspectives

## Natural scientist

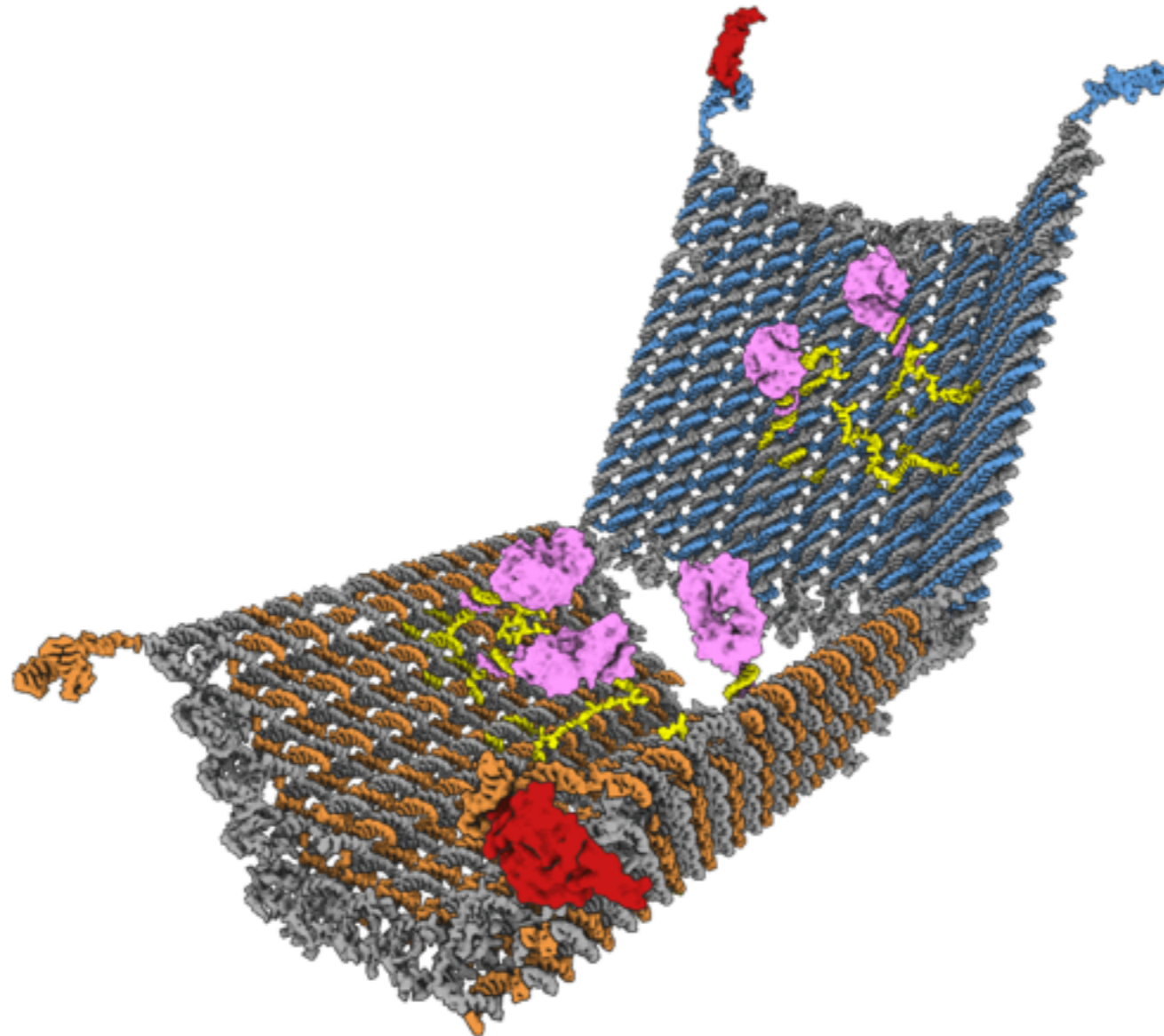
How does computation occur in the physical/biological world?



# Three perspectives

## Engineer

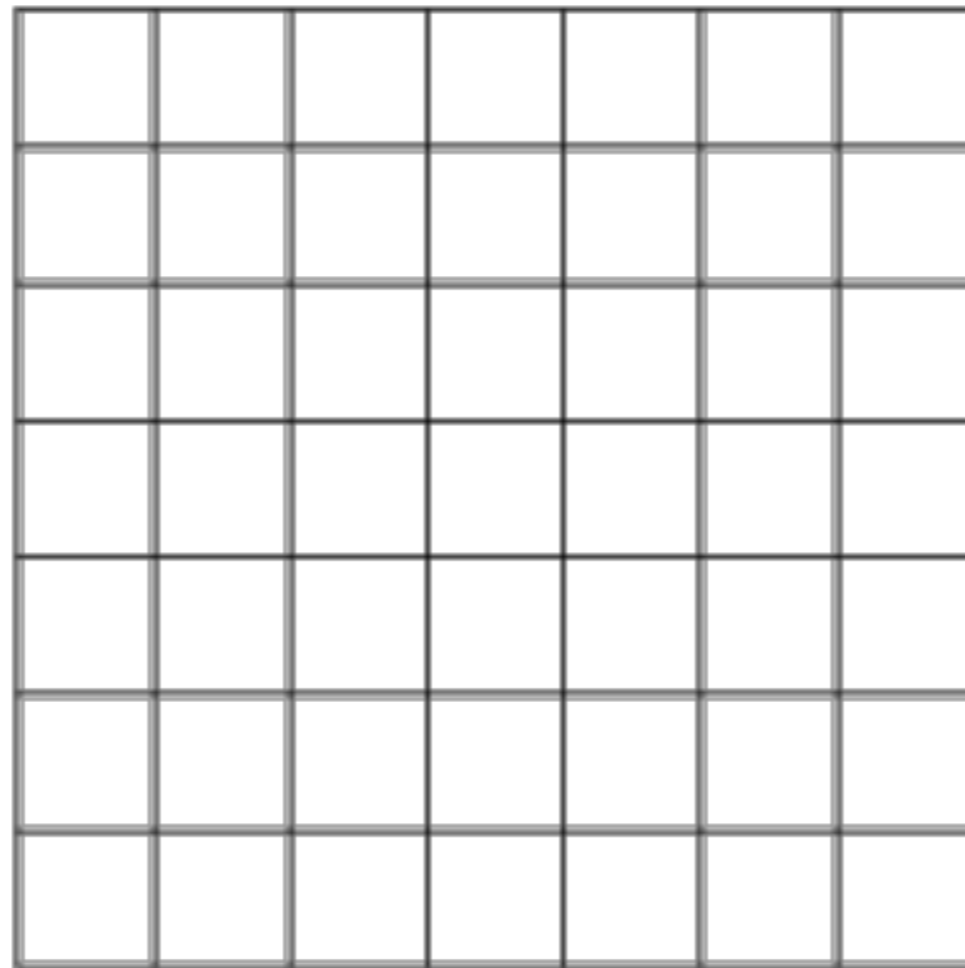
How can we use computational power in nanotechnology?



# Three perspectives

## Computer scientist

How can I compute using extremely simple systems?



# Three perspectives

## Natural scientist

How does computation occur in the physical/biological world?

## Engineer

How can we use computational power in nanotechnology?

## Computer scientist

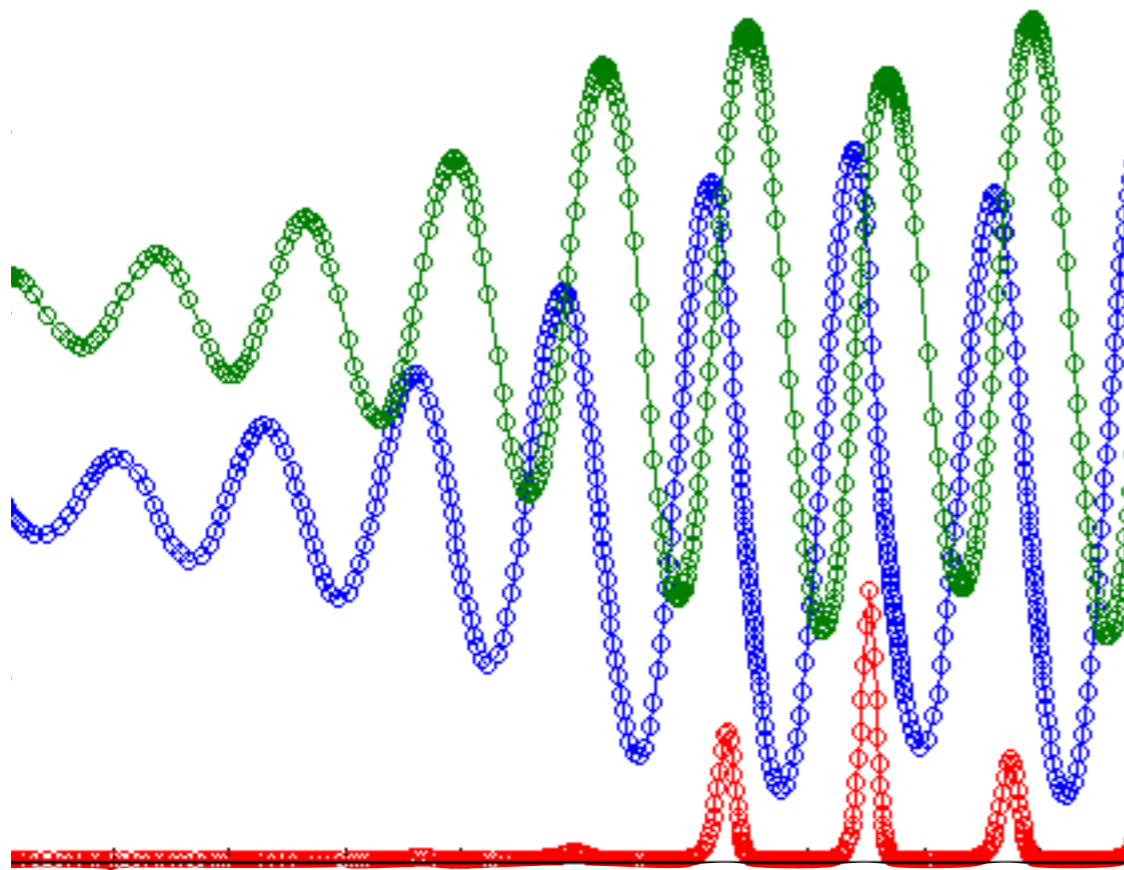
How can I compute using extremely simple systems?





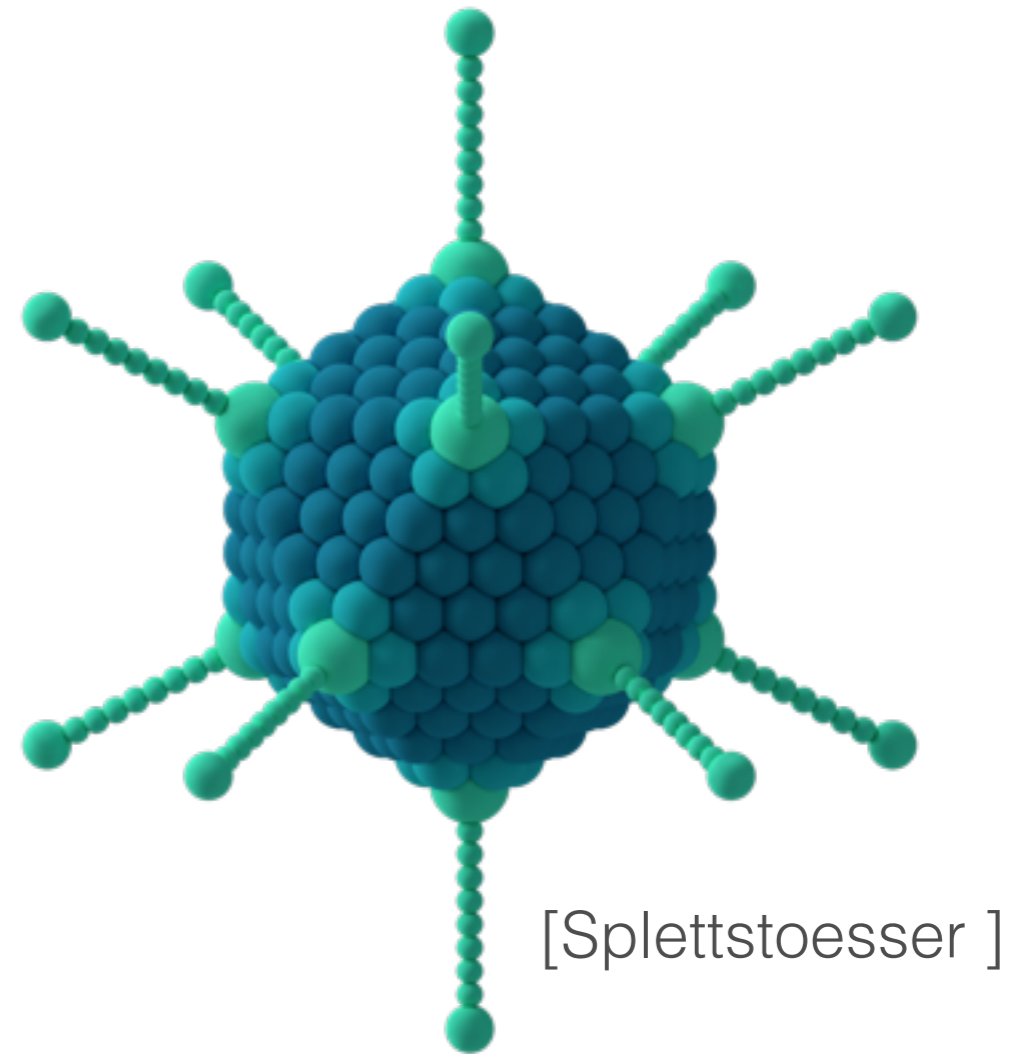
# Two things biology does...

Control concentrations



**Dynamic Reaction  
networks**

Build things



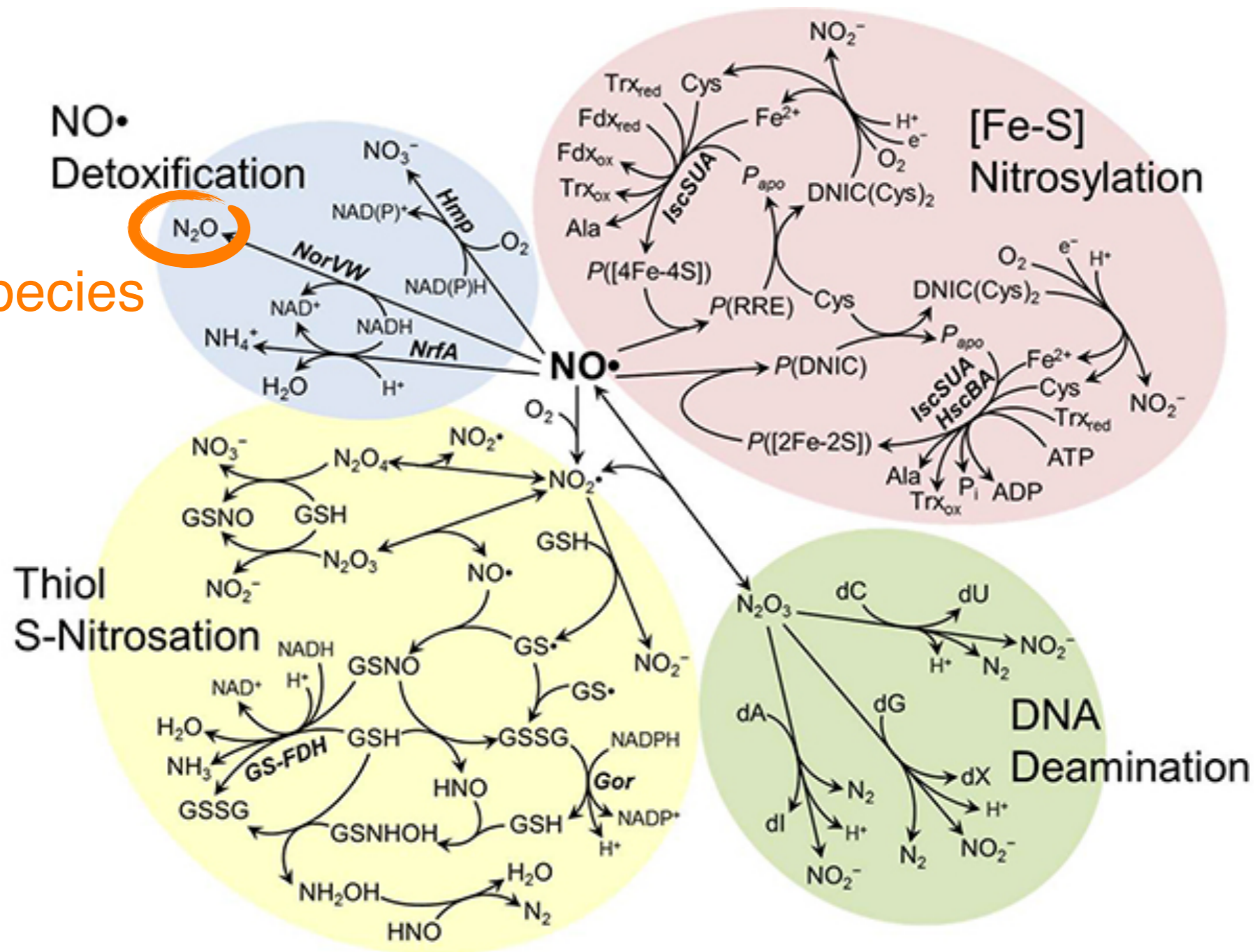
**Steuerelemente  
Assembly Code  
programming**

