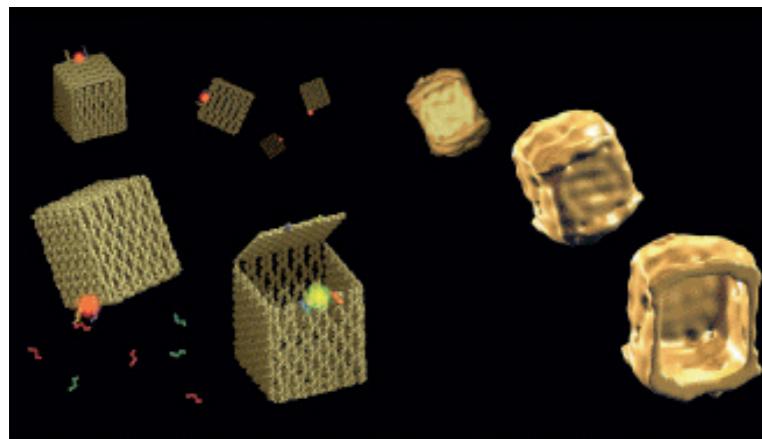


Oritatami: A computational model for cotranscriptional folding

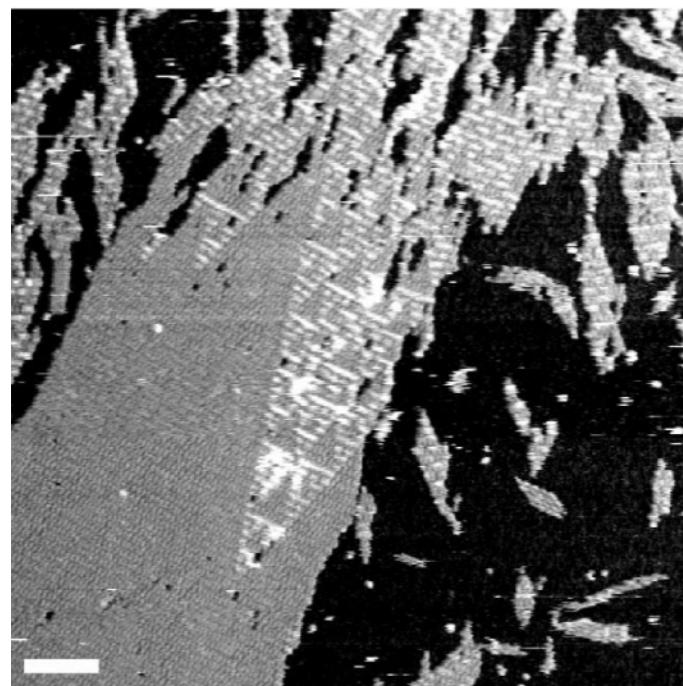
Nicolas Schabanel
CNRS - LIP, ENS Lyon & IXXI - France

Context: Biomolecular Computing & Engineering

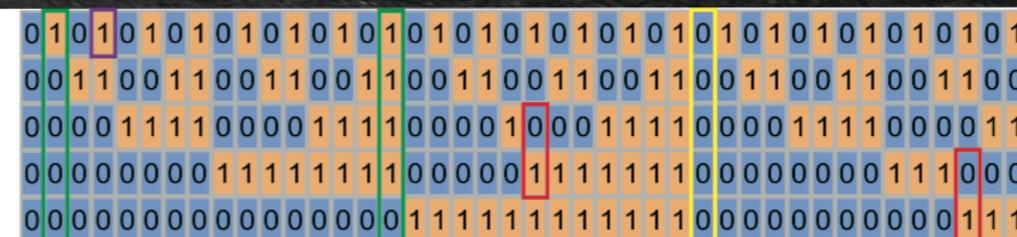
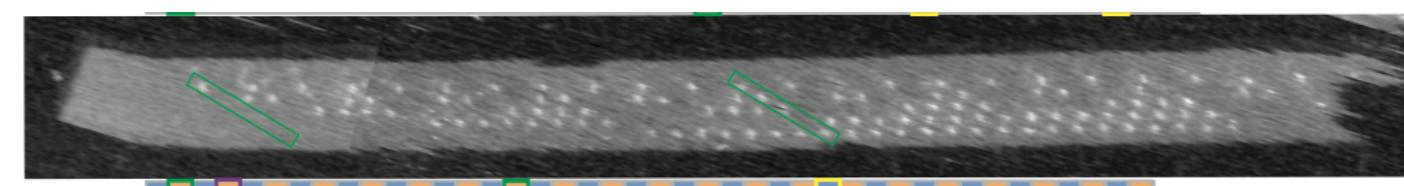
—~100 nm