Part I

# Chemical Reaction Networks

# Chemical Reaction Networks

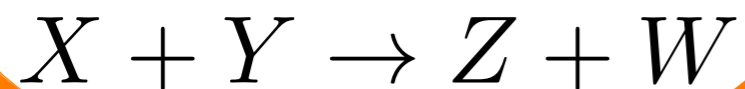
chemical species



# Chemical Reaction Networks

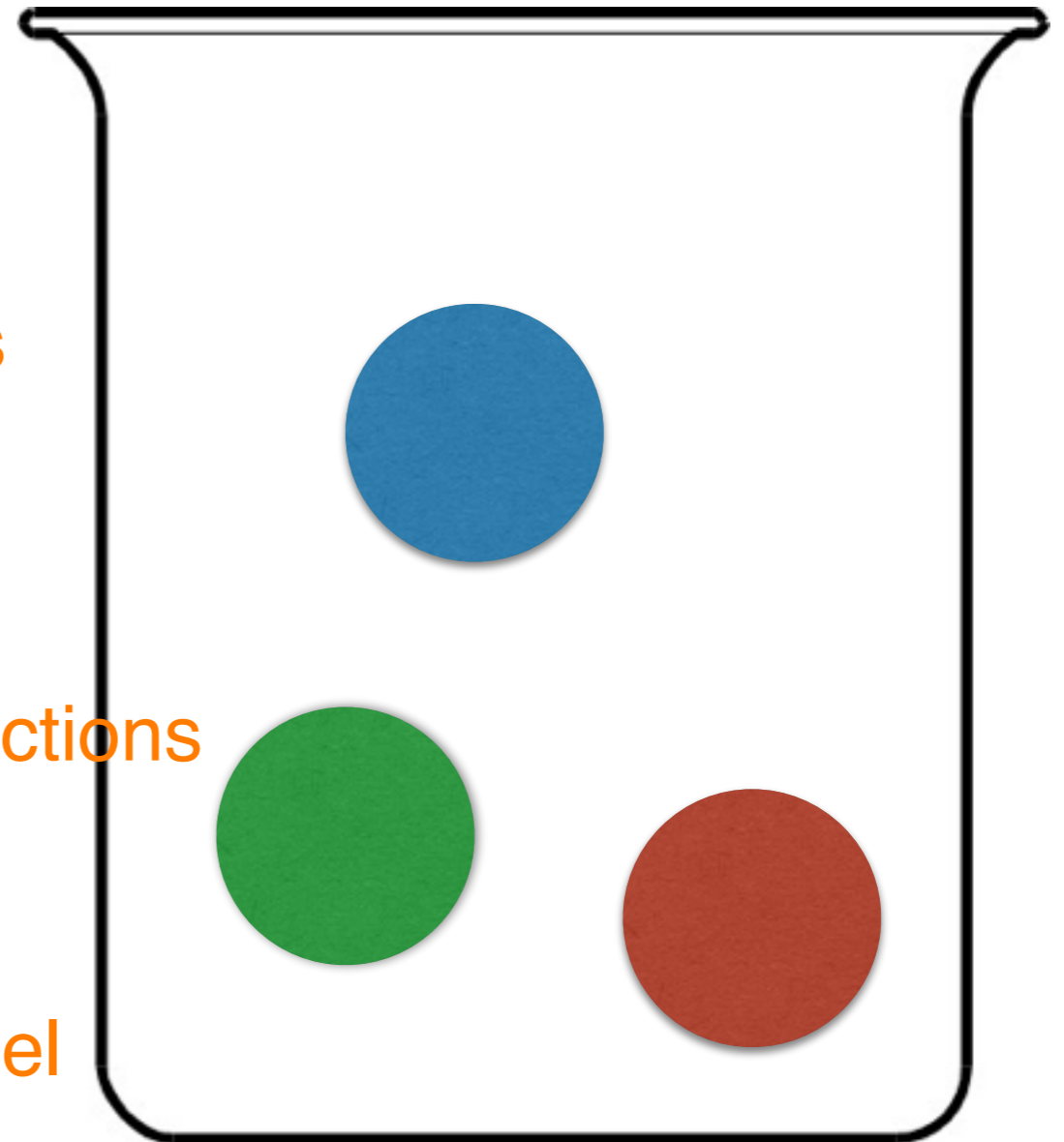
$A, B, C, W, X, Y, Z,$

Finite\* set of species



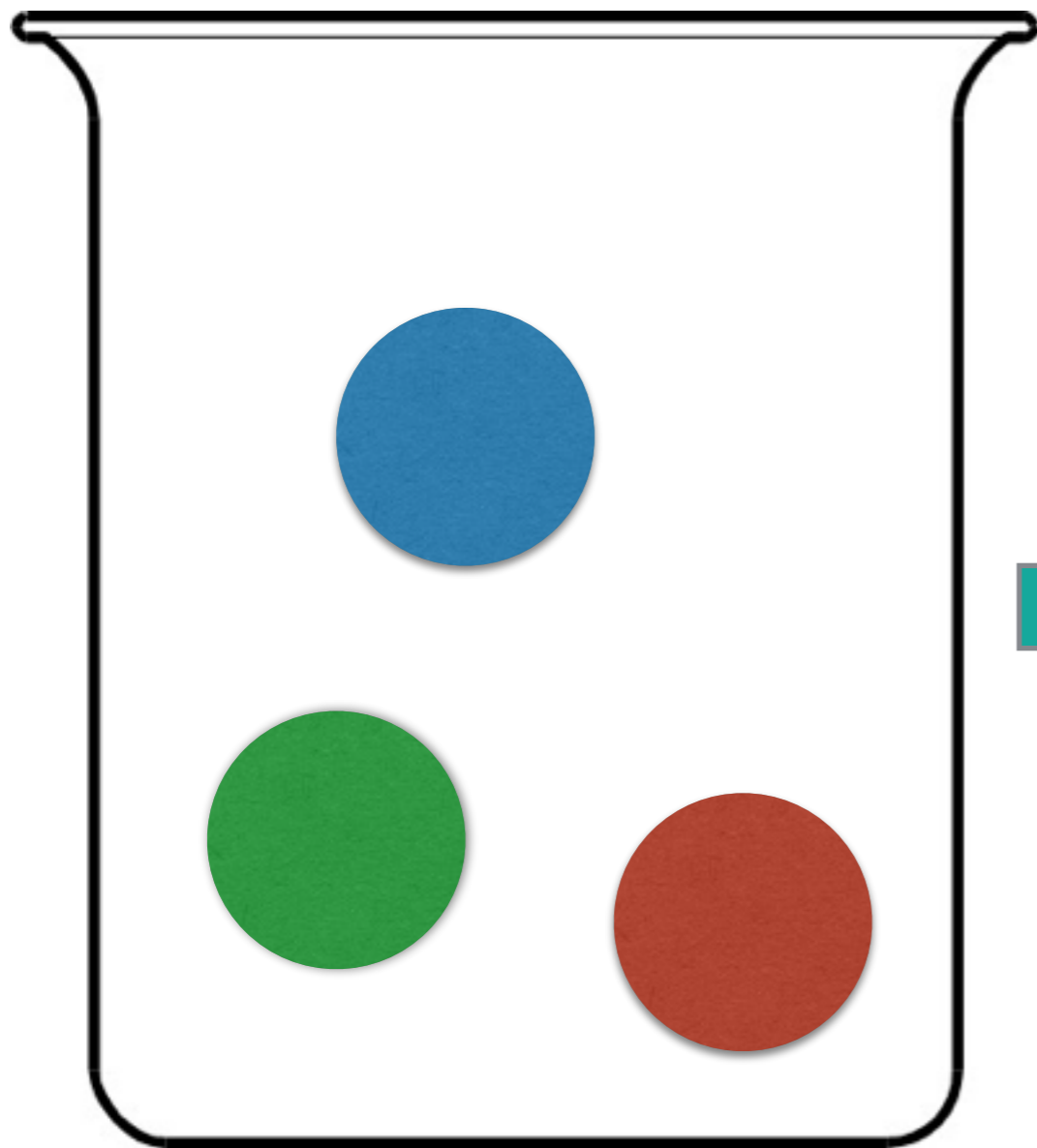
Finite\* set of reactions

Well-mixed reaction vessel

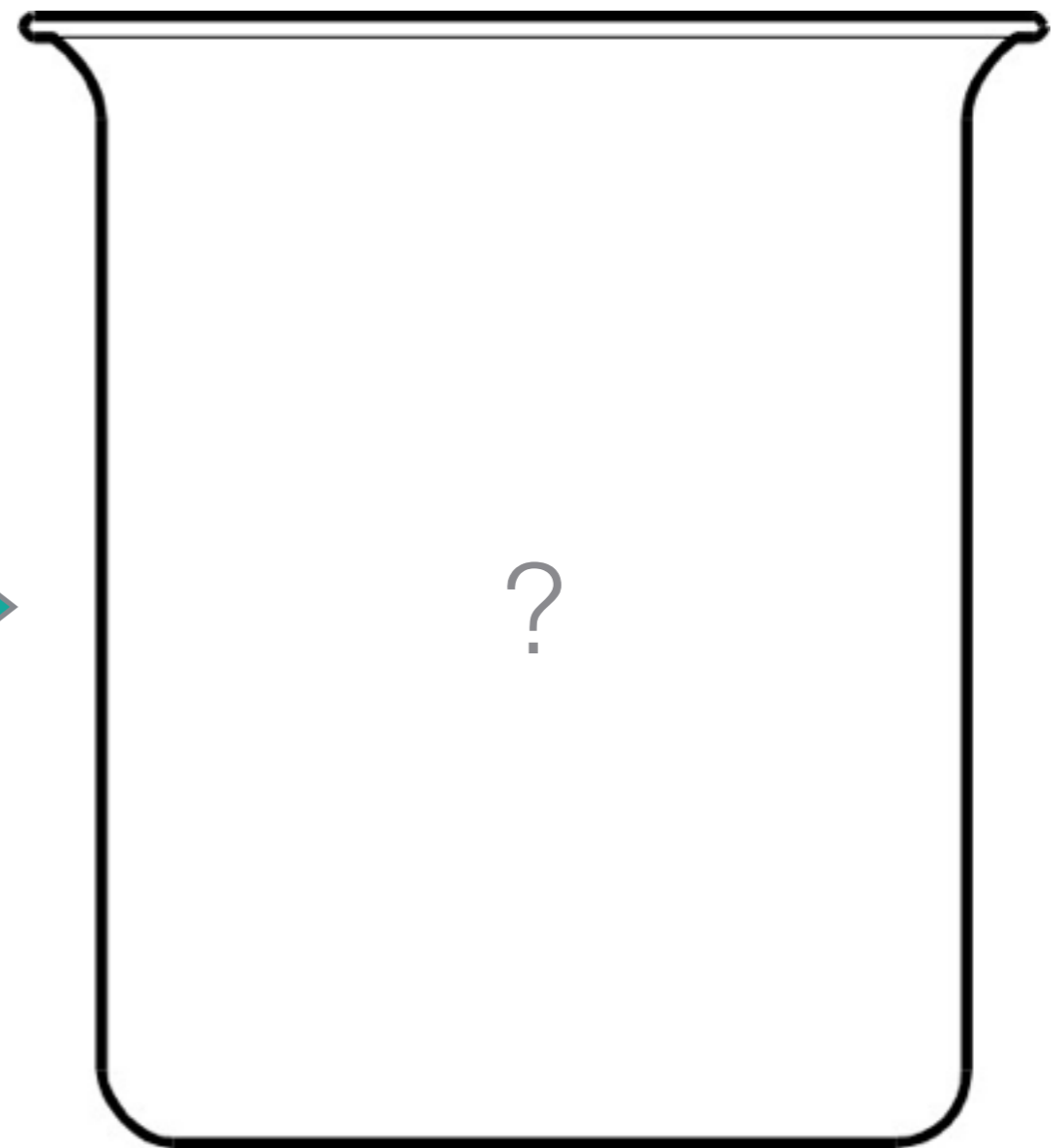


\*usually

# CRN Dynamics

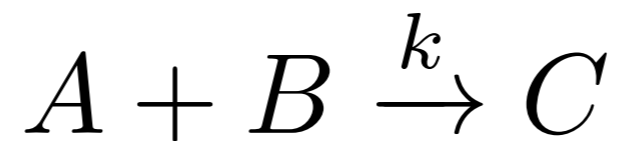


time  $t$



time  $(t + \varepsilon)$

# CRN Dynamics



“Mass action” regime

Concentrations

$$[A], [B], [C] \in \mathbb{R}^+$$

Described by ODE

$$\frac{d[A]}{dt} = -k[A][B]$$

$$\frac{d[B]}{dt} = -k[A][B]$$

$$\frac{d[C]}{dt} = k[A][B]$$

“Kinetic” regime

Counts

$$\#(A), \#(B), \#(C) \in \mathbb{Z}^+$$

State is a continuous time Markov chain (“Gillespie dynamics”)

Equivalent to population protocols

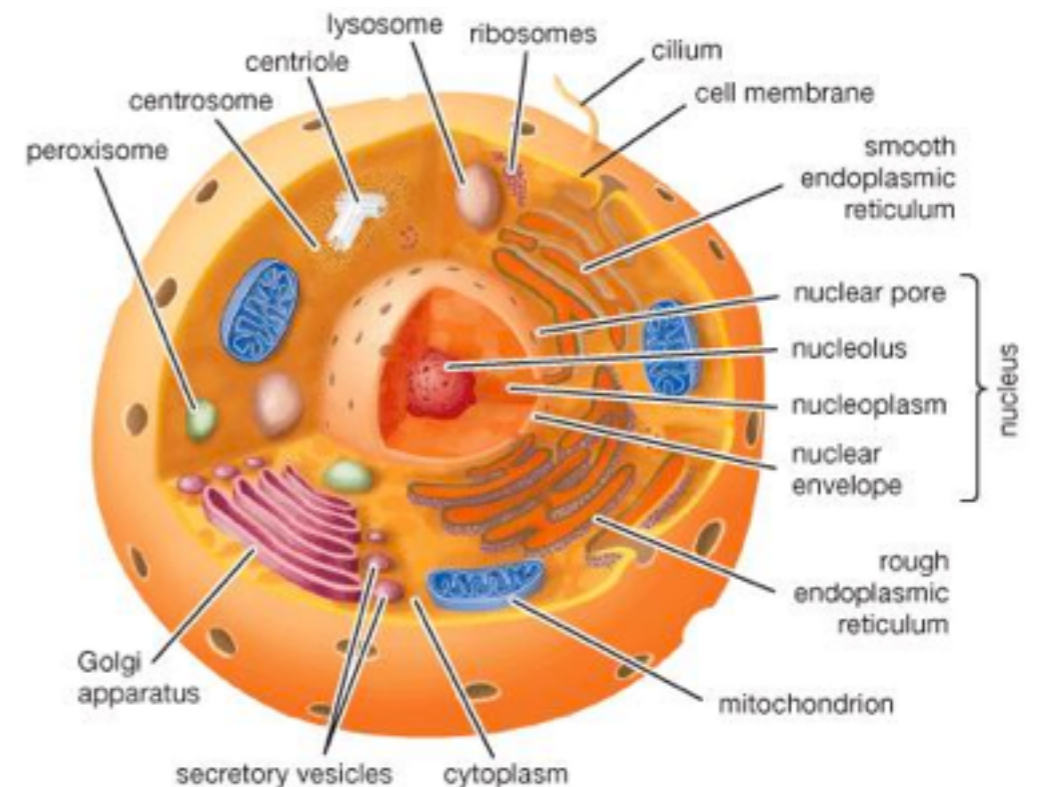
# CRN Dynamics

“Mass action” regime



“Kinetic” regime

vs.



Kinetic model approaches mass action model as counts grow towards infinity.

# Mass action CRNs

**Theorem.** Any polynomial ODE can be approximated arbitrarily well by a mass action CRN.

## Key ideas

Proof due to [Berleant 2014], much older proof via Michaelis-Menten enzyme kinetics

For each variable  $x$ , have species  $X^+$  and  $X^-$  that “cancel quickly”  $X^+ + X^- \xrightarrow{\text{fast}} \emptyset$

Linear terms are easy

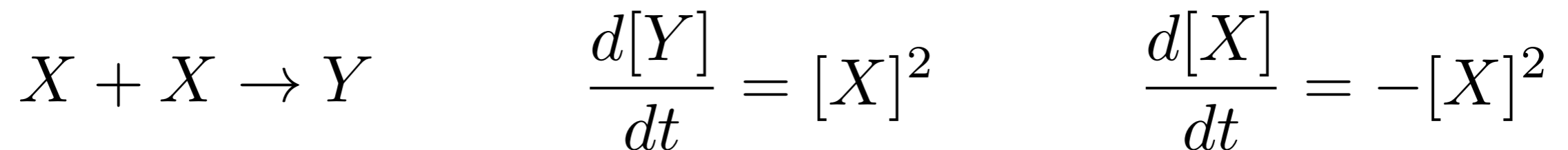


# Mass action CRNs

**Theorem.** Any polynomial ODE can be approximated arbitrarily well by a mass action CRN.

## Key ideas

To implement quadratic terms, use multiple reactants:

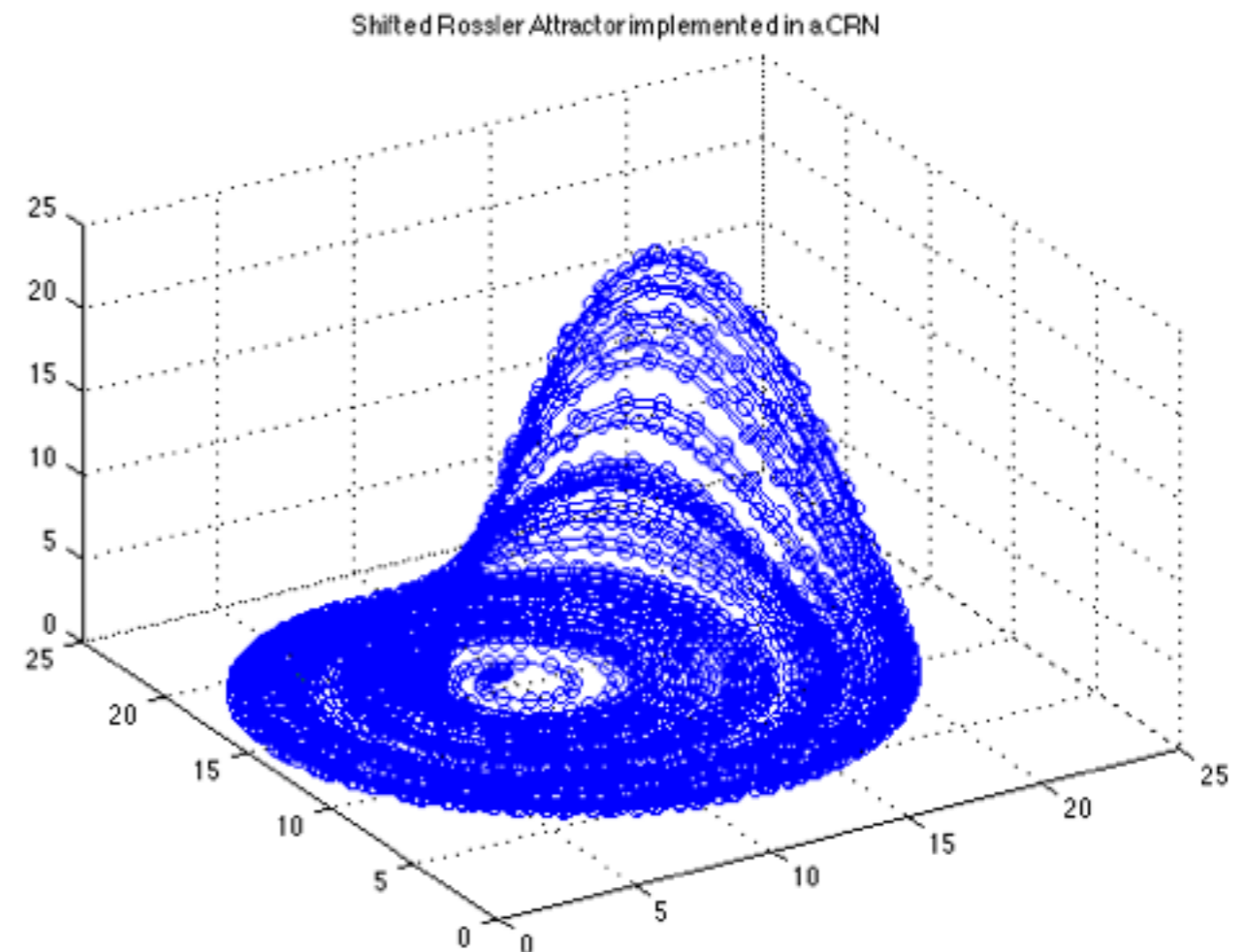


Use special reactants to break higher degree terms into several parts

# Mass action CRNs

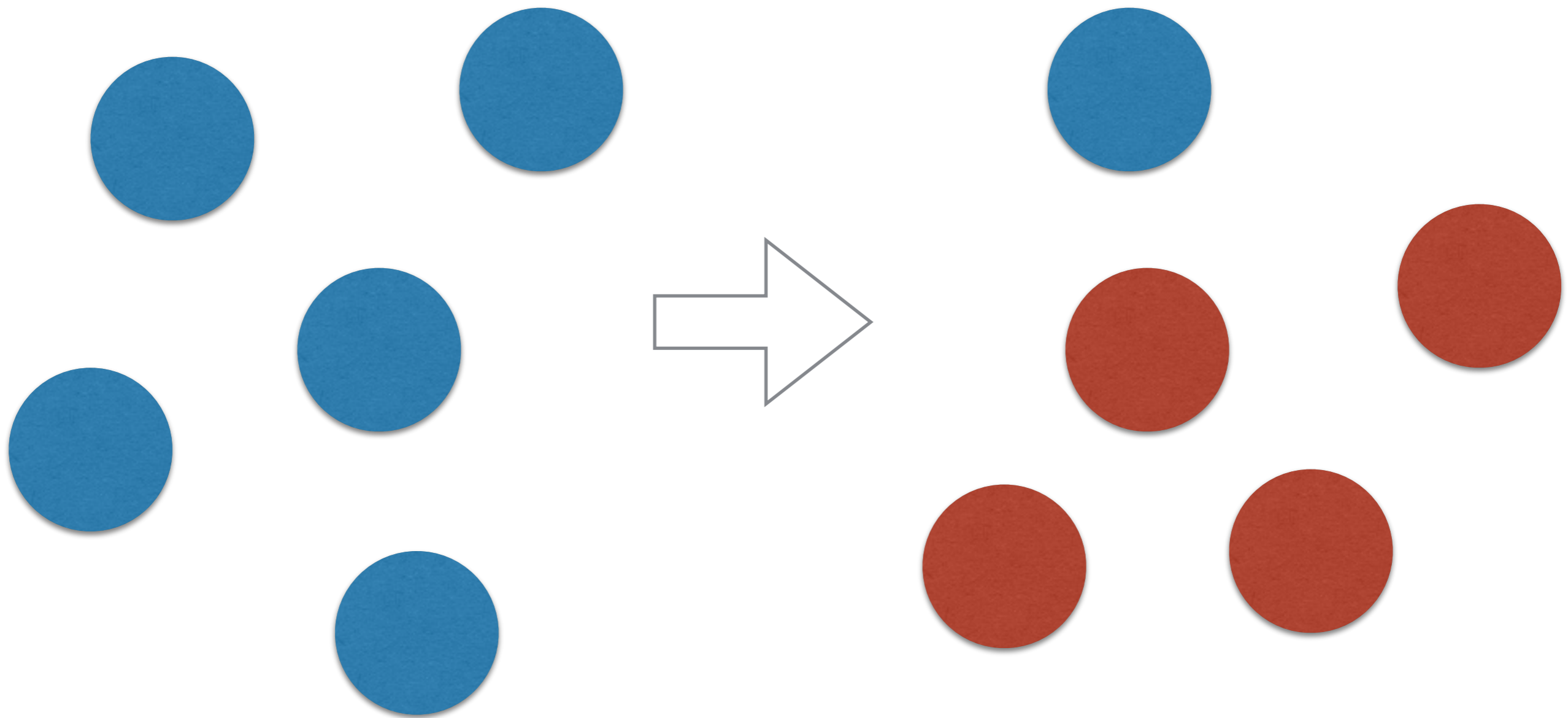
**Theorem.** Any polynomial ODE can be approximated arbitrarily well by a mass action CRN.

$$\begin{aligned}\frac{dx}{dt} &= -z - y \\ \frac{dy}{dt} &= x + ay \\ \frac{dz}{dt} &= b + z(x - c)\end{aligned}$$



# Kinetic CRNs

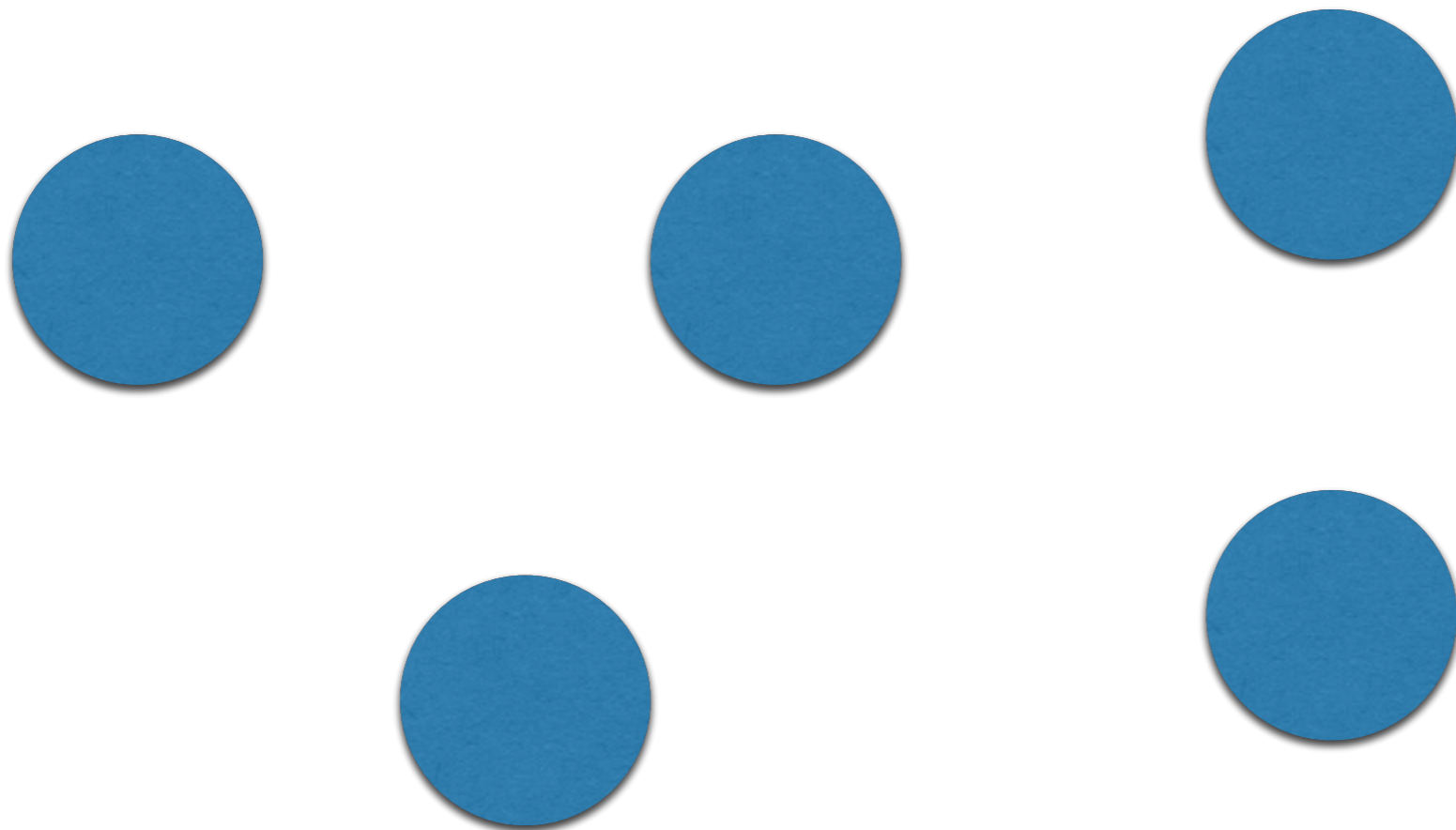
## Stable leader election



# Kinetic CRNs

## Stable leader election

$A + A \rightarrow A + B$  solves leader election in  $\mathcal{O}(n)$   
expected time (equivalently  $\mathcal{O}(n^2)$  pairwise interactions)



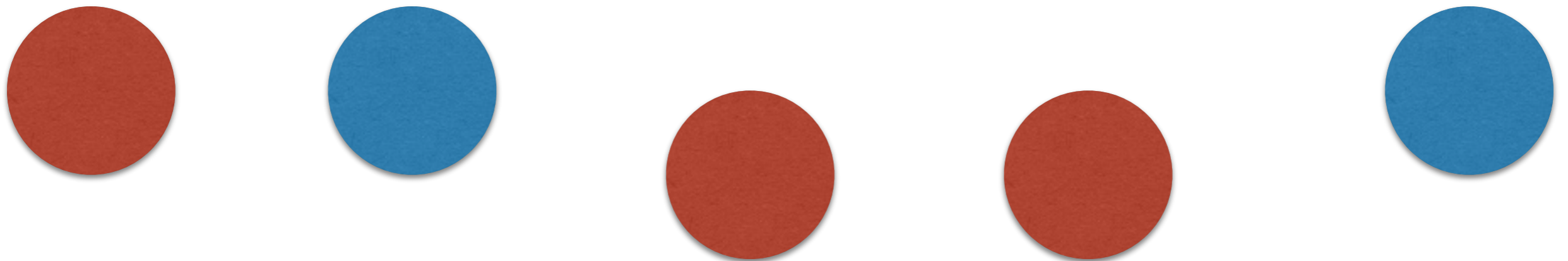
# Kinetic CRNs

## Stable leader election

**Theorem.** Stable leader election requires  $\Omega(n^2)$  pairwise interactions.

[Doty and Soloveichik, 2015]

**Intuition:** No matter what, there is always a “bottleneck” somewhere, where two low concentration species need to find each other to know who will be the leader.

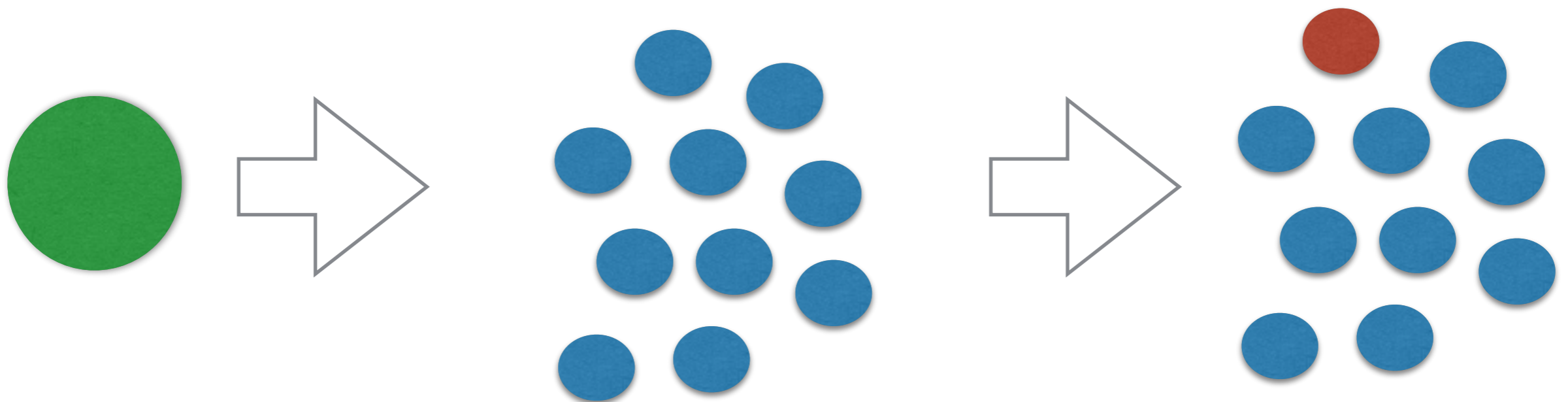


# Extensions of kinetic CRNs

## Stable leader election

Allowing a super-constant number of CRN species gives better protocols [Alistairh and Gelashvili, 2015], [Alistarh, Aspnes, Eisenstat, Gelashvili, Rivest, 2017], etc.

Can have substantial impact on *descriptive complexity* in some applications



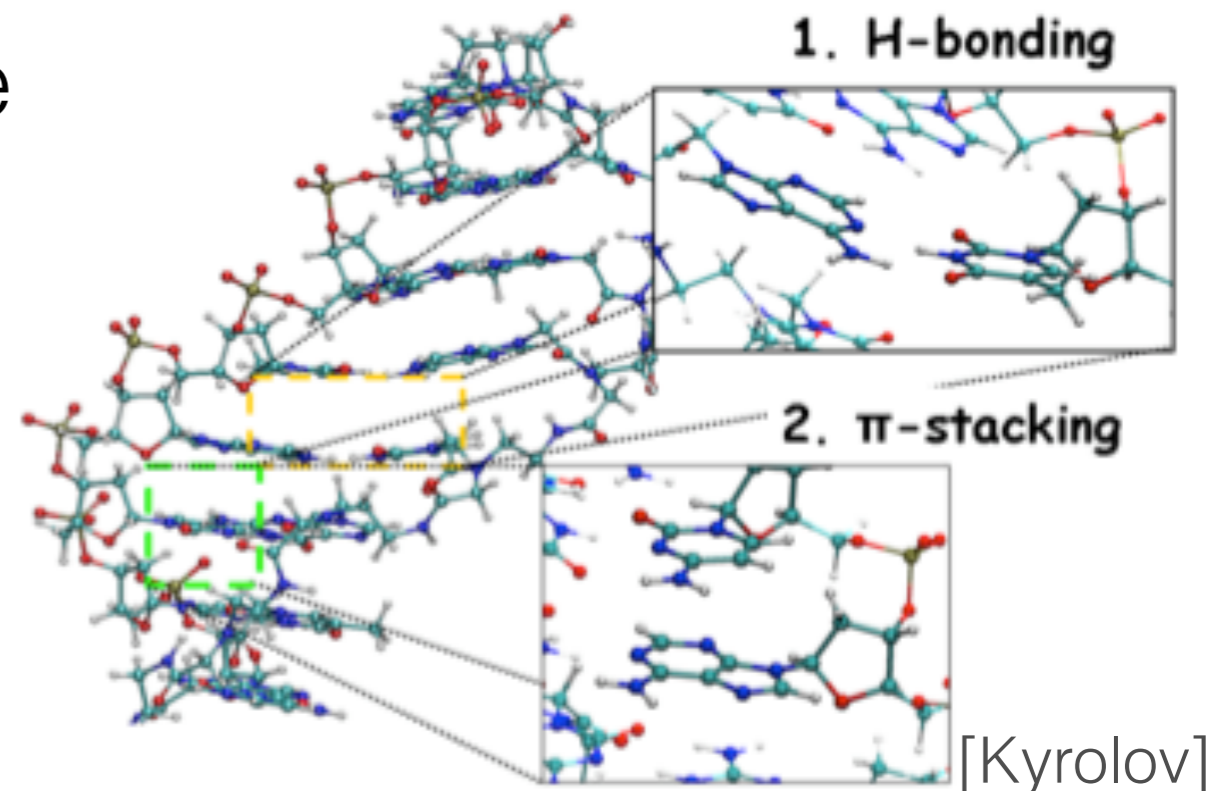
# Implementing CRNs

## DNA as a substrate for molecular engineering

Very predictable secondary structure due to Watson-Crick complementarity

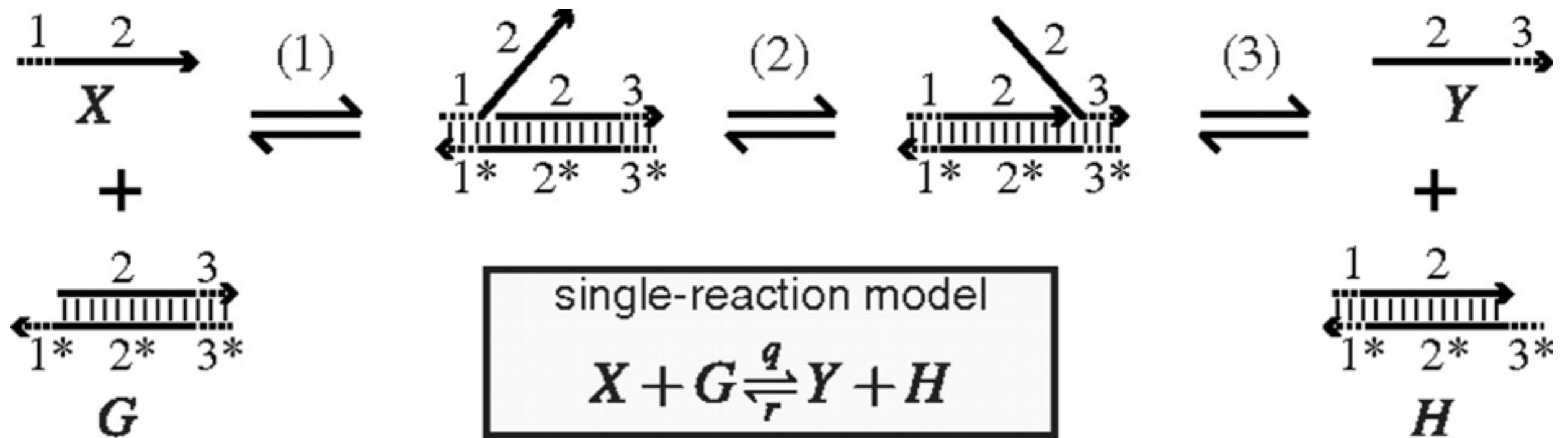
Easy to filter out garbage because of pi-stacking

Cheap and easy to synthesize



# Implementing CRNs

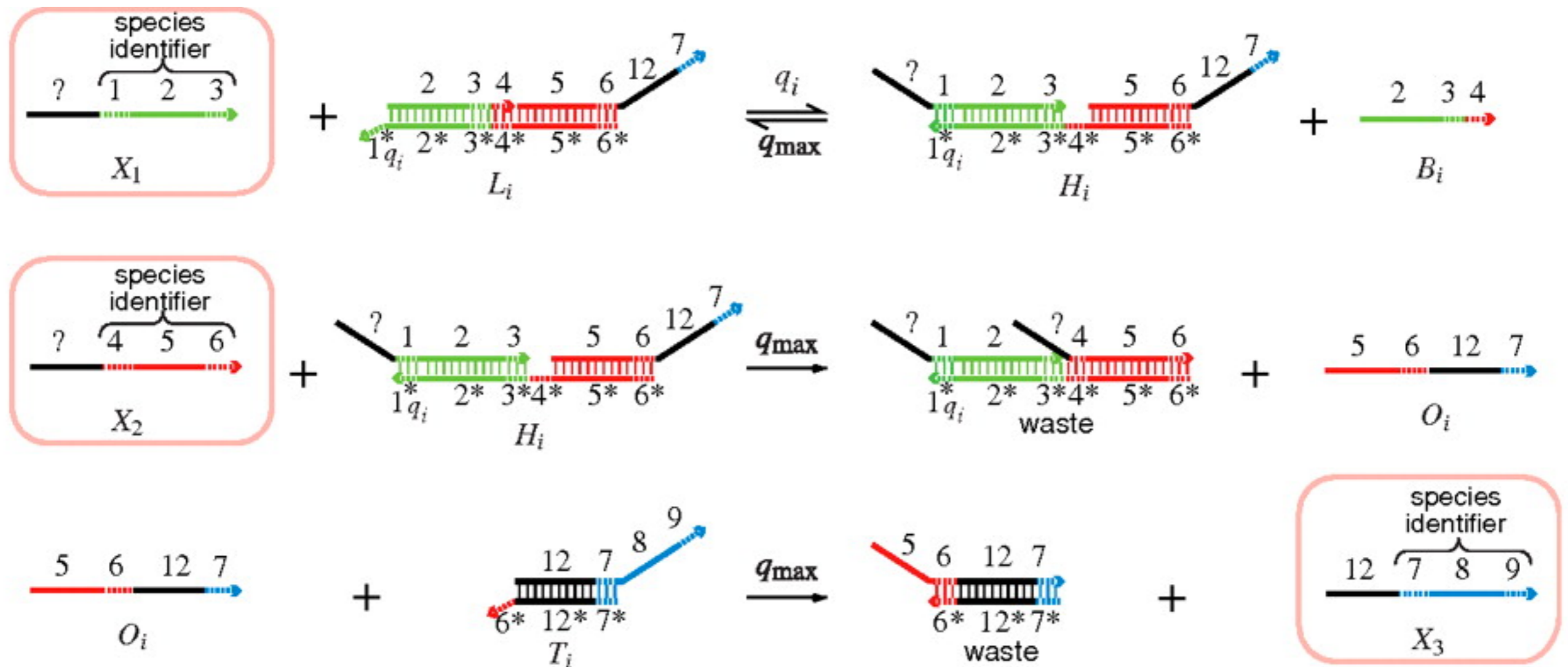
## Toehold-mediated branch migration





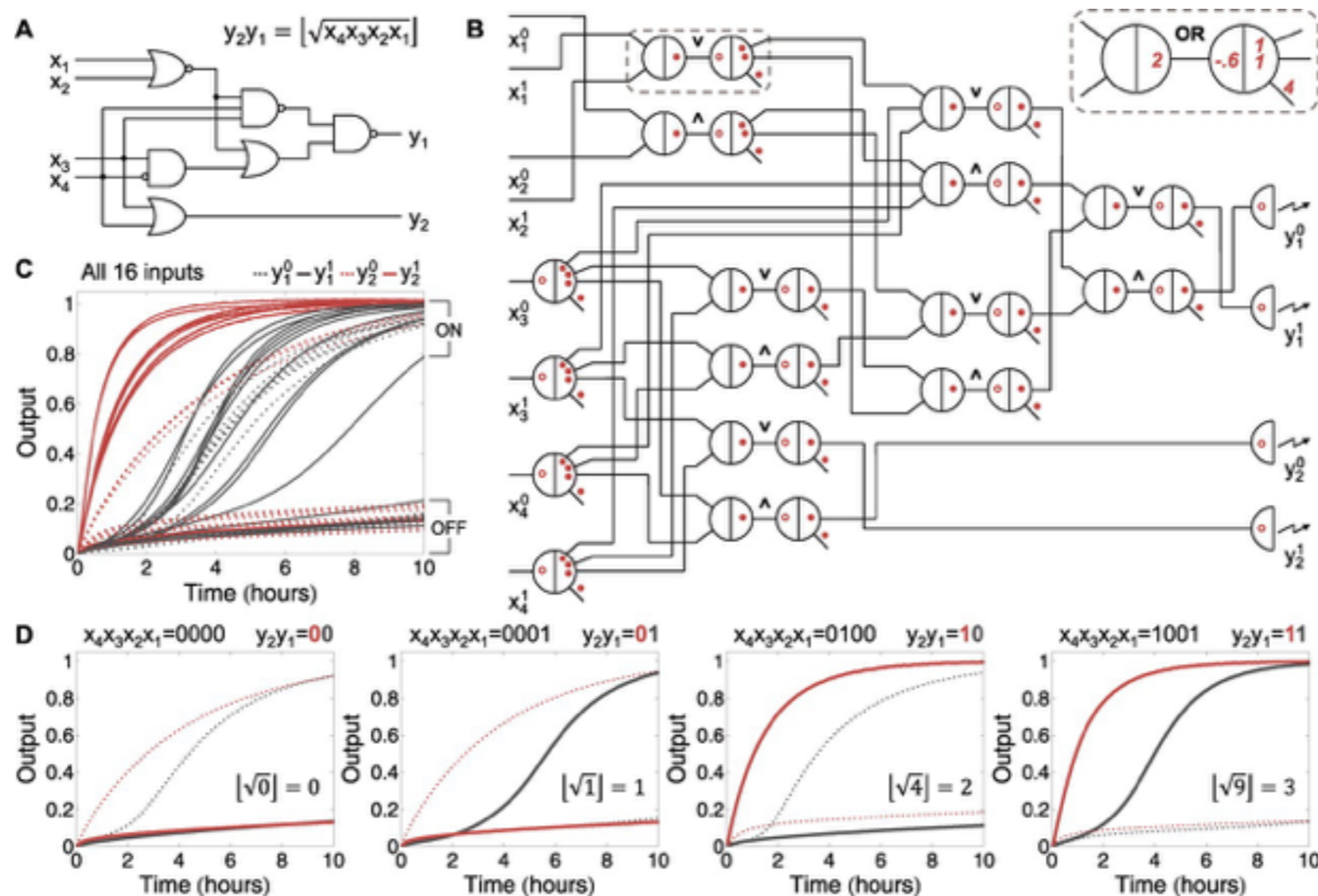
# Implementing CRNs

## DNA strand displacement circuits



# Implementing CRNs

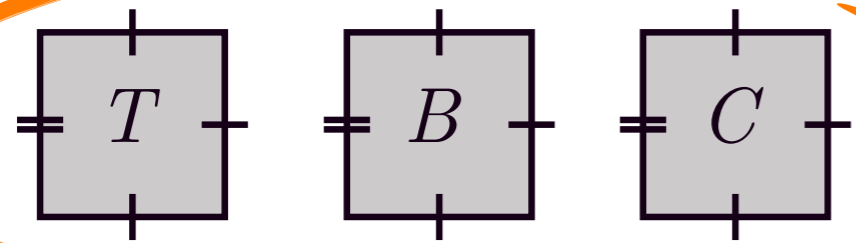
Difficulty of design is related to # of species!



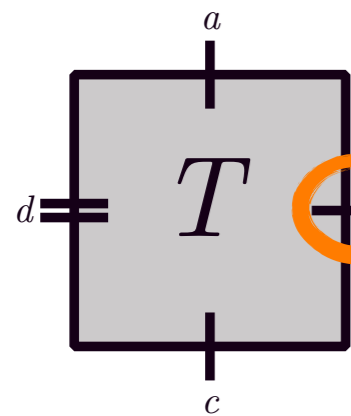
Part II

# Tile Assembly Models

# Abstract Tile Assembly Model

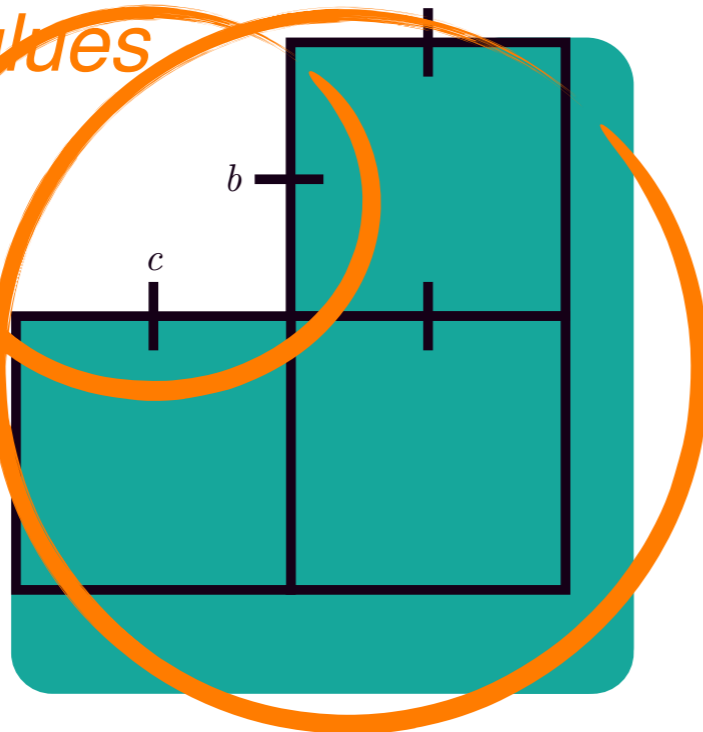


finite set of *tiles*

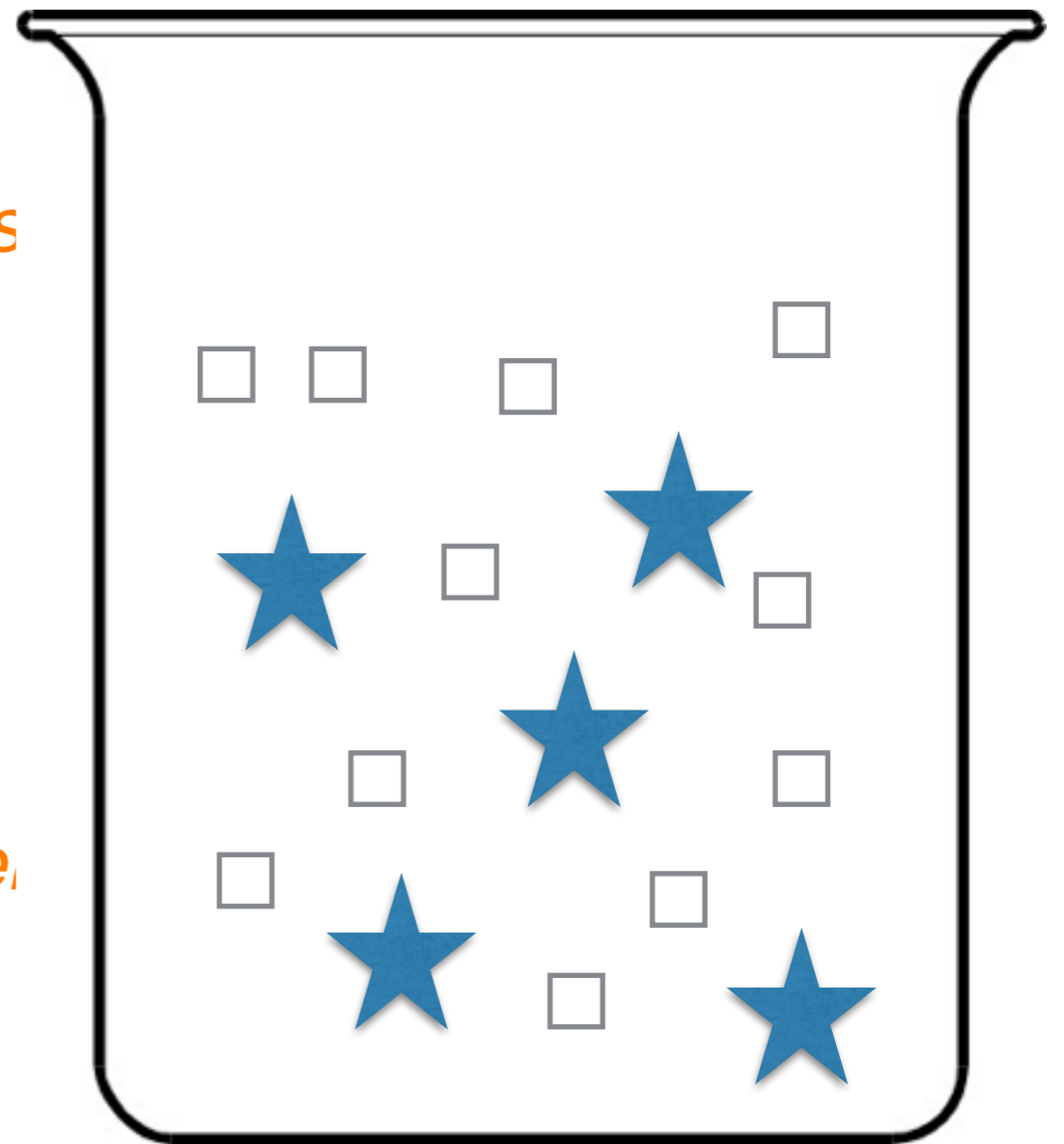


*glues*

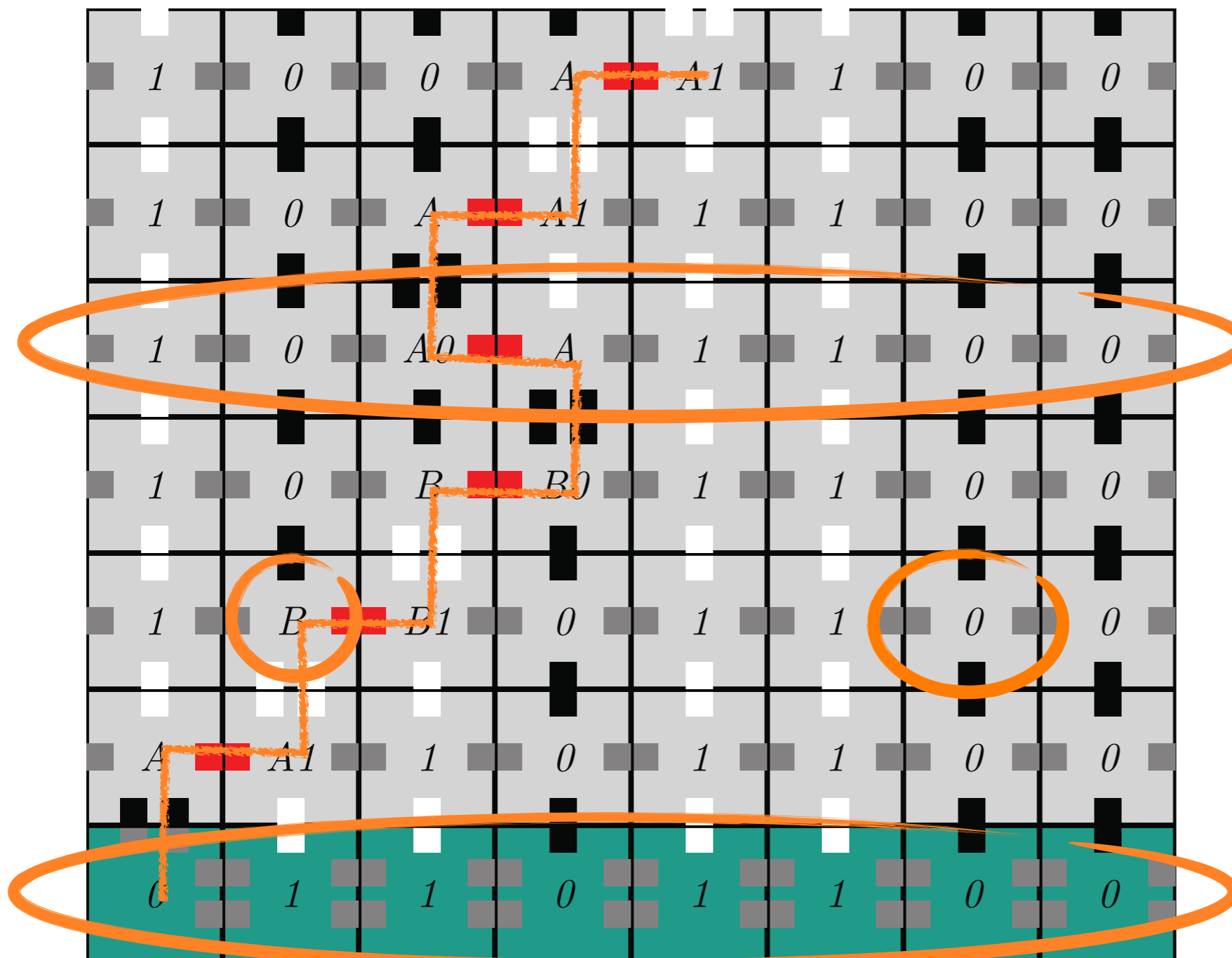
temperature



*assembly*



# Computation with Tiles



head moves left/right

each row represents a single Turing machine operation

position and state of head is recorded

hard-coded seed tiles specify input

# Temperature in the aTAM

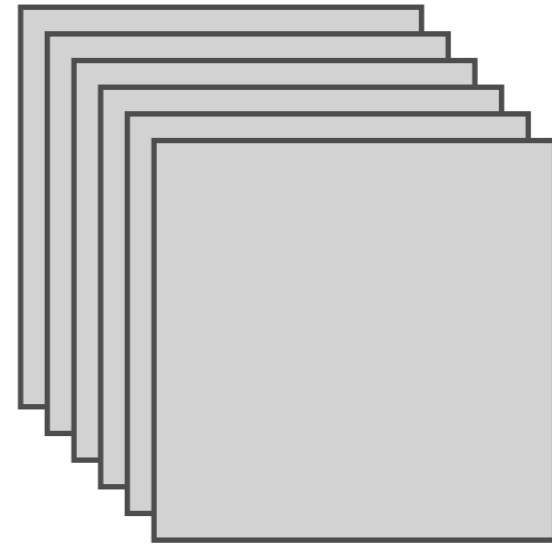
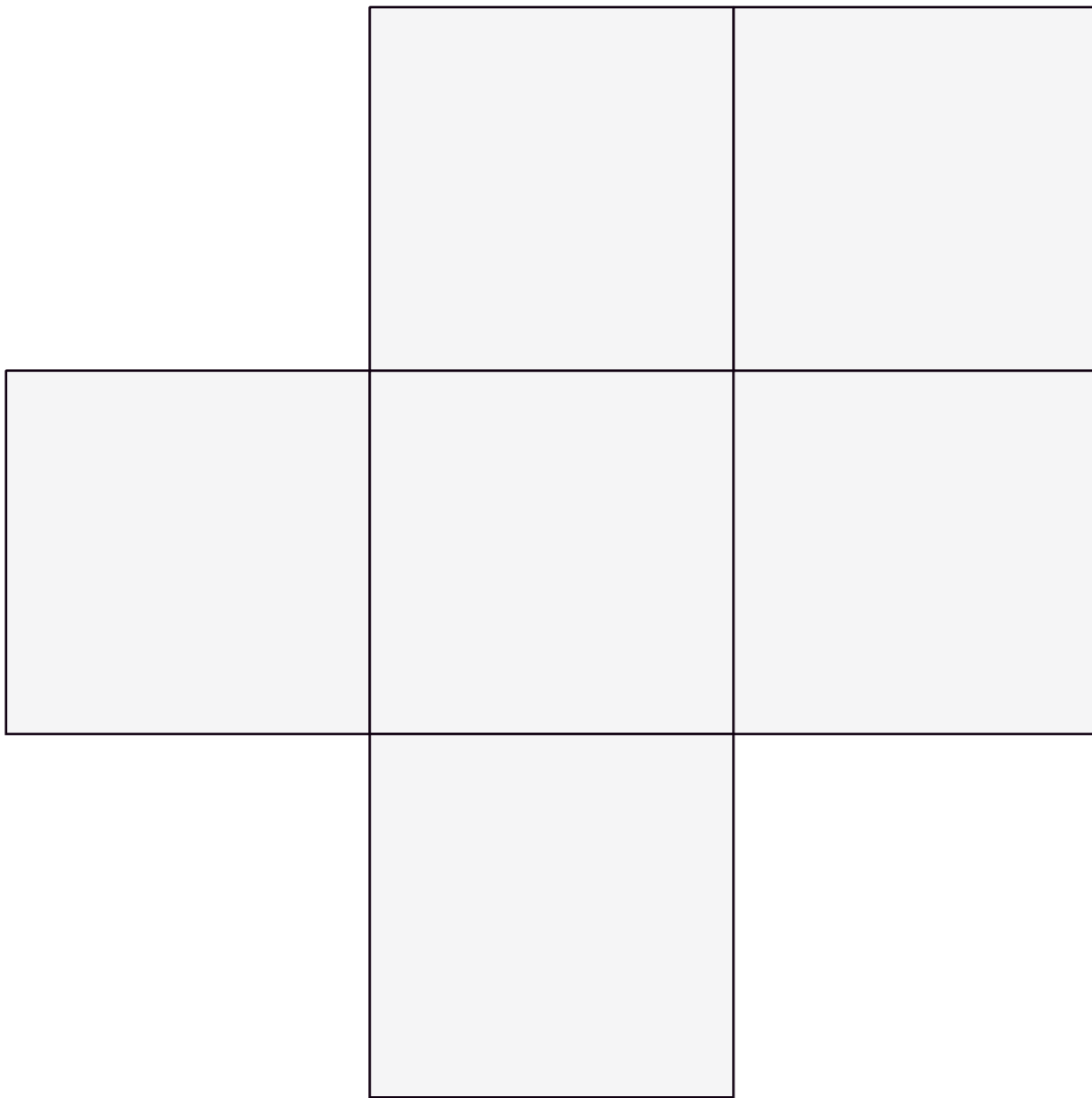
All of our proofs rely on temperature 2

Allows “cooperative binding”, i.e. merging of information

The aTAM at temperature 1 is *believed* to be very weak...

**Possibly the biggest open problem in the field!**

# Finite Shape Construction



Always possible  
with  $N$  tile types!

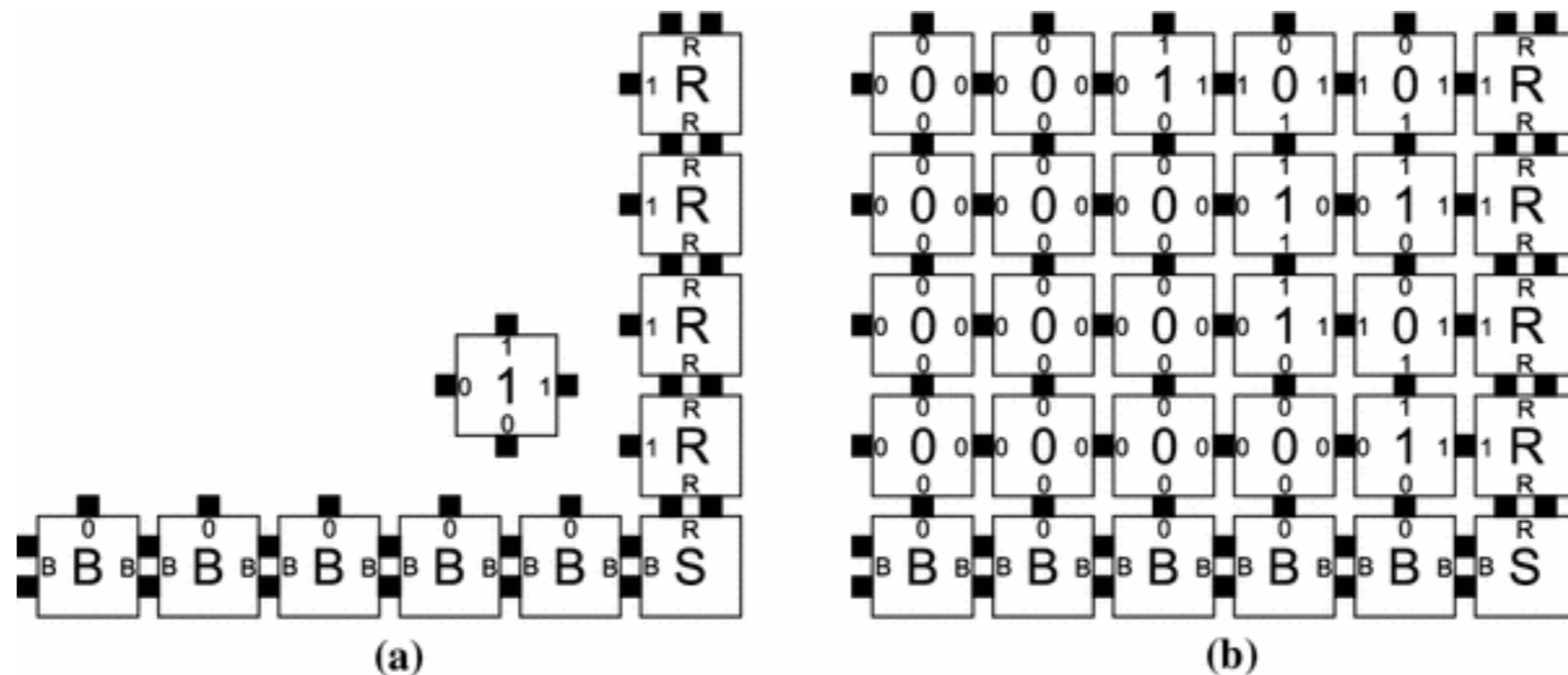
# Constructing squares

**Theorem.** An aTAM program with  $\mathcal{O}(\log n)$  tile types can construct an  $n \times n$  square.

[Rothemund and Winfree, 2000]

## Proof idea:

Build a “binary counter” using  $\mathcal{O}(1)$  tile types



[image due to Patitz, 2014]



# Constructing squares

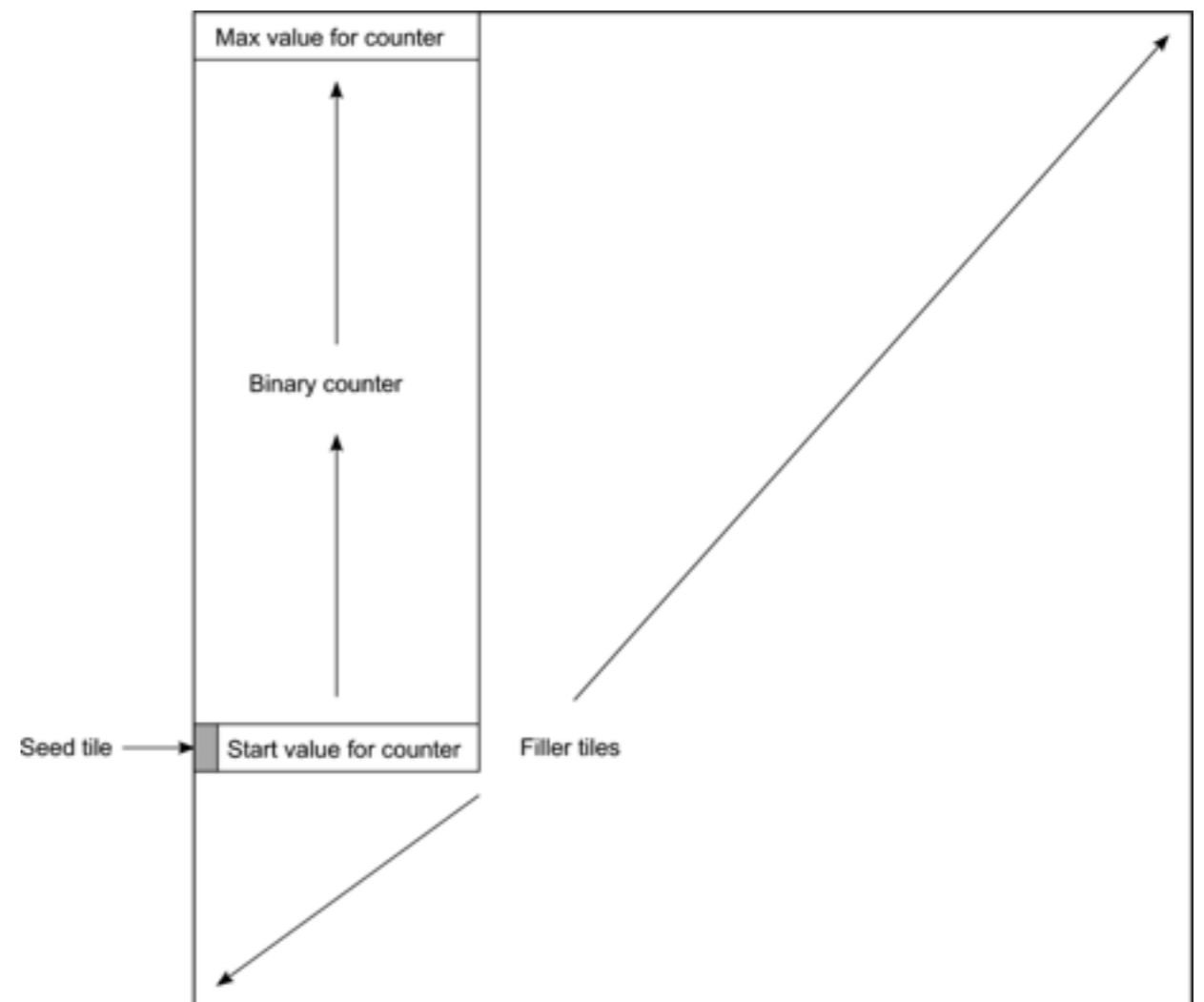
**Theorem.** An aTAM program with  $\mathcal{O}(\log n)$  tile types can construct an  $n \times n$  square.

[Rothemund and Winfree, 2000]

## Proof idea:

Encode binary counter input in  $\mathcal{O}(\log n)$  tile types.

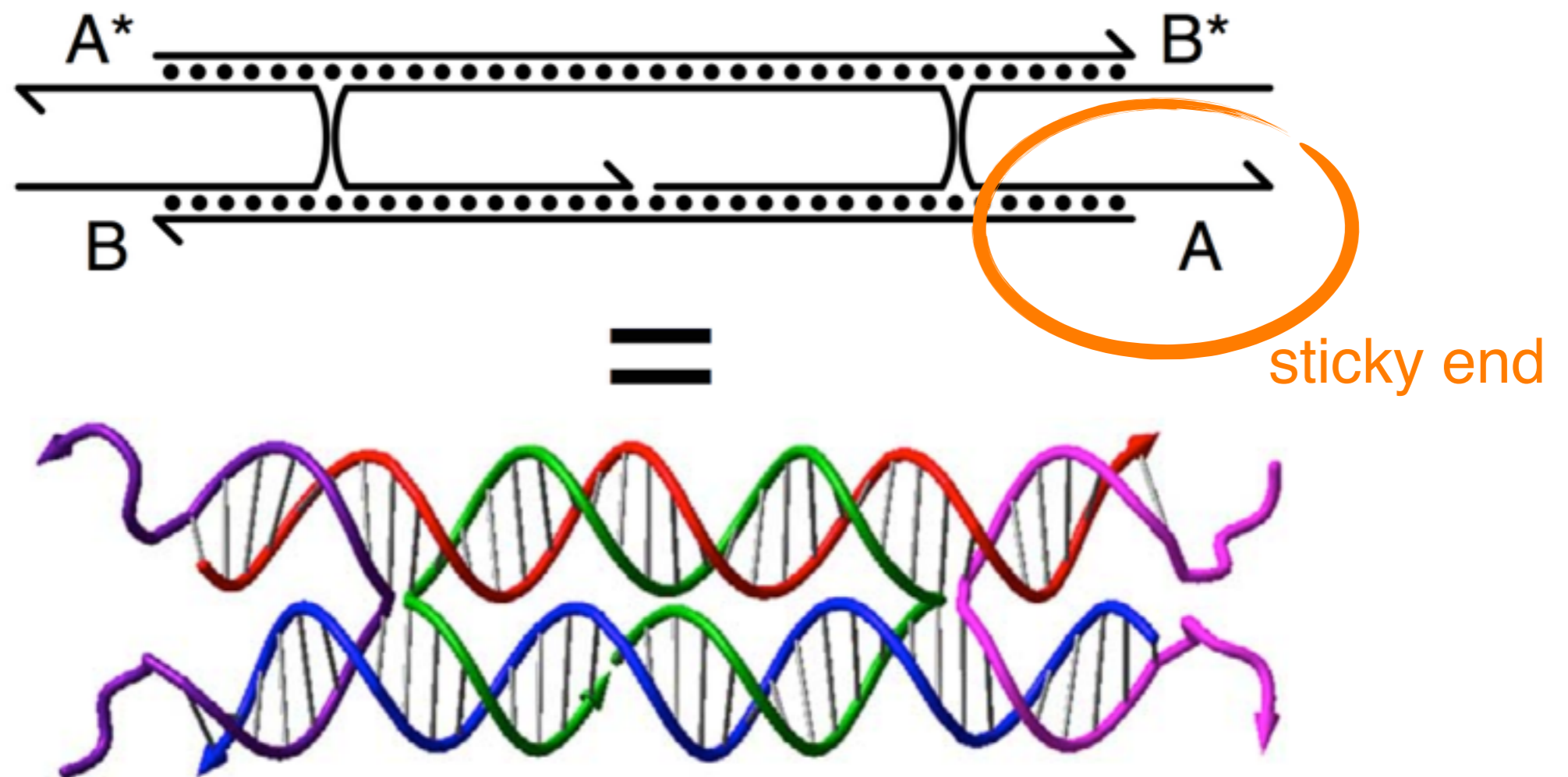
Fill in gaps with  $\mathcal{O}(1)$  filler tile types



[image due to Patitz, 2014]

# Tile Assembly Model

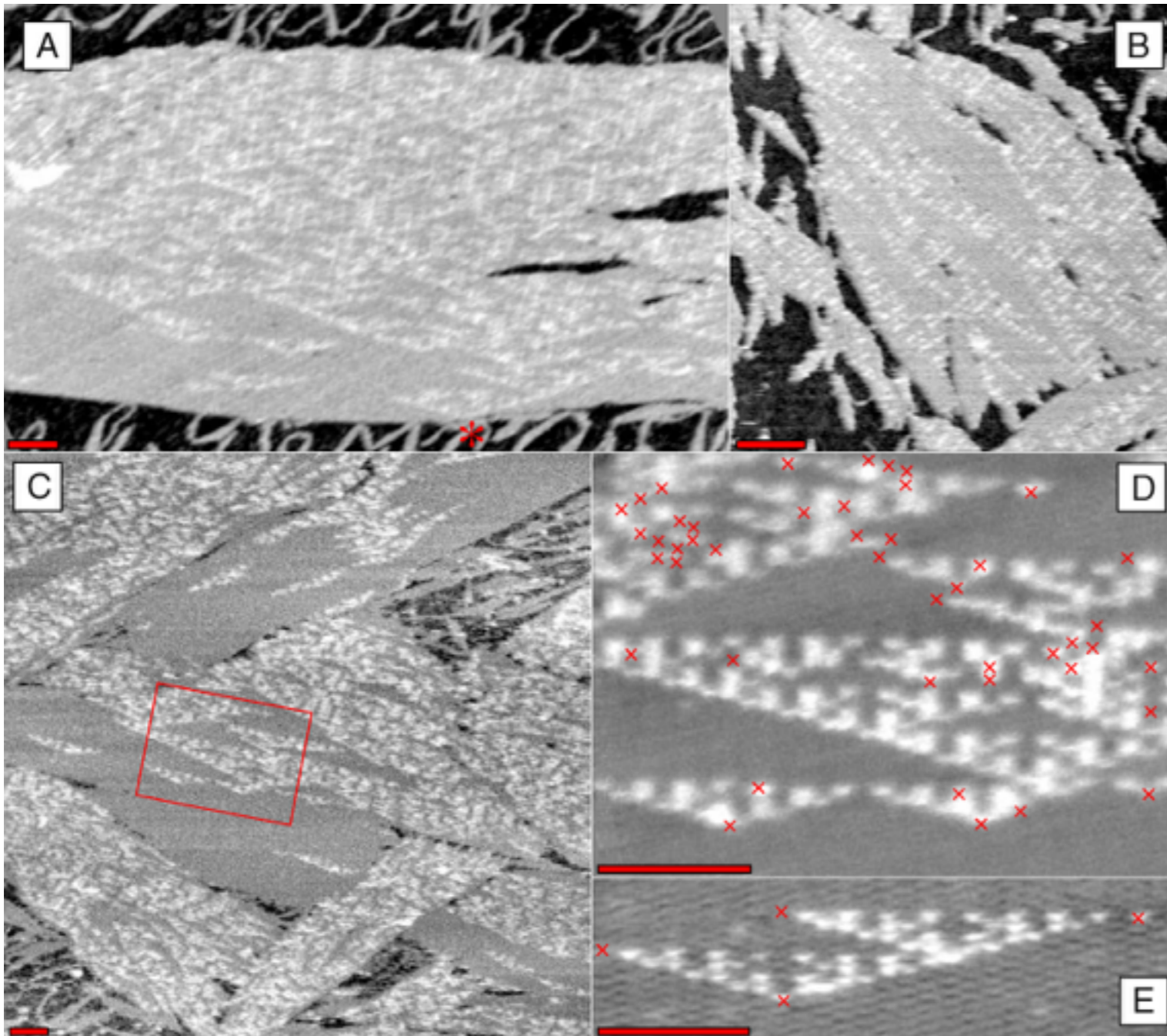
## Double-crossover motif



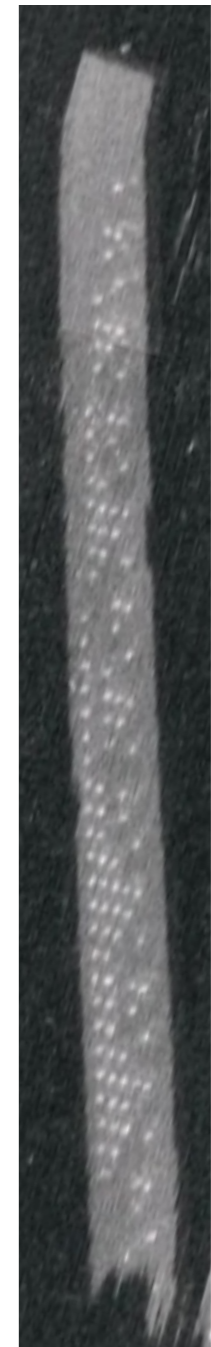
[Fu and Seeman, 1993]

[Winfree, 1998]

# Tile Assembly Model



[Rothemund, Papadakis, Winfree, 2004]



[Evans, 2014]

# Constructing squares

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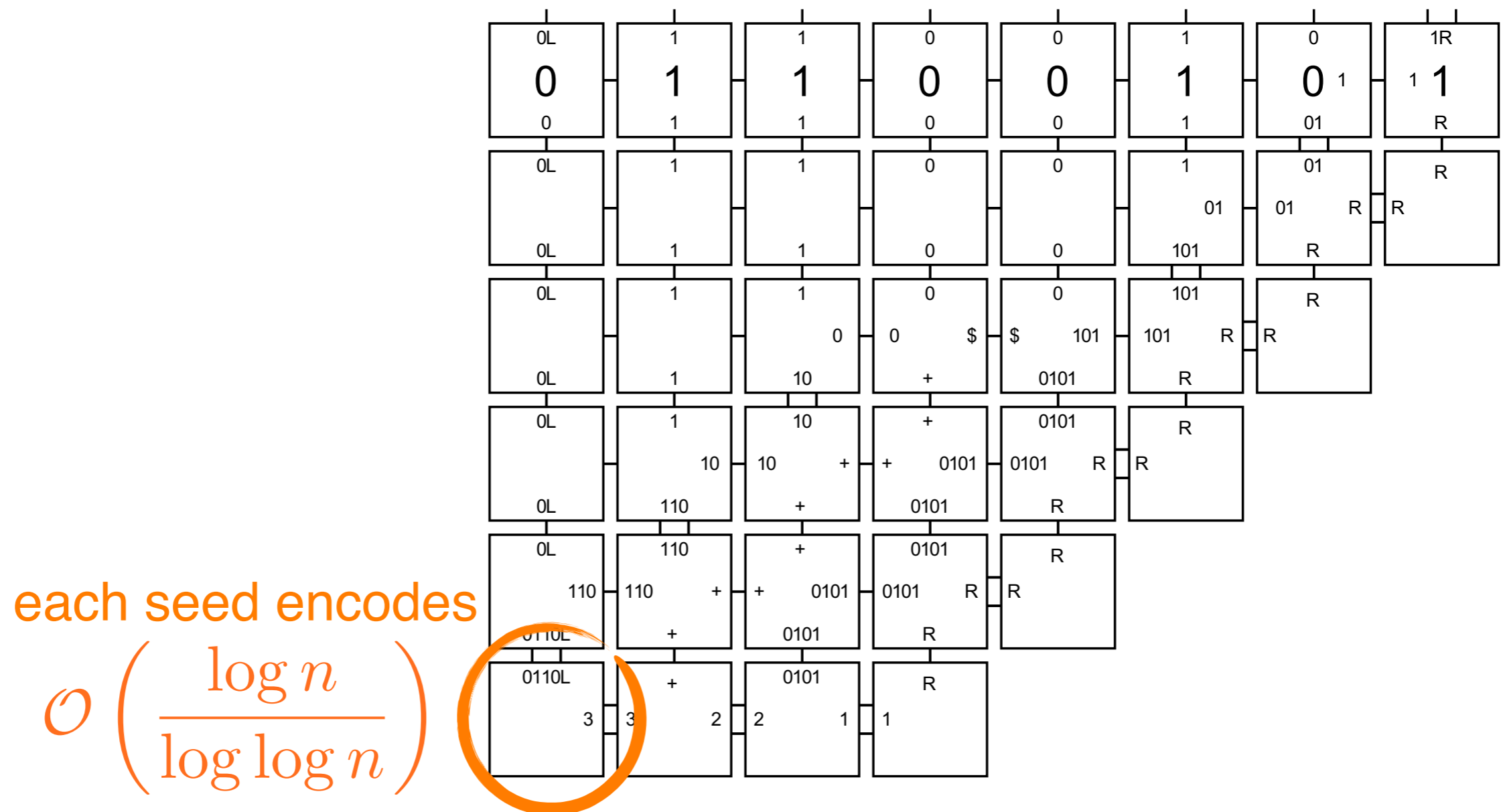
**Theorem.** There is an aTAM program with  $\mathcal{O}\left(\frac{\log n}{\log \log n}\right)$  tile types can construct a  $n \times n$  square.

[Adleman, Cheng, Goel, and Huang, 2001]

Better input encoding!

# Optimal encoding of binary strings

$n$  bit binary string to encode with tiles



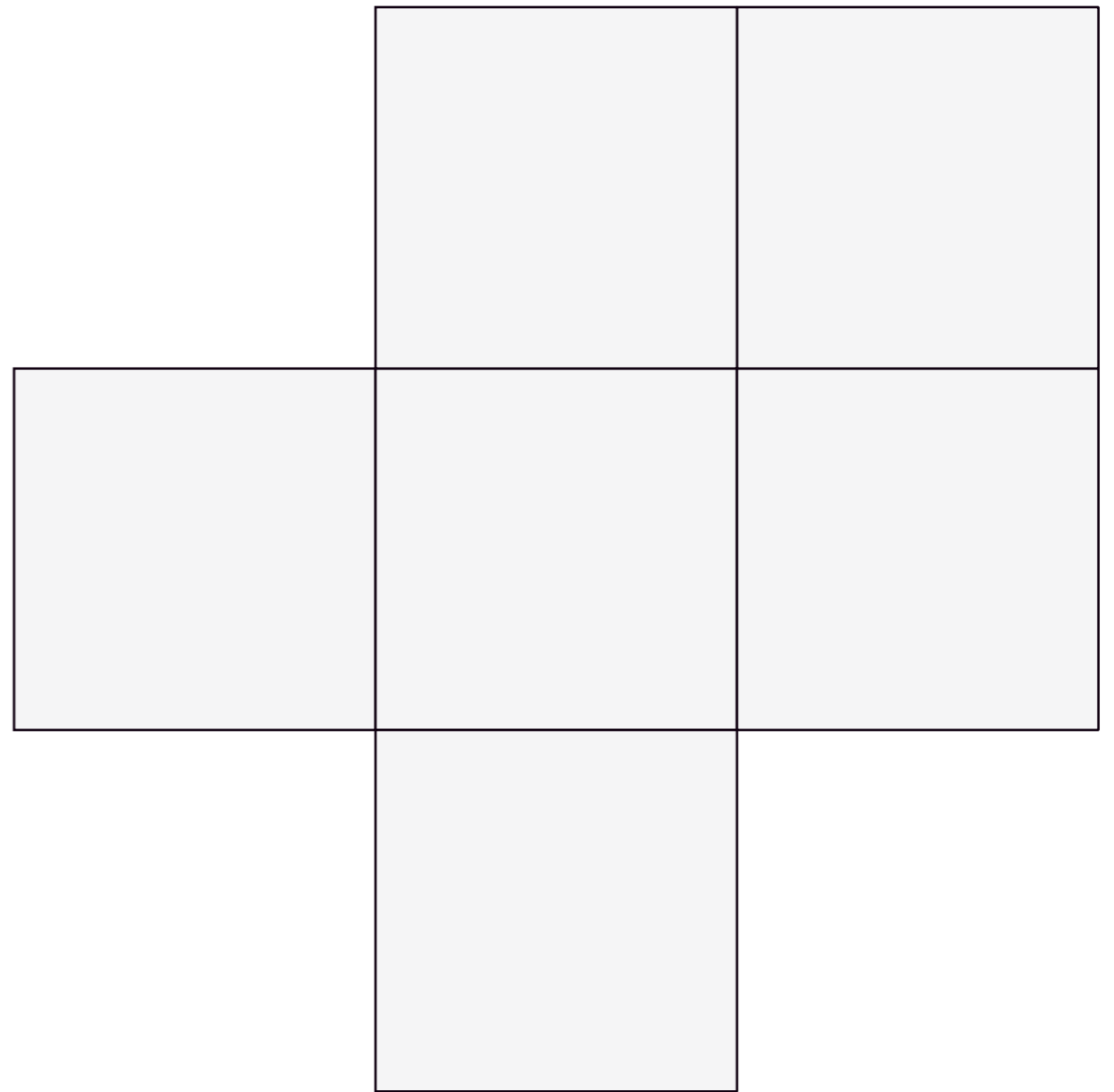


# Finite Shape Construction

Kolmogorov complexity

$$K_U(\mathcal{S}) =$$

size of the smallest  
program for  $U$  that  
outputs  $\mathcal{S}$



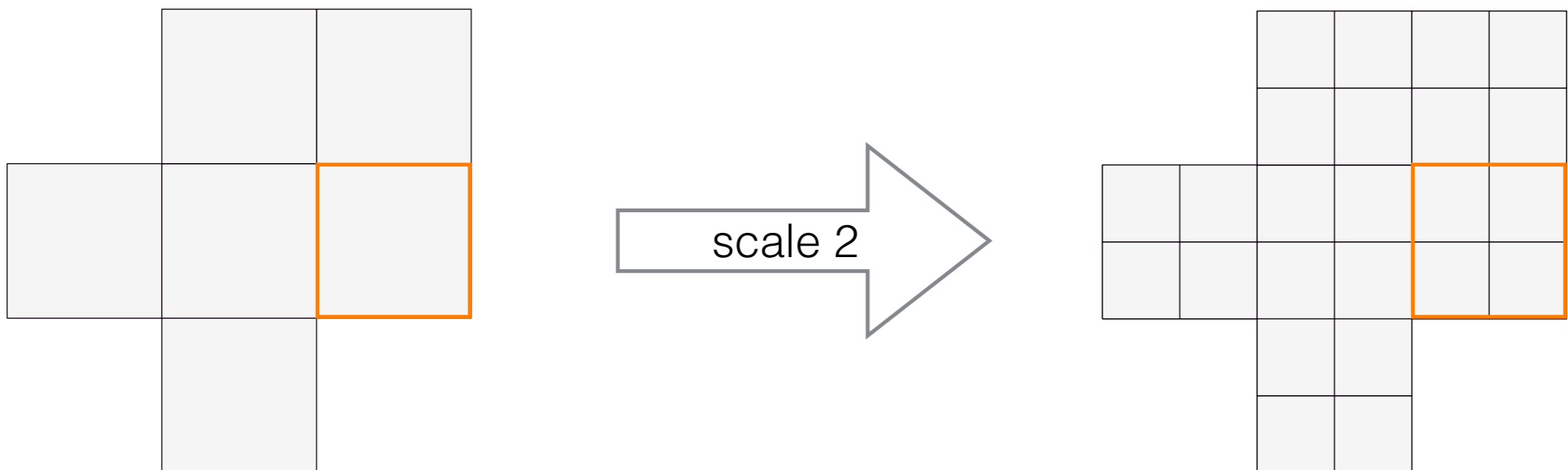
# Shape Construction in the aTAM

**Theorem.** For any shape  $\mathcal{S}$ , there is an aTAM tile set  $T$  that constructs  $\mathcal{S}$  at some scale such that

$$|T| \in \Theta \left( \frac{K_U(\mathcal{S})}{\log K_U(\mathcal{S})} \right)$$

optimal input encoding

[Soloveichik and Winfree, 2007]





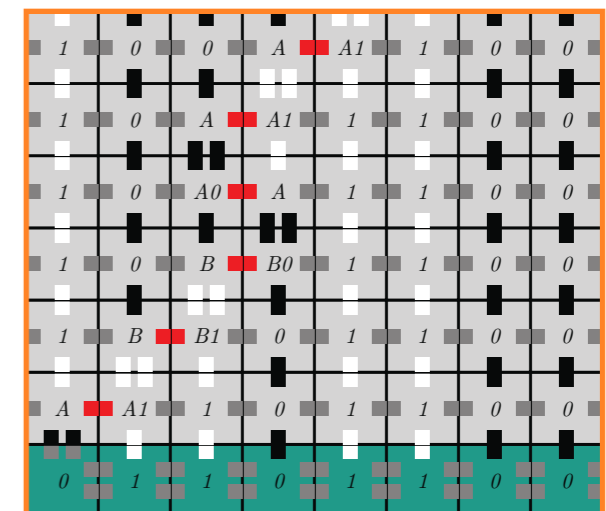
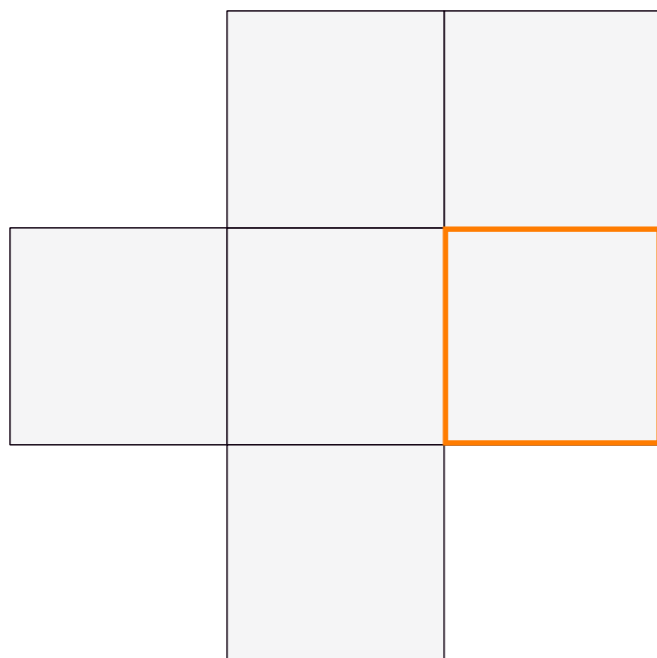
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optimal input encoding

[Soloveichik and Winfree, 2007]



# But wait, there's more!

## aTAM is extremely well studied

aTAM is intrinsically universal [Doty, Lutz, Patitz, Schweller, Summers, Woods, 2012]

classification of shapes by difficulty [Aggarwal<sup>†</sup>, Cheng, Goldwasser, Kao, Moisset de Espanes, Schweller, 2005]

# But wait, there's more!

## Dozens of variants

2-handed tile assembly model

hierarchical tile assembly model

kinetic tile assembly model

polyomino tile assembly model

flipping tile assembly model

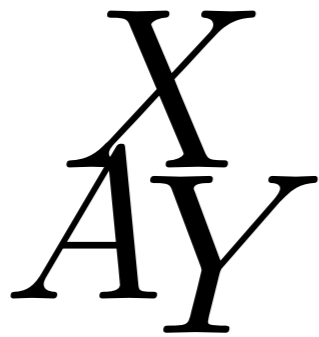
xTAM has been studied for many, many  $x$

*“One tile to rule them all”* in non-square tile systems

[Demaine, Demaine, Fekete, Patitz, Schweller, Winslow, Woods, 2012]

# Locality: friend and foe

CRNs



$D$

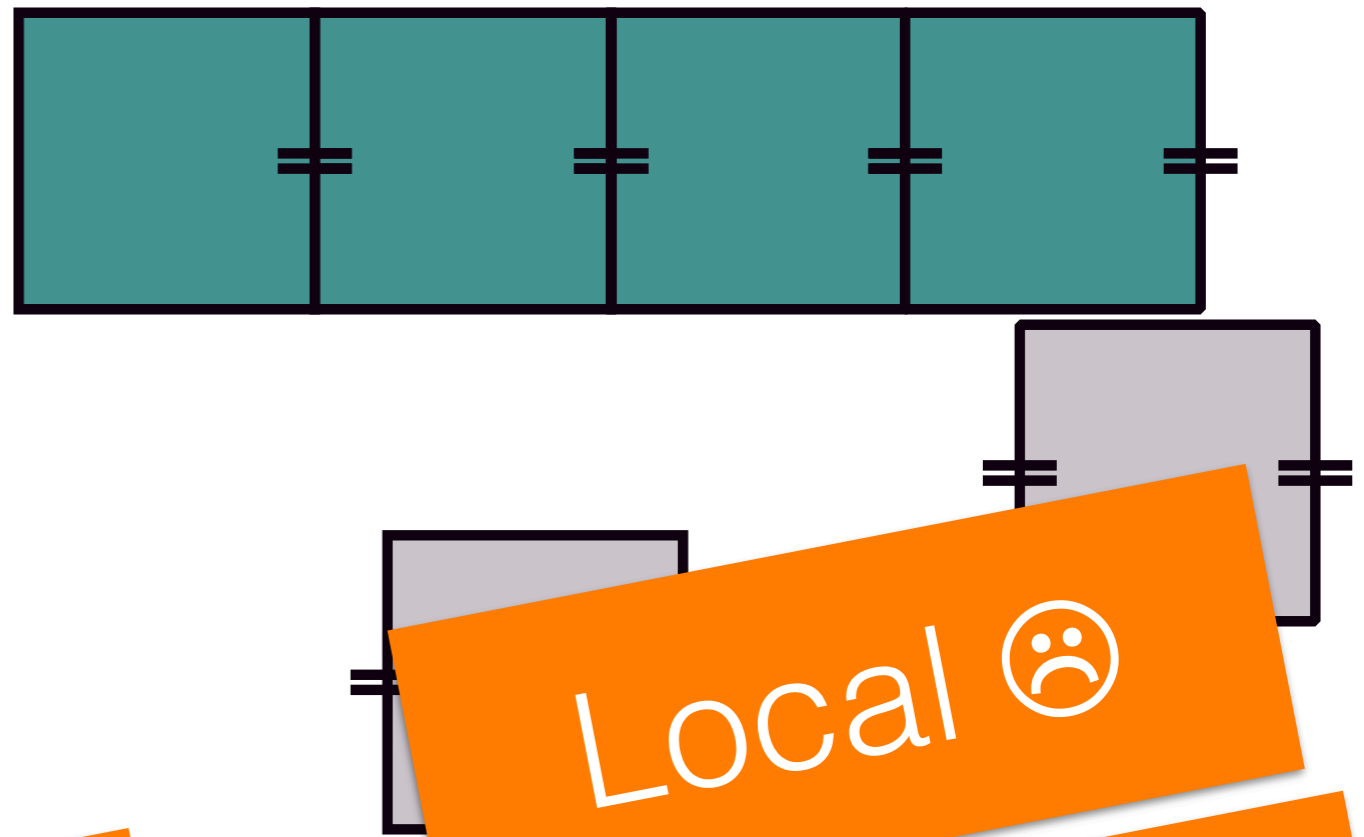
$B$

$C$

Non-local 😊

No geometry 😞

Tile assembly model



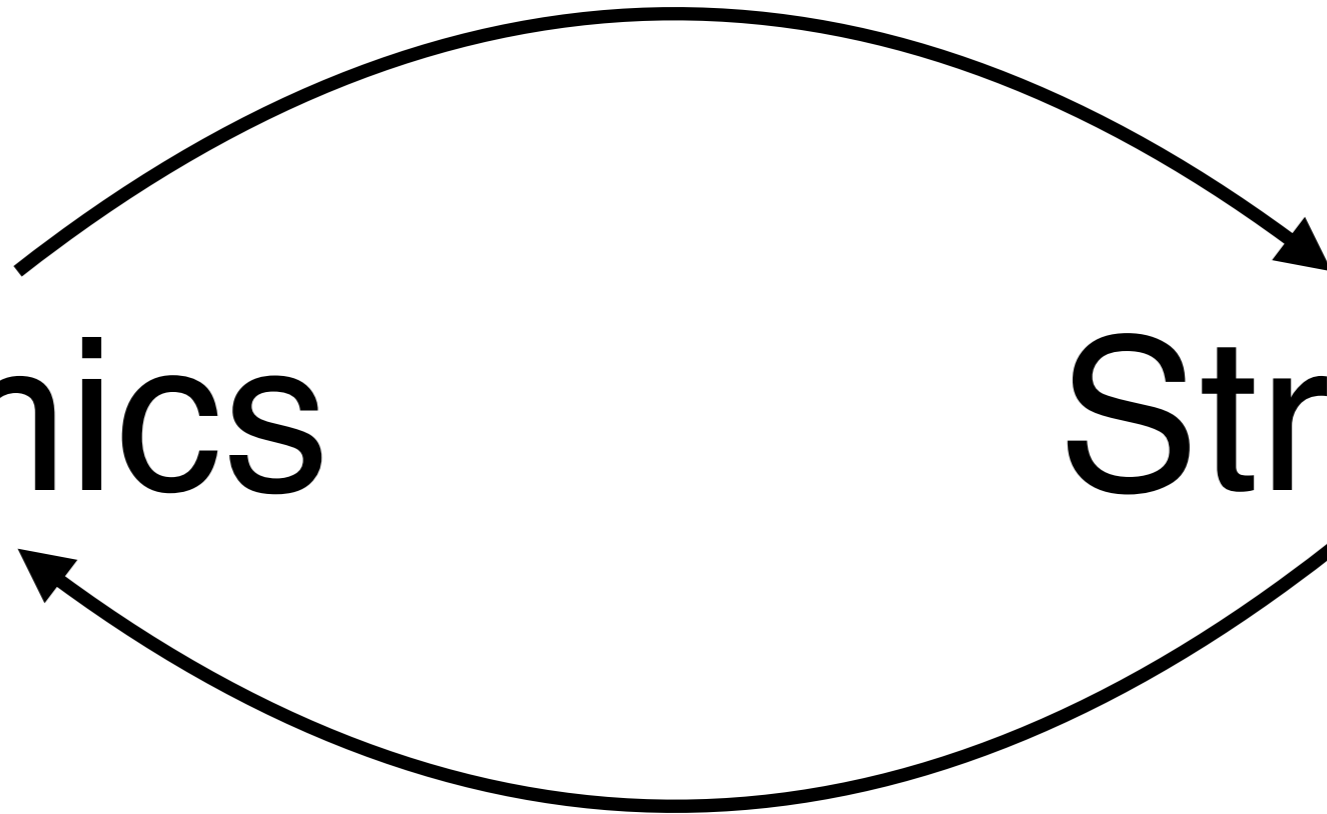
Local 😞

Geometry 😊

In nature...

**Dynamics**

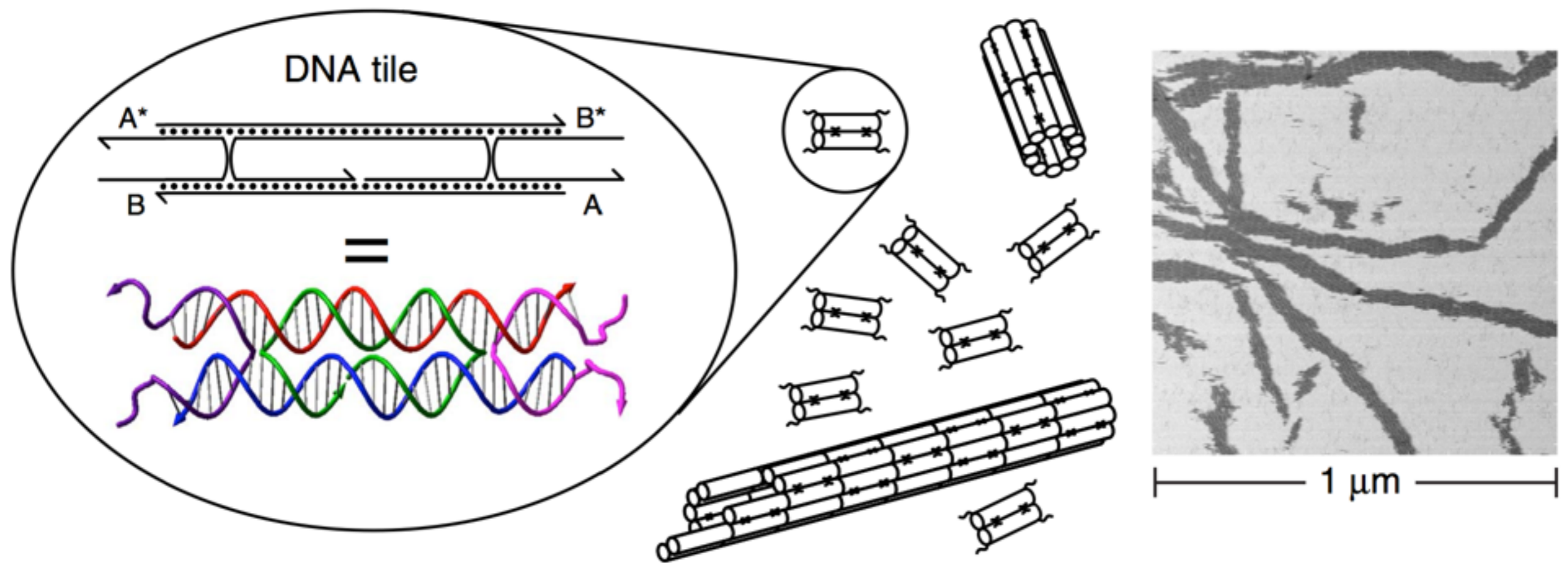
**Structure**



# Part III

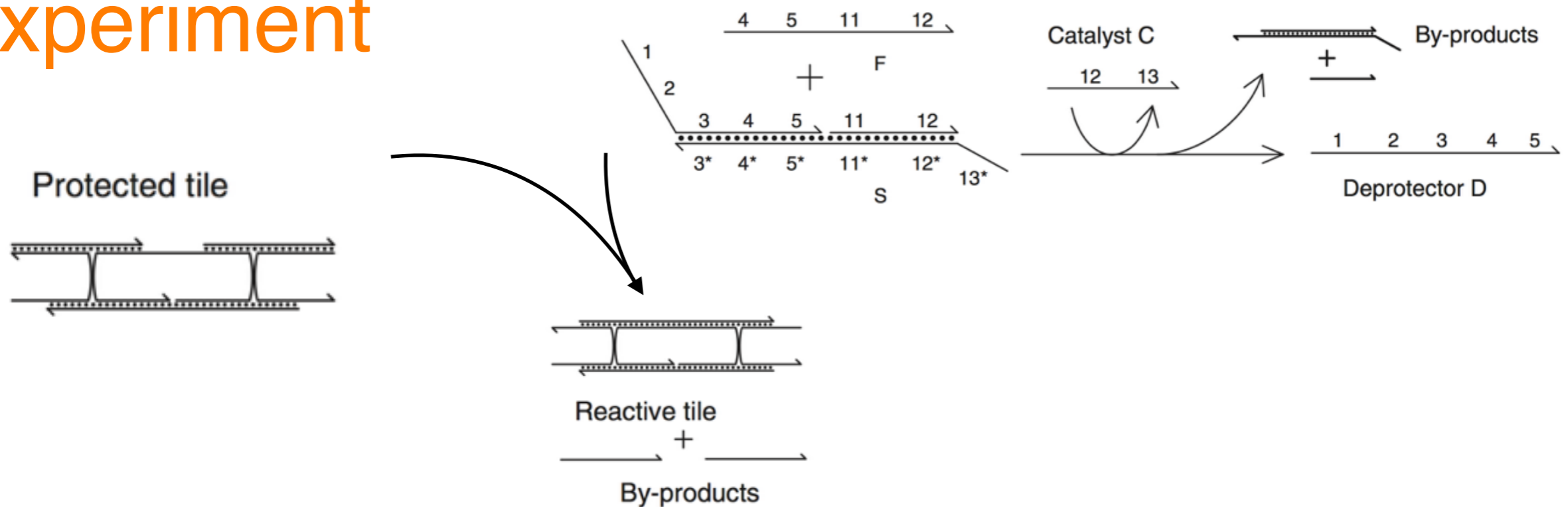
## Hybrid models of molecular programming

# CRN Control of Tile Self-Assembly

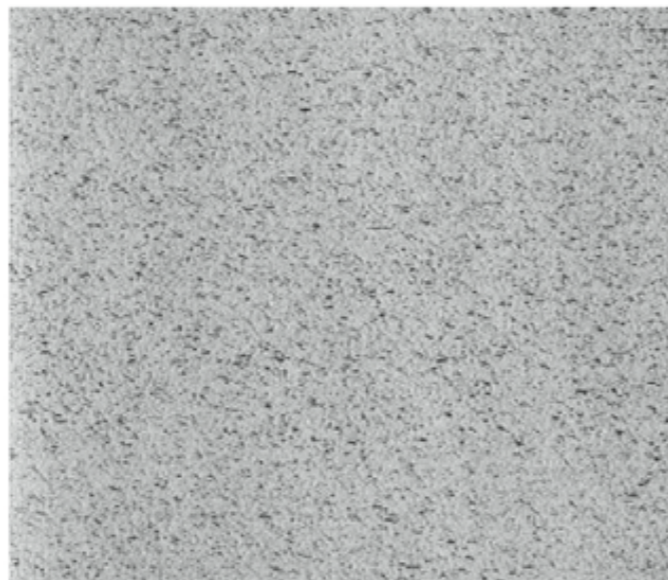


# CRN Control of Tile Self-Assembly

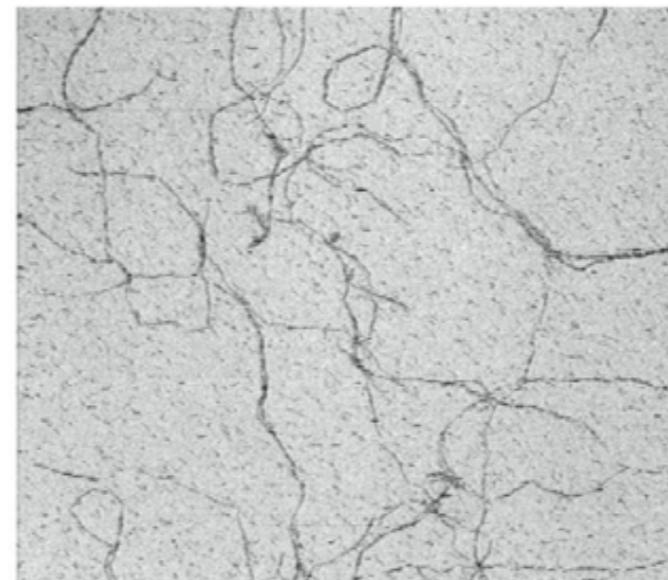
## Experiment



No catalyst (No sink)



0.1× catalyst (No sink)



6.5 μm

[Zhang, et al. 2013]



# CRN Control of Tile Self-Assembly

Theory



# CRN Control of Tile Self-Assembly

## Theory

**“A theoretical framework is needed to characterize what molecular behaviors can or cannot be achieved by integrated DNA tile and strand-displacement systems....”**

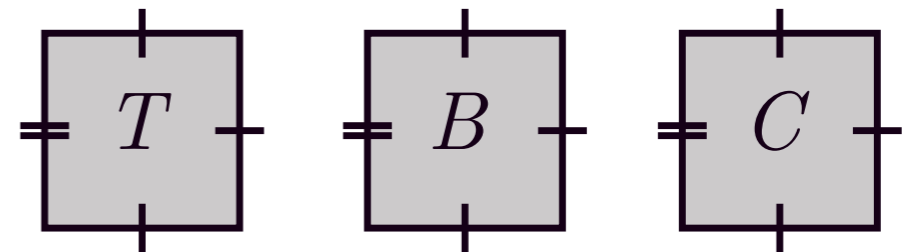
[D. Y. Zhang, R. F. Hariadi, H. M. T. Choi, and E. Winfree, “Integrating DNA strand-displacement circuitry with DNA tile self-assembly,” Nat Commun, vol. 4, Jun. 2013.]

# Chemical Reaction Network-Controlled Tile Assembly Model (CRN-TAM)

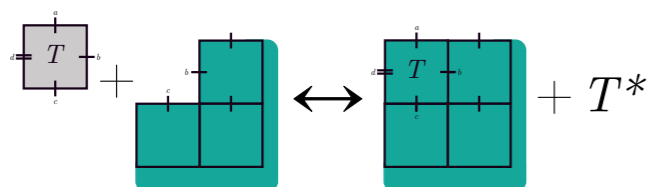
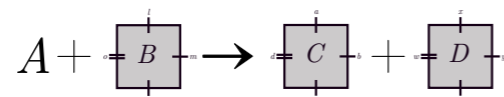
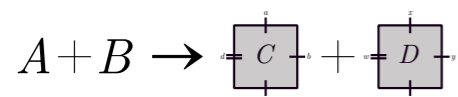
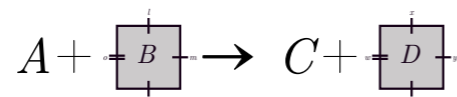
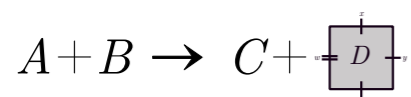
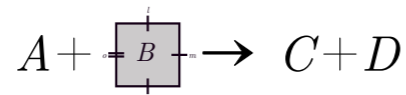
Program includes:

$A, B, C, X, Y, Z, \dots$

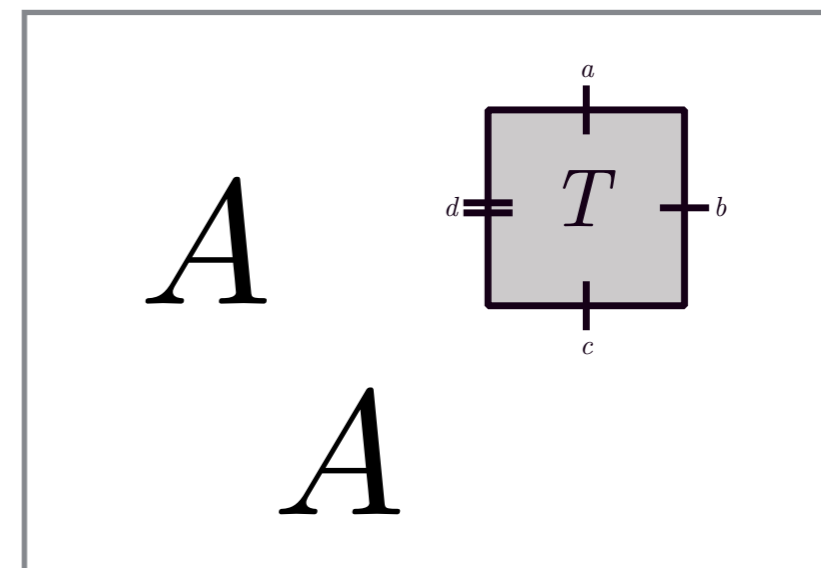
finite set of *signals*



finite set of *tiles*



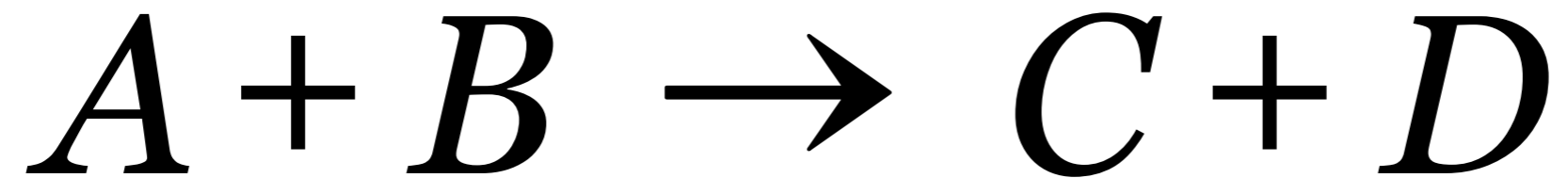
tile assembly reactions



initial state

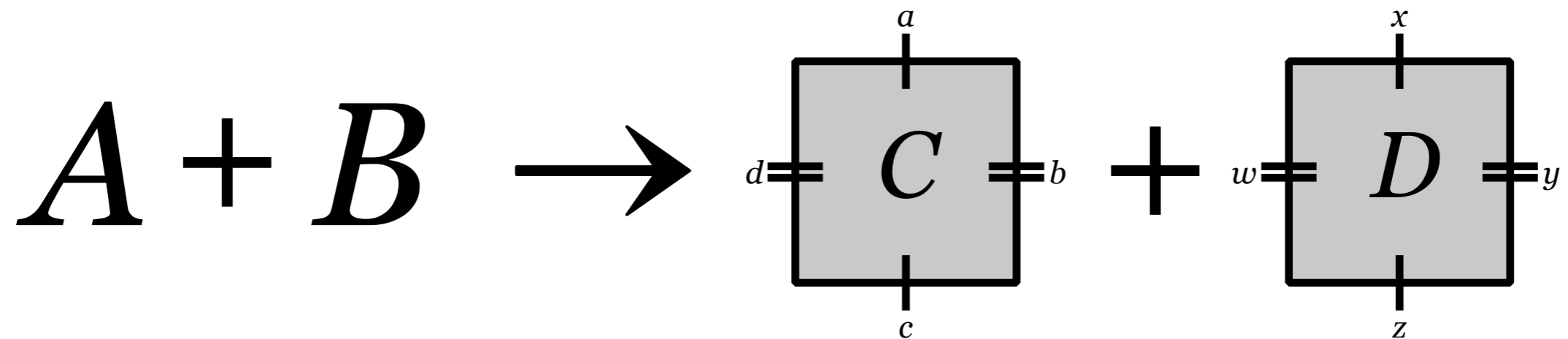
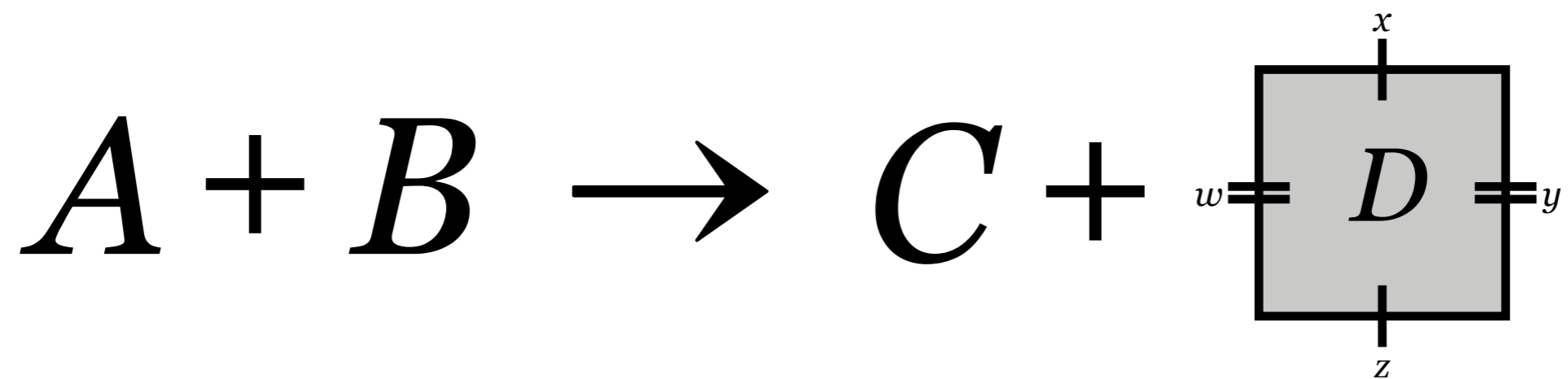
# Chemical Reaction Network-Controlled Tile Assembly Model (CRN-TAM)

## Normal CRN reactions



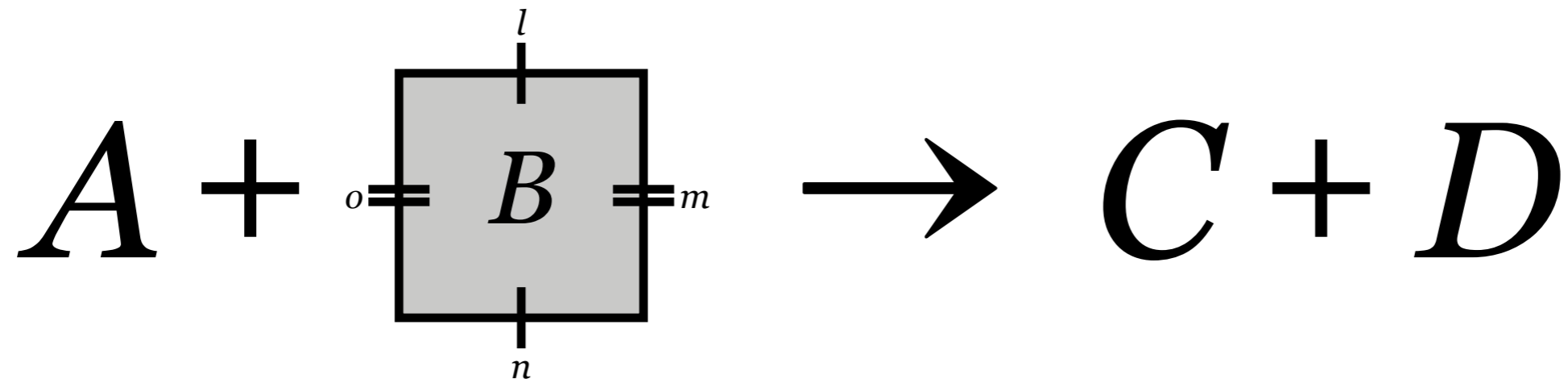
# Chemical Reaction Network-Controlled Tile Assembly Model (CRN-TAM)

## Creating tiles



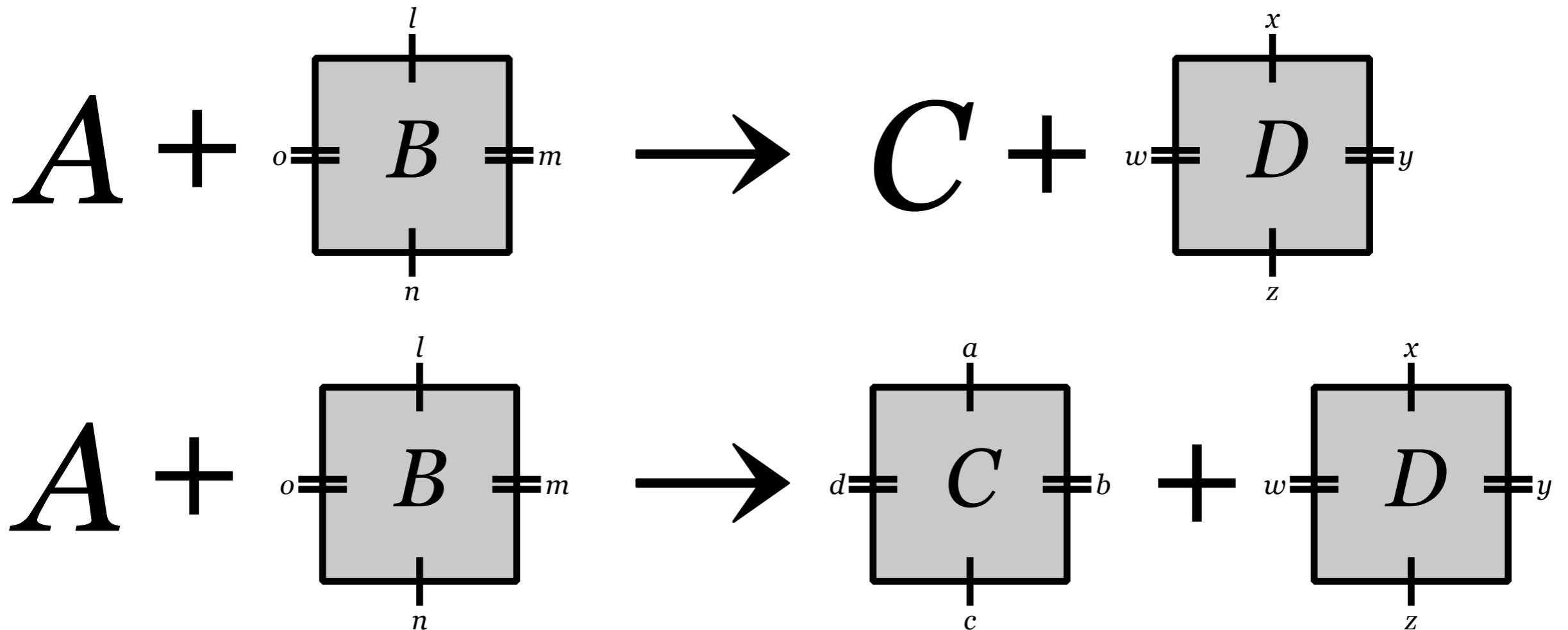
# Chemical Reaction Network-Controlled Tile Assembly Model (CRN-TAM)

## Deleting tiles



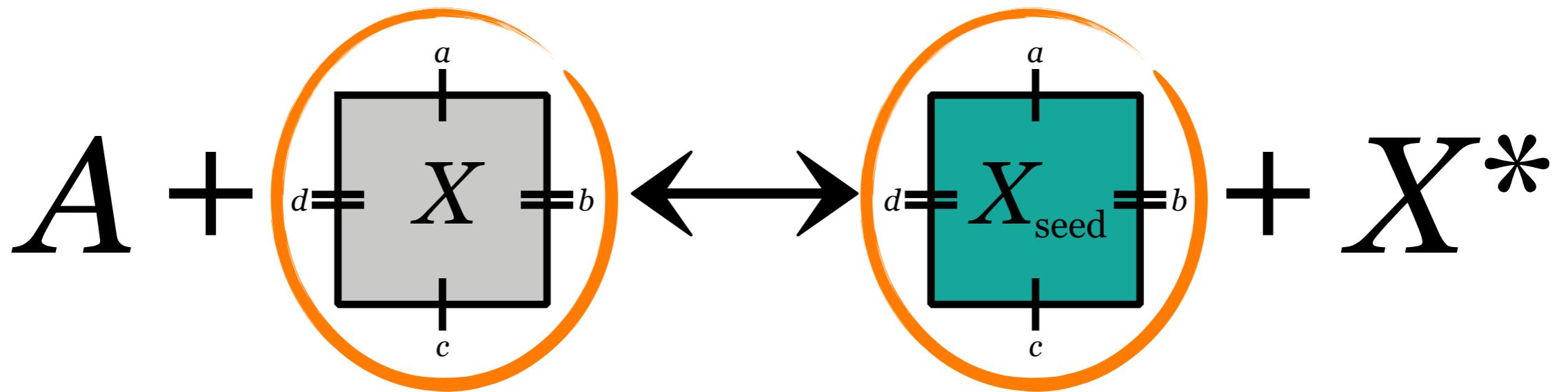
# Chemical Reaction Network-Controlled Tile Assembly Model (CRN-TAM)

## Relabelling tiles



# Chemical Reaction Network-Controlled Tile Assembly Model (CRN-TAM)

## Activating/deactivating tiles



“inactive” tile

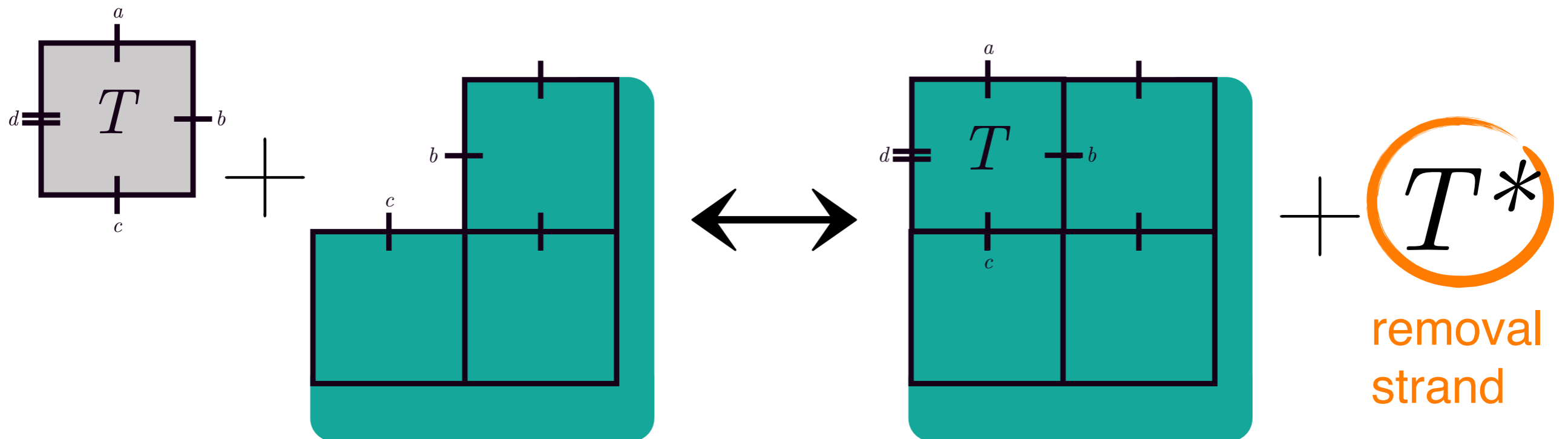
“active” seed assembly

Variable # of assemblies!



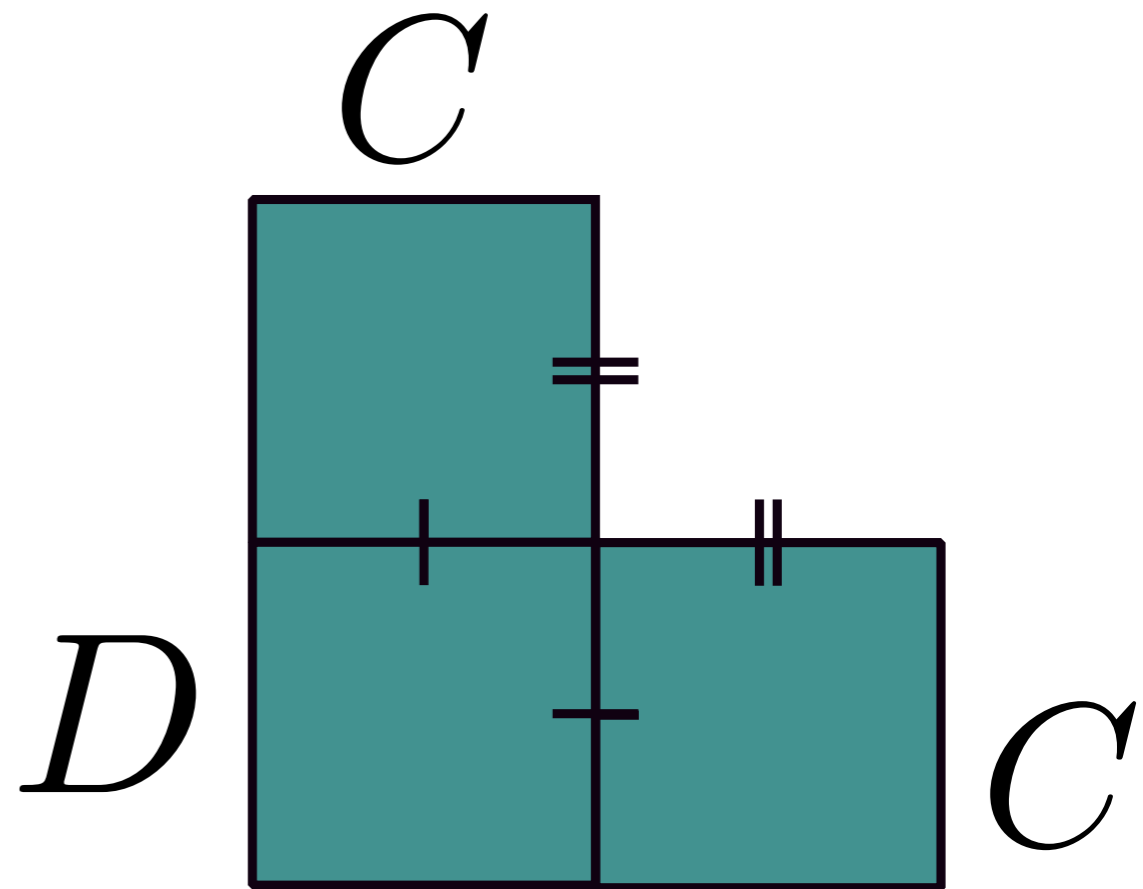
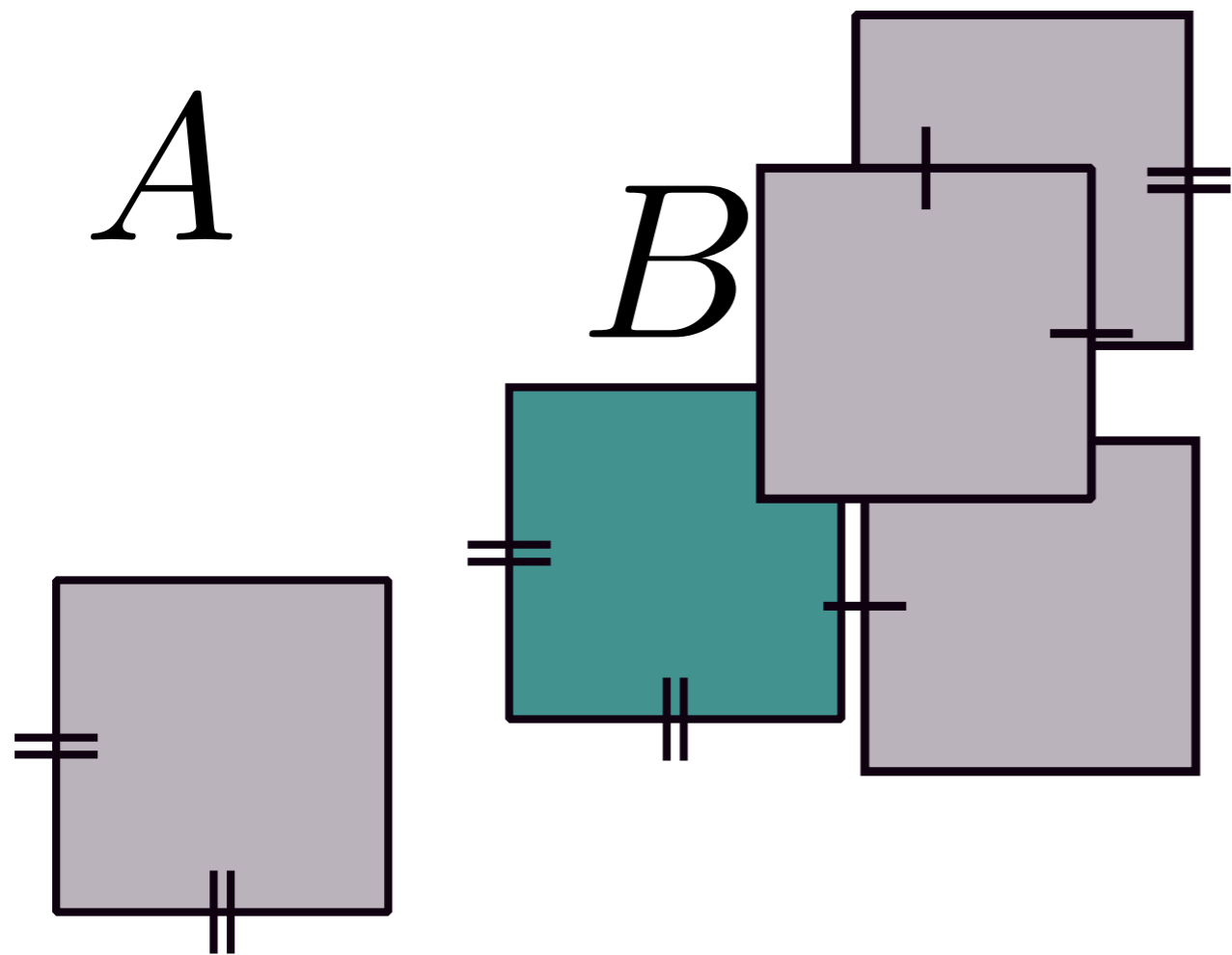
# Chemical Reaction Network-Controlled Tile Assembly Model (CRN-TAM)

## Tile attachment/detachment



Feedback from structure!

# Example



$$A + \begin{array}{|c|} \hline \text{=} \\ \hline \text{=} \\ \hline \end{array} \leftrightarrow \begin{array}{|c|} \hline \text{=} \\ \hline \text{=} \\ \hline \end{array} + B$$

$$C + C \rightarrow \begin{array}{|c|} \hline \text{+} \\ \hline \text{-} \\ \hline \end{array}$$

$$B \rightarrow \begin{array}{|c|} \hline \text{+} \\ \hline \text{-} \\ \hline \end{array} + \begin{array}{|c|} \hline \text{-} \\ \hline \text{=} \\ \hline \end{array}$$

$$D \rightarrow$$

# Program Complexity

number of signals of reactions

$$K_{CT}^T(P) = |S| + |T| + |R| + |I| \text{ size of initial state}$$
$$\equiv |S| + |T| + |R| + \sum_{z \in (S \cup T)} \log(I(z) + 1)$$

# Building skinny shapes

[pattern designed by Kevin Li, software by S]

Current assembly



binary  
counter

CRN species

Main

North

East

South

West

Time



# Turing Machines

**Theorem.** The CRN-TAM is Turing-universal at temperature  $\tau = 2$ .

*Proof.* The aTAM is Turing-universal at temperature  $\tau = 2$ .

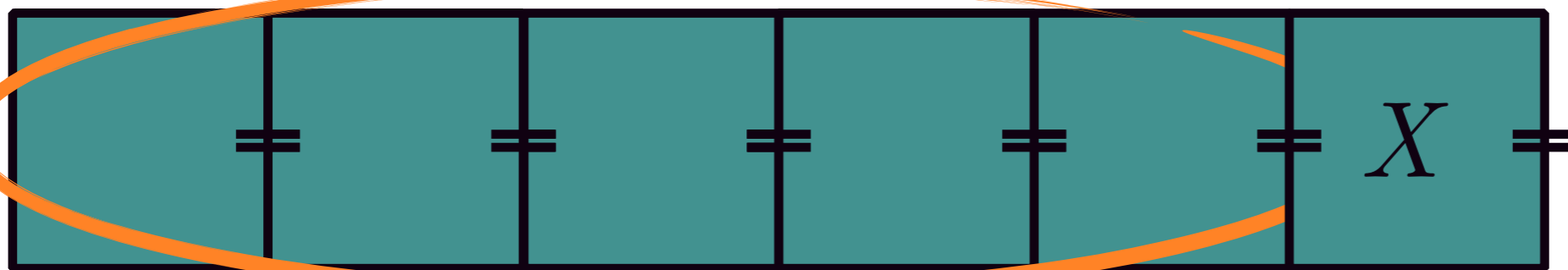
(Simulation of computation histories)

Requires  $\Omega(s \times t)$  space!

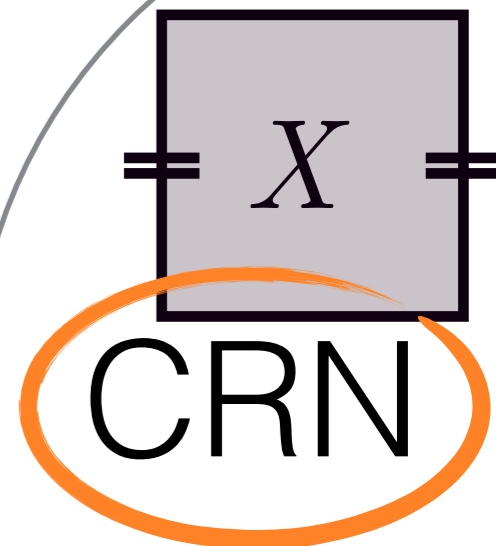
(Probably) requires temp. 2!

# Stack Machines

## Push operation



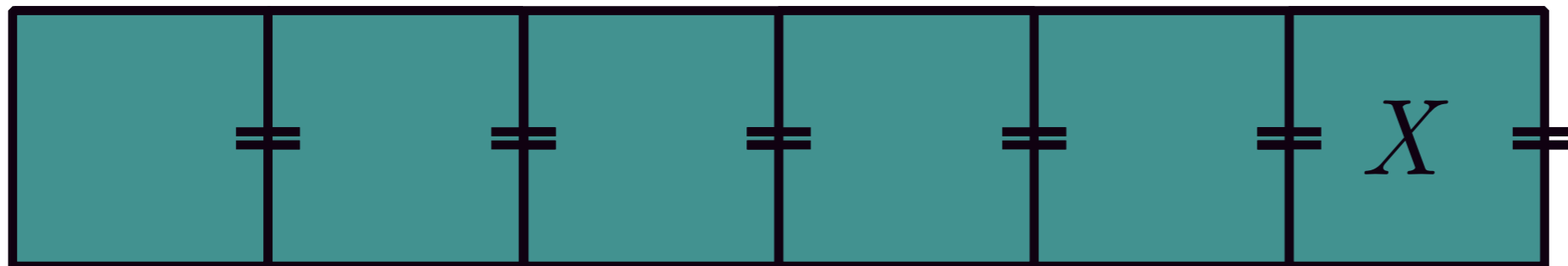
stack encoded as linear assembly  $X^*$  finite state encoded in the CRN



**Theorem.** Turing machines  $\Leftrightarrow$  multi-stack machines.

# Stack Machines

## Pop operation



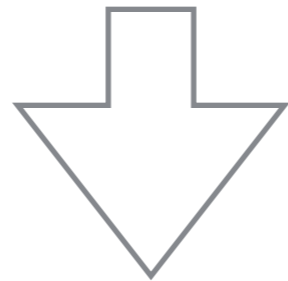
CRN

$X^*$

**Theorem.** Turing machines  $\Leftrightarrow$  multi-stack machines.

# Stack Machines

**Theorem.** Turing machines  $\Leftrightarrow$  multi-stack machines.



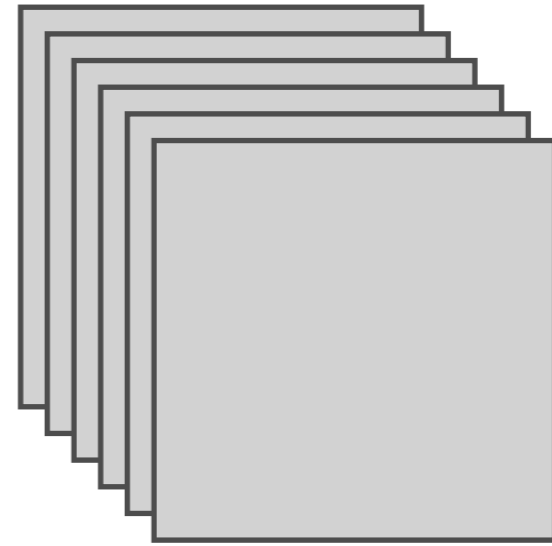
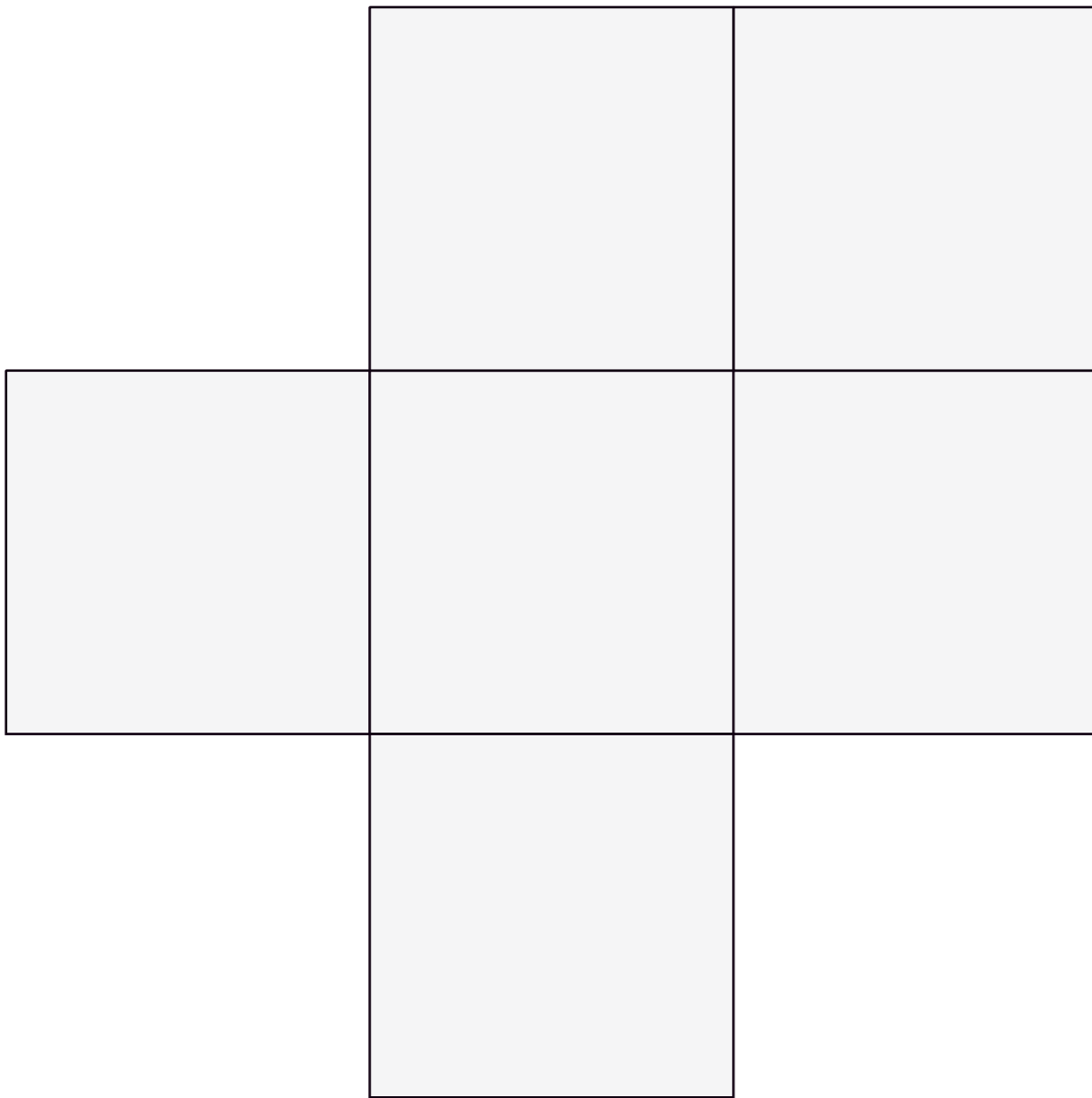
**Theorem.** The CRN-TAM is Turing universal at all temperatures  $\tau \geq 1$  using  $\mathcal{O}(1)$  space in one dimension.

Only  $\Theta(s)$  space!

Temperature 1!



# Finite Shape Construction



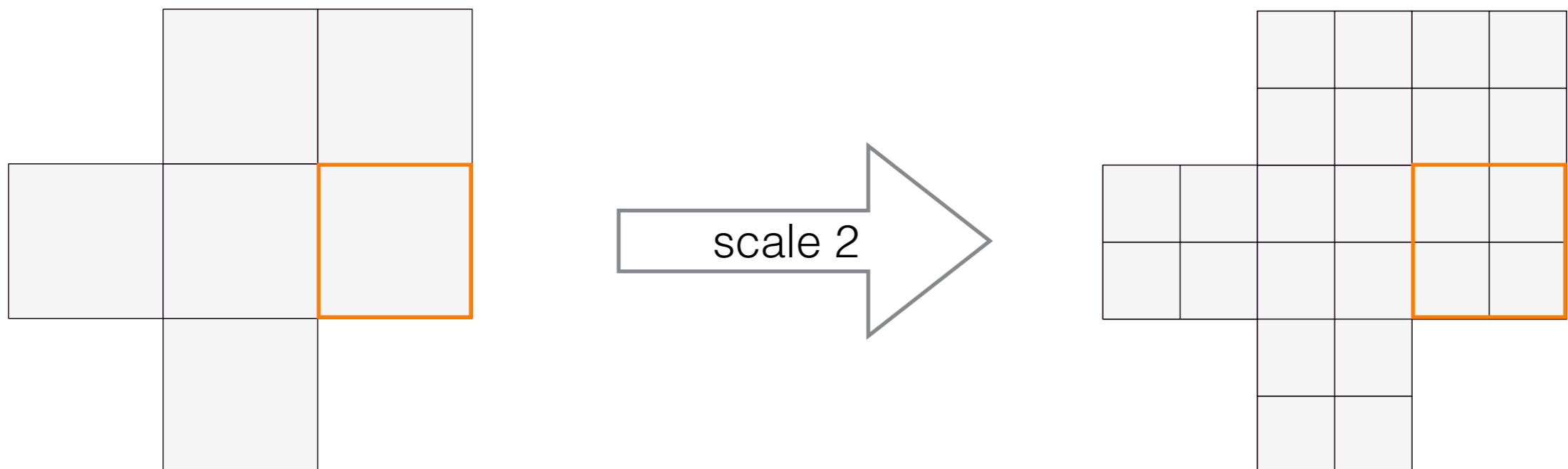
# Shape Construction in the aTAM

**Theorem.** For any shape  $\mathcal{S}$ , there is an aTAM tile set  $T$  that constructs  $\mathcal{S}$  at some scale such that

$$|T| \in \Theta \left( \frac{K_U(\mathcal{S})}{\log K_U(\mathcal{S})} \right)$$

[Soloveichik and Winfree, 2007]

conversion from “bits” to “tiles”



# Shape Construction in the aTAM

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[Soloveichik and Winfree, 2007]

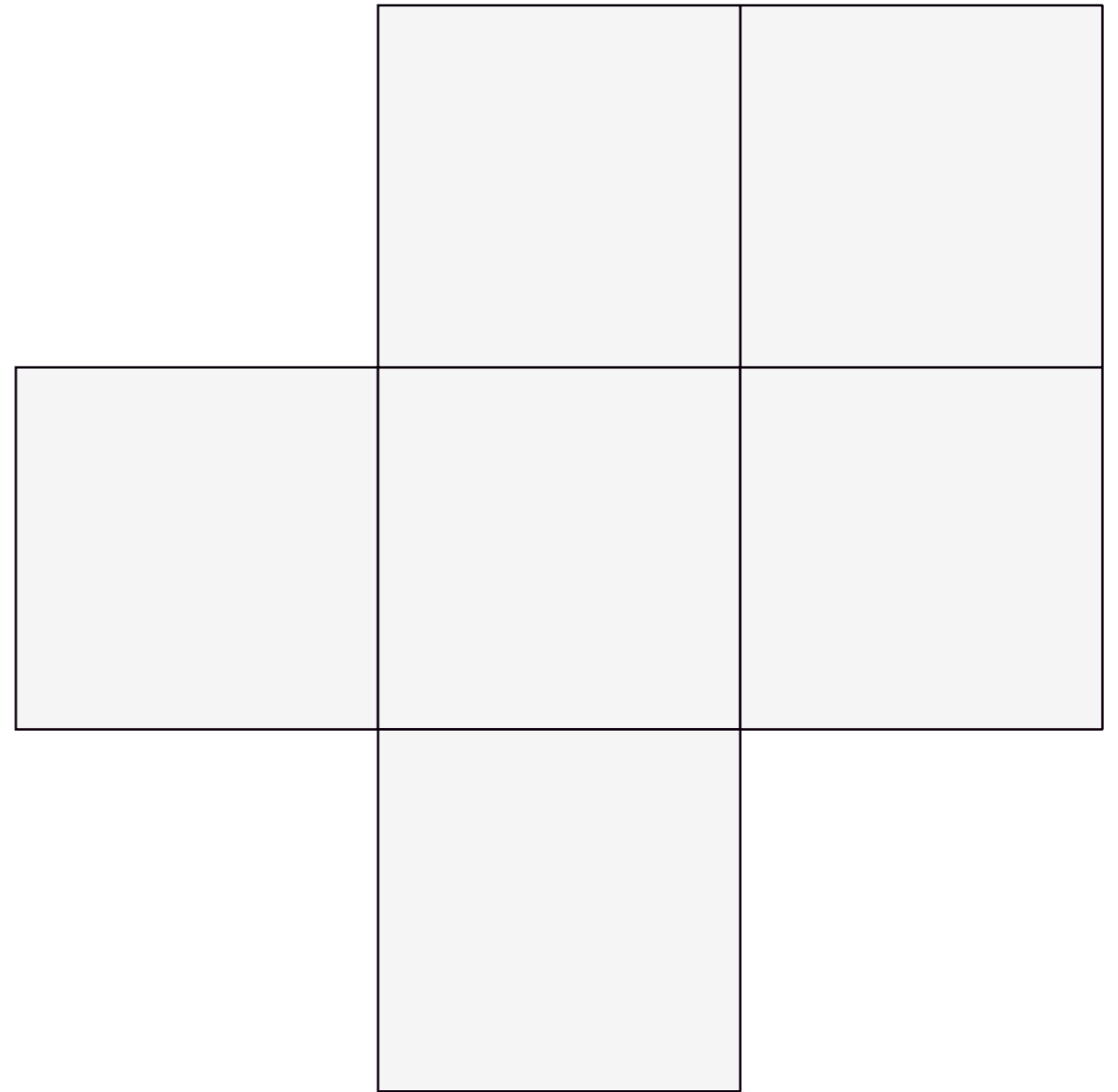
Huge scale = huge shapes!

# Shape Construction in the CRN-TAM

## CRN-TAM complexity

$$K_{\text{CT}}^{\tau}(\mathcal{S}) =$$

size of the smallest  
CRN-TAM program  
that constructs  $\mathcal{S}$



# Shape Construction in the CRN-TAM

**Theorem.** For any shape  $\mathcal{S}$ , the CRN-TAM complexity of  $\mathcal{S}$  at **scale 2** and any temperature  **$\tau \geq 1$**  is:

$$K_{CT}^\tau(\text{scale}_2(\mathcal{S})) \in \Theta\left(\frac{K_U(\mathcal{S})}{\log K_U(\mathcal{S})}\right)$$

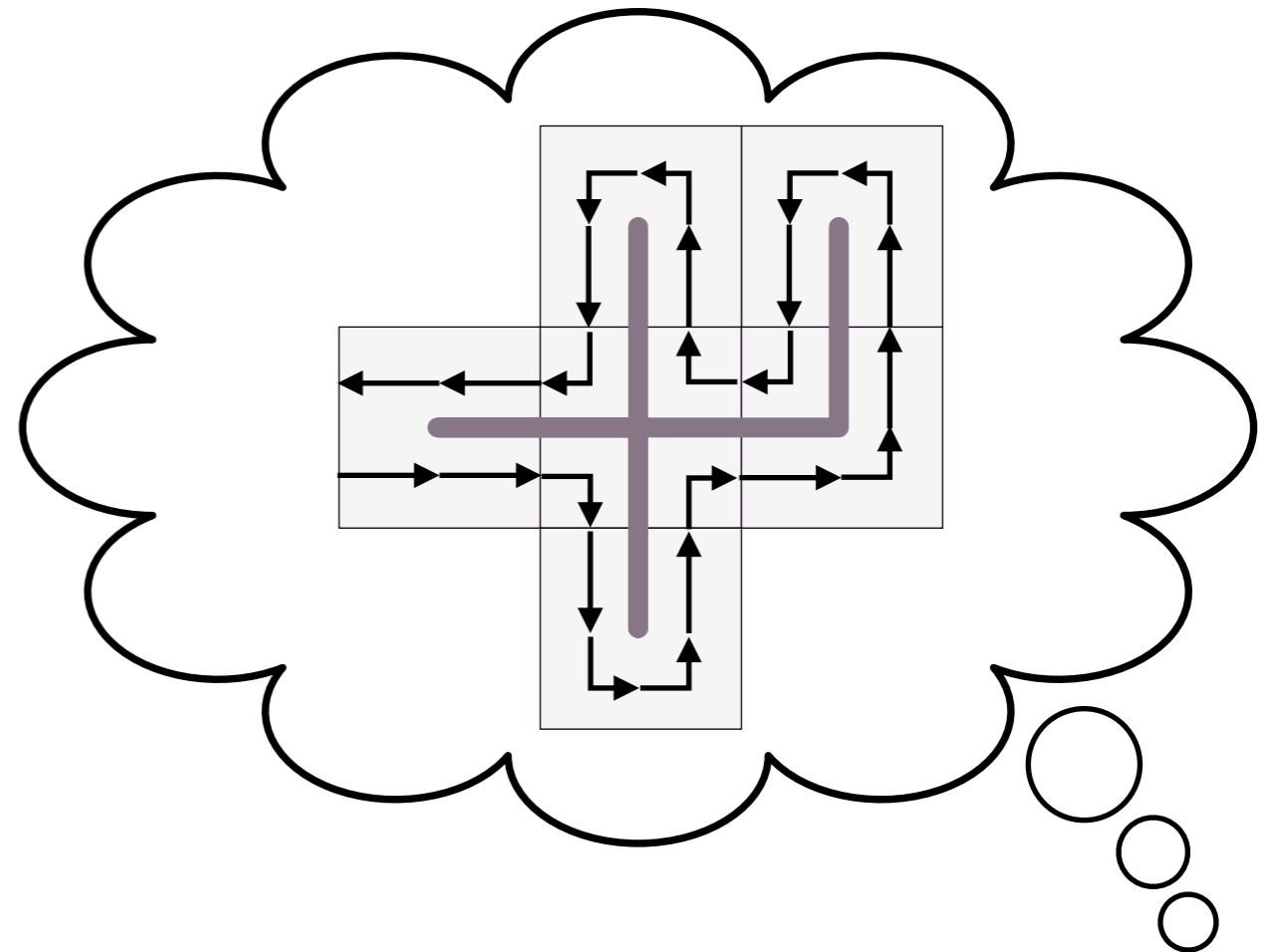
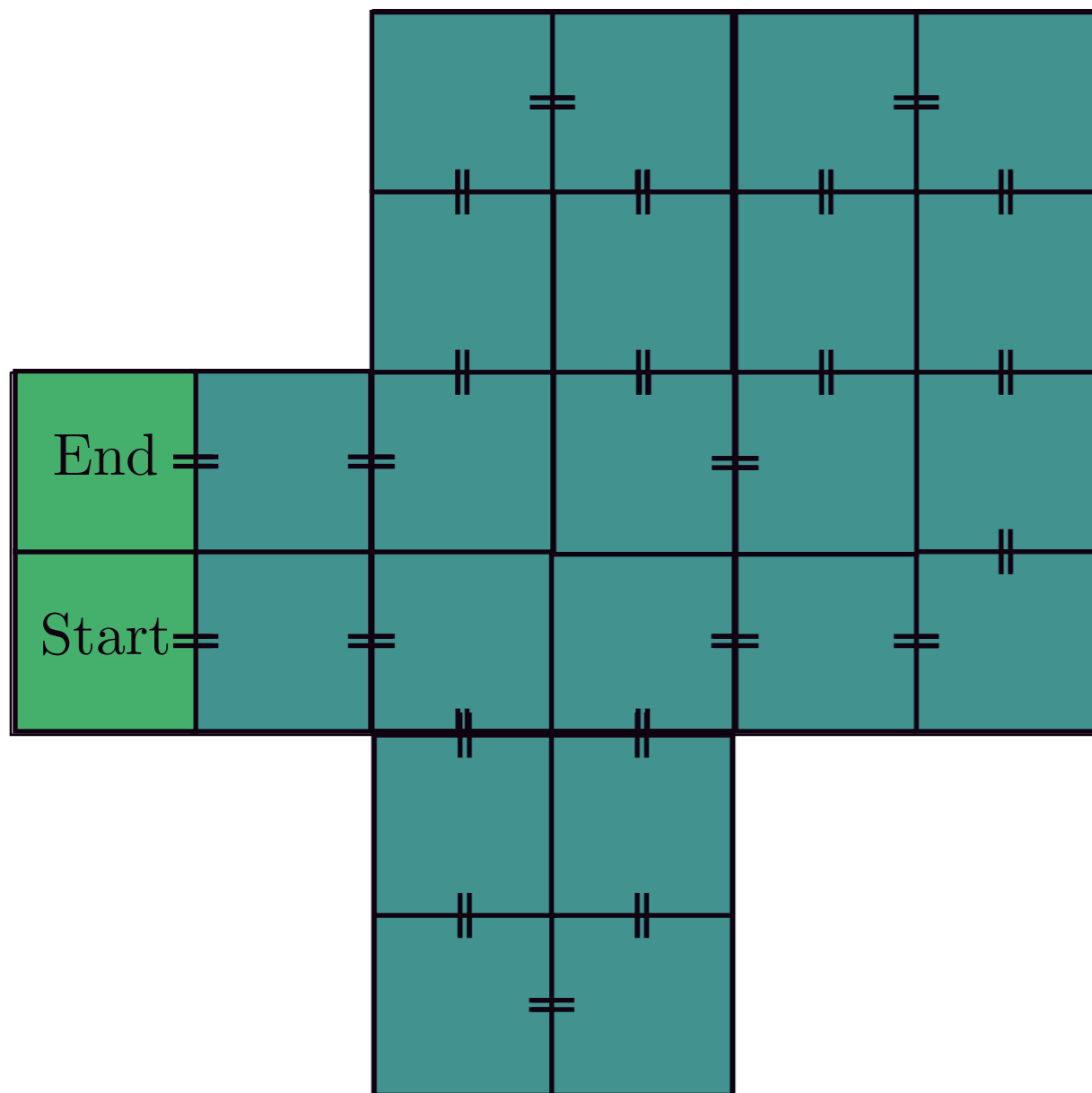
[S and Winfree, 2015]

same conversion from “bits” to “CRN-TAM complexity”

Constant scale!

Temperature 1!

# Shape Construction in the CRN-TAM



010010000100001010101010001010

program outputting  $S$

Universal Turing  
Machine

# Shape Construction in the CRN-TAM

## Program components

Universal Turing machine (constant complexity)

Path tiles (constant complexity)

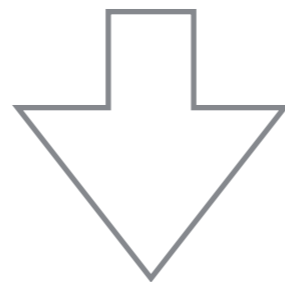
Depth-first search (constant complexity)

**Universal Turing machine program ( $K_U(\mathcal{S})$  bits)**

**Theorem.** A binary string of length  $n$  can be encoded in a (temperature 1) CRN-TAM program with complexity  $\Theta(n/\log n)$ .

# Shape Construction in the CRN-TAM

**Theorem.** A binary string of length  $n$  can be encoded in a (temperature 1) CRN-TAM program with complexity  $\Theta(n/\log n)$ .



**Theorem.** For any shape  $\mathcal{S}$ , the CRN-TAM complexity of  $\mathcal{S}$  at scale 2 and any temperature  $\tau \geq 1$  is:

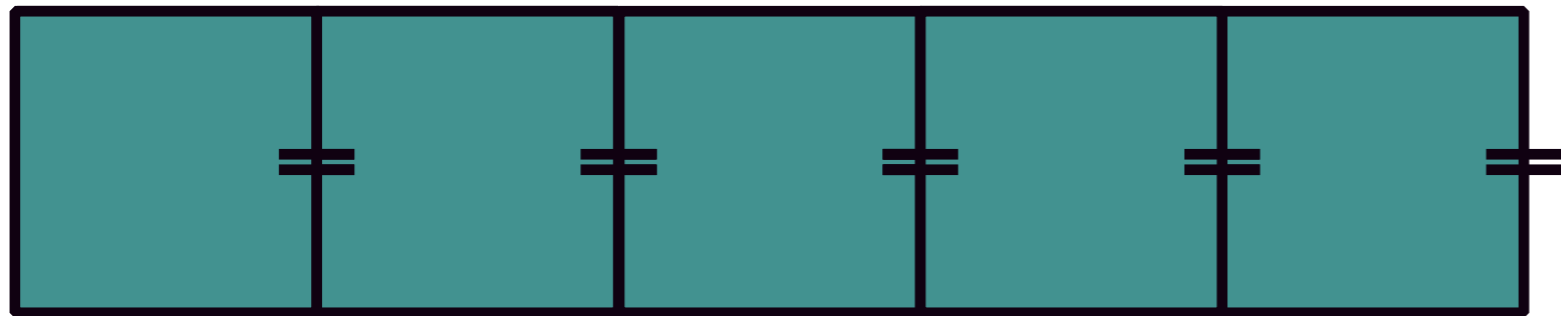
$$K_{\text{CT}}^{\tau}(\text{scale}_2(\mathcal{S})) \in \Theta \left( \frac{K_U(\mathcal{S})}{\log K_U(\mathcal{S})} \right)$$



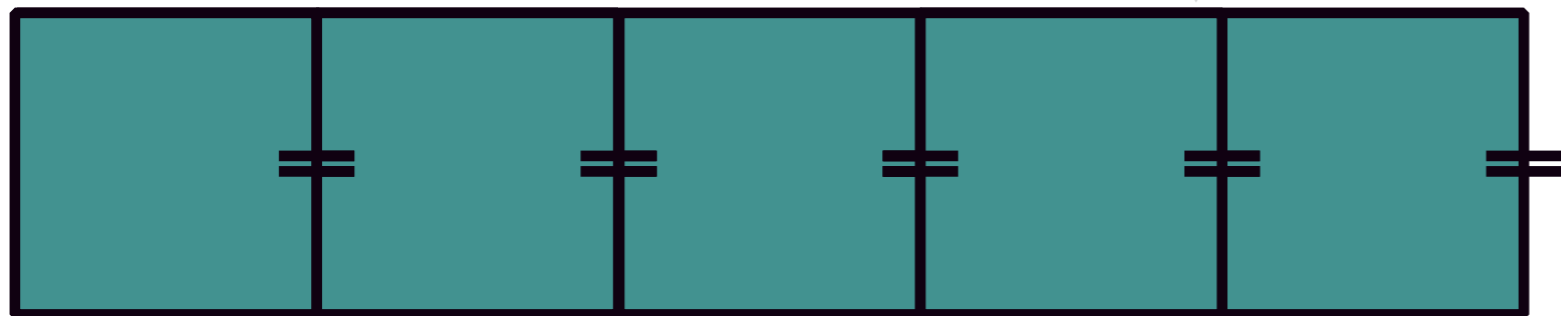
# Parallelism in the CRN-TAM

Previous constructions  
were carefully engineered  
to avoid parallelism!

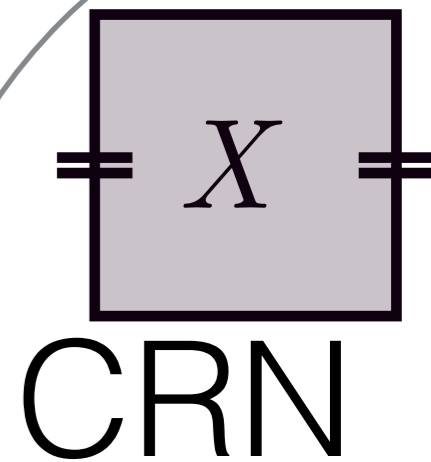
# A problem with stack machines...



same tile species



?



Shared state = limited parallelism!

# A problem with stack machines...

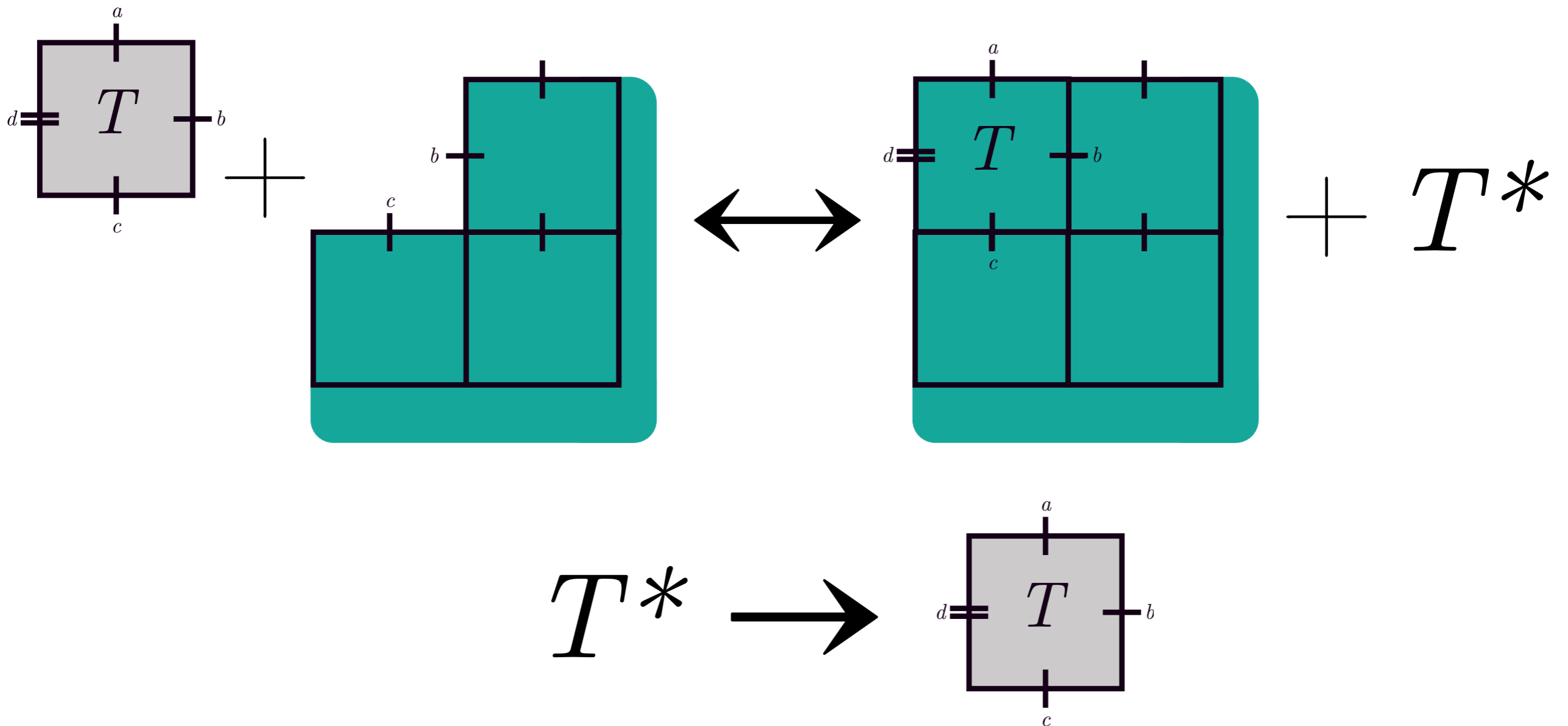
**Definition.** A CRN-TAM program that decides a language is *scalable* if it still works with arbitrarily many copies in the same reaction vessel.

**Theorem.** Every scalable CRN-TAM program uses  $\Omega(t(n))$  space to simulate a Turing machine that takes time  $t(n)$ .

“Stack machines” are not scalable!

# Computation with Tiles

Maintaining  $\Theta(V)$  tiles of each type





# Time Complexity of Tile Computation

Seems straightforward to analyze, but...

Assembly process is asynchronous, so tiles could attach in any order!

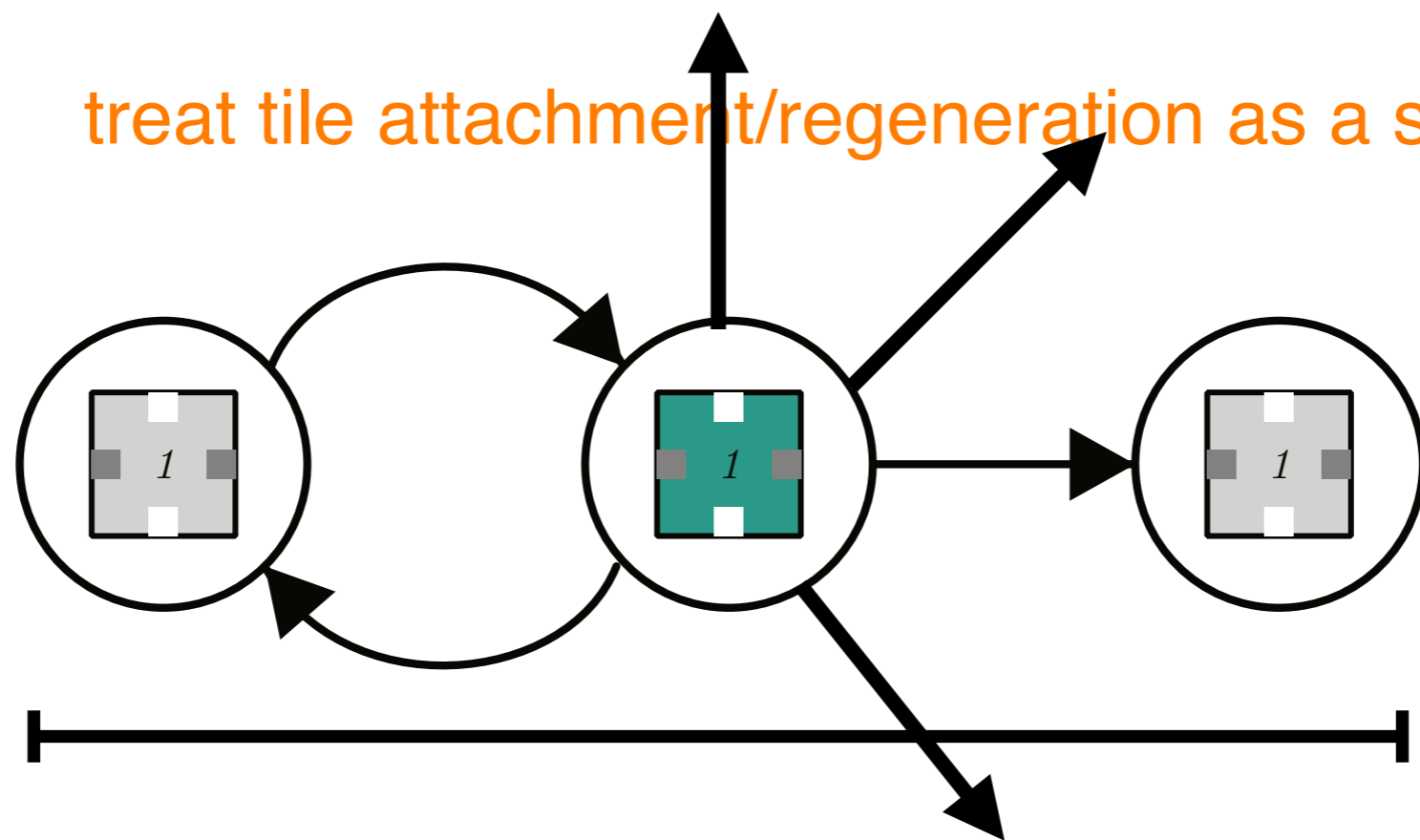
Tile consumption and re-generation could be delayed, so tile concentrations...

Don't know when assembly is complete before knowing the answer (just the last piece of the "backbone")!

**Absolute chaos!**

# Time Complexity of Tile Computation

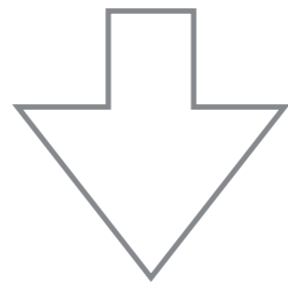
## Sentinel process



transit time has phase-type distribution (well studied)  
Restricting particular reactions only  
*increases* time complexity!

# Time Complexity of Tile Computation

**Theorem.** The sentinel process takes  $\Theta(t(n))$  time.



**Theorem.** CRN-TAM computation with tiles takes  $\Theta(t(n))$  time.

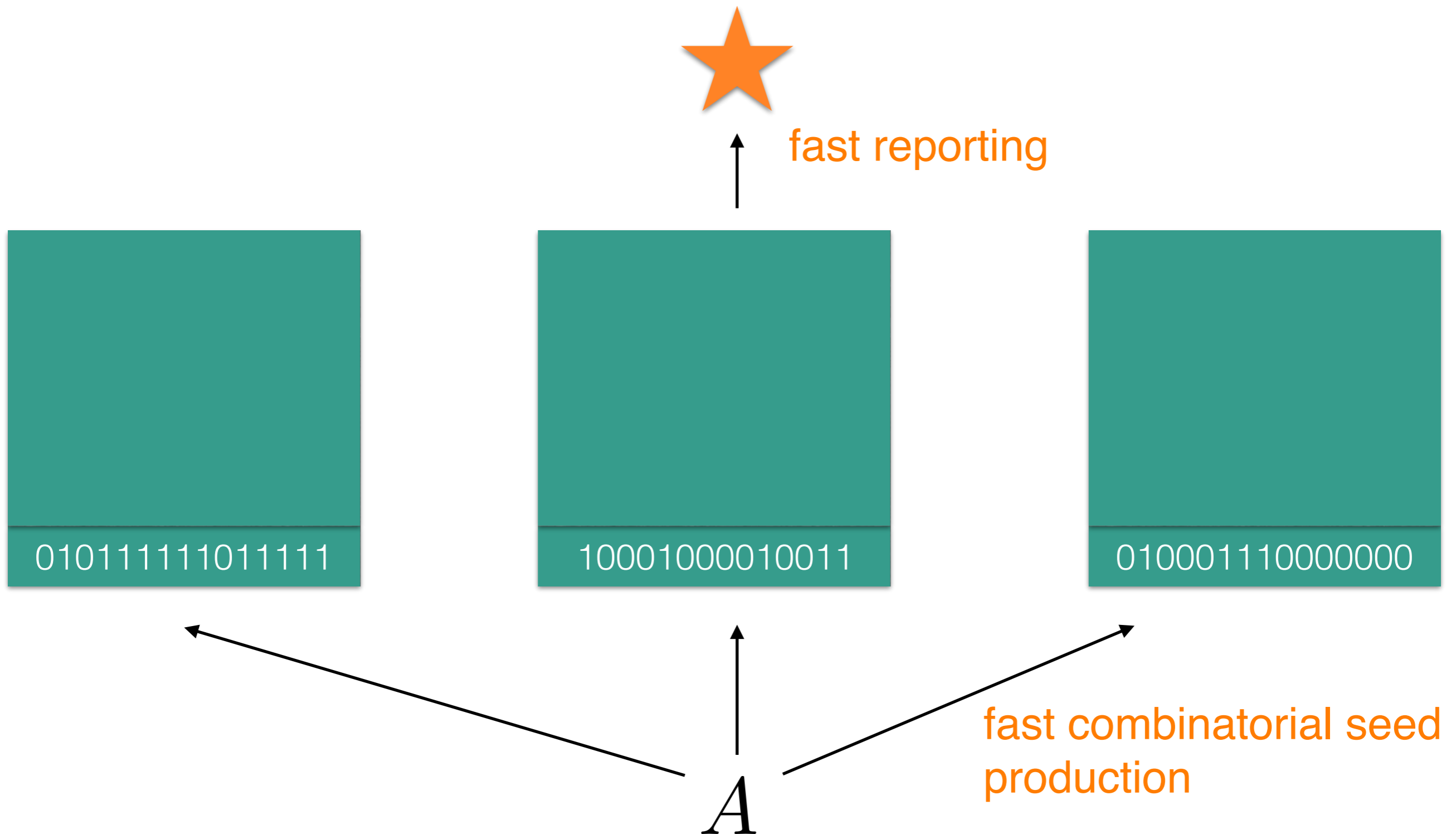
[S and Winfree, 2016]

Same time as stacks!

Scalable!



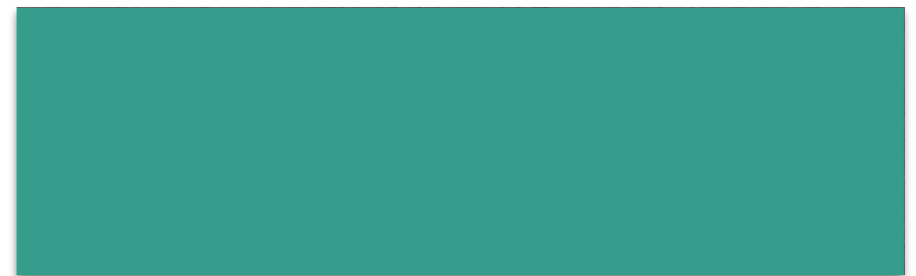
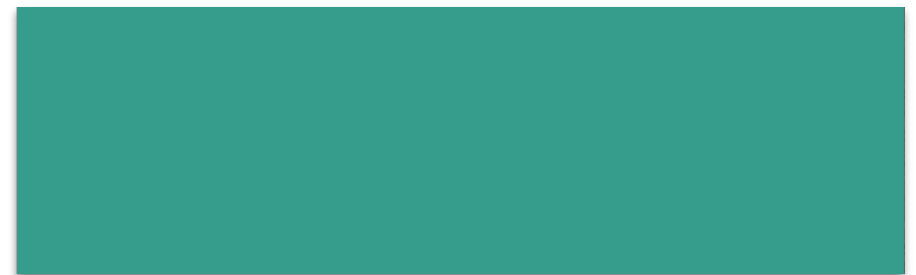
# Towards Parallel Computation



# Limits and Open Questions

## Message routing in a well-mixed CRN

*A*



What parallelism can/cannot be implemented in the CRN-TAM?

# Three perspectives

## Natural scientist

How does computation occur in the physical/biological world?

## Engineer

How can we use computational power in nanotechnology?

## Computer scientist

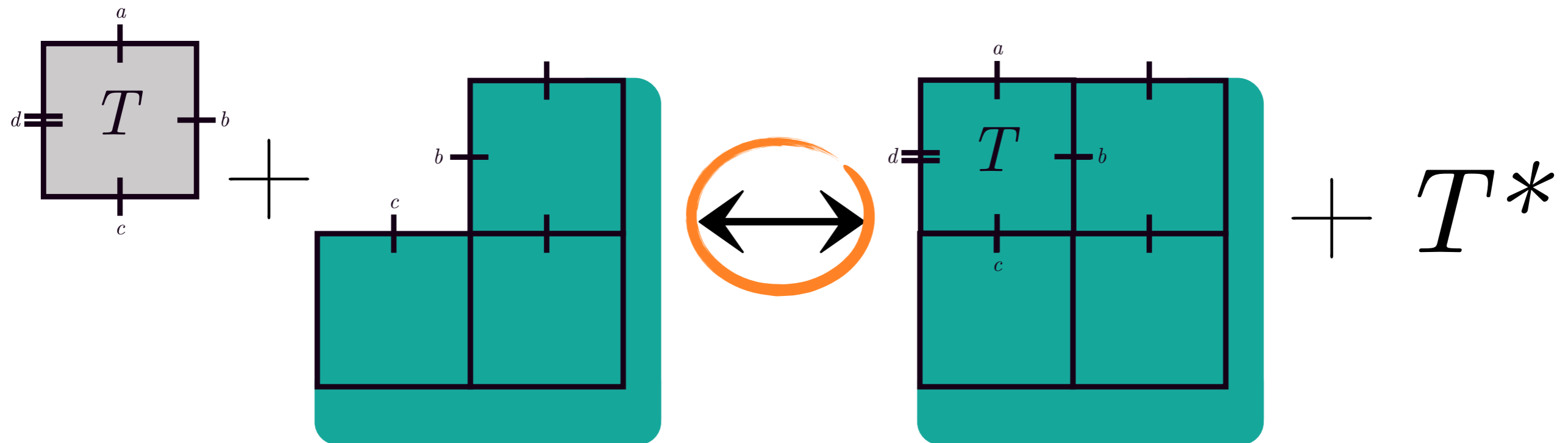
How can I compute using extremely simple systems?



Thanks!

# Chemical Reaction Network-Controlled Tile Assembly Model (CRN-TAM)

## Tile attachment/detachment



“reversible” based on binding strength  $b$

- 1) Attachment only if  $b \geq \tau$
- 2) Detachment only if  $b = \tau$