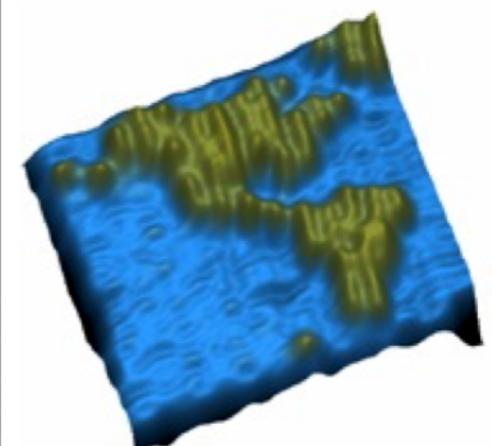
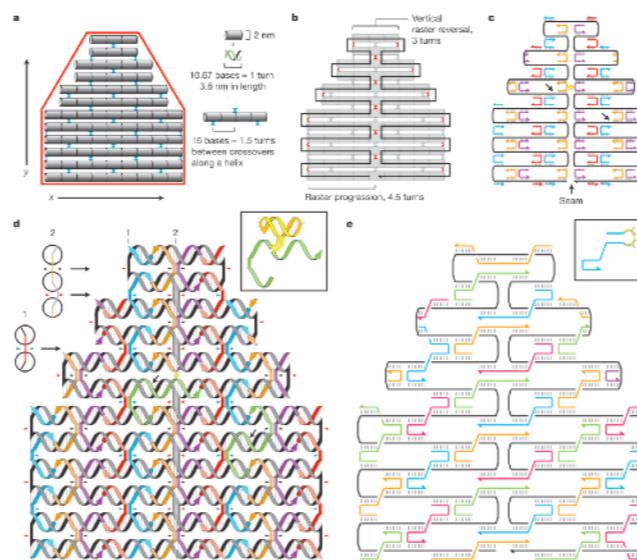
Andersen et al, 2009



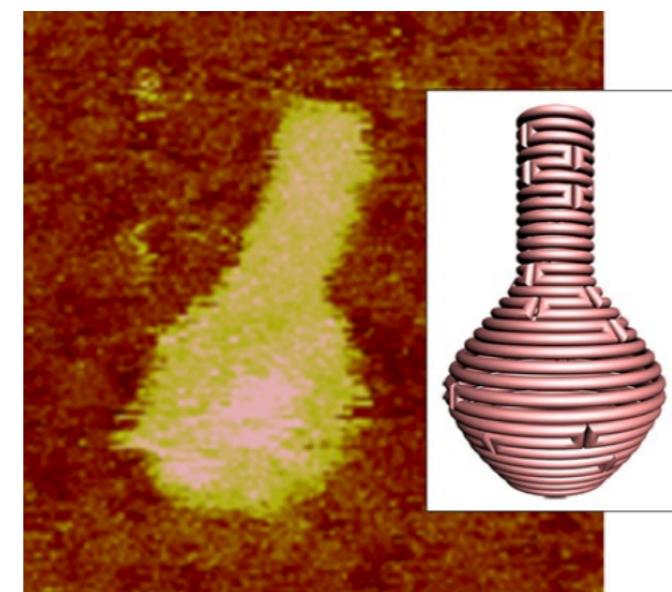
Fujibayashi et al, 2007



Constantine Evans, PhD Thesis, Caltech 2014



Rothenmund, Nature 2006



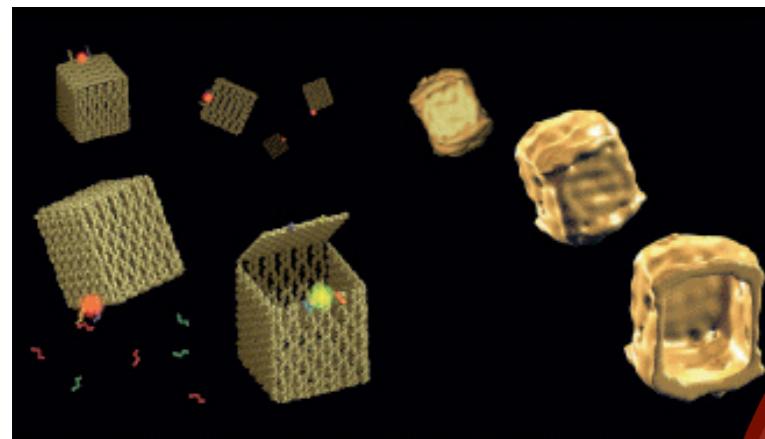
Han et al, Science 2011



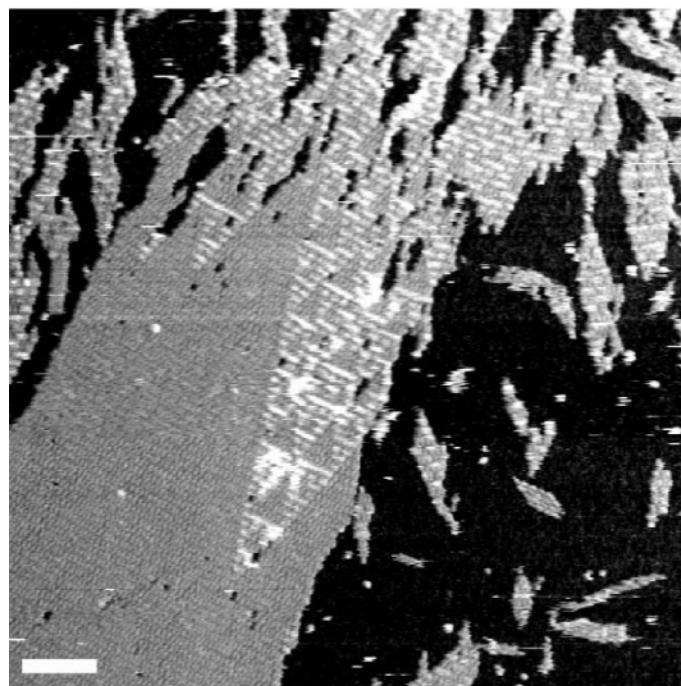
Wei, Dai, Yin, Nature 2013

Context: Biomolecular Computing & Engineering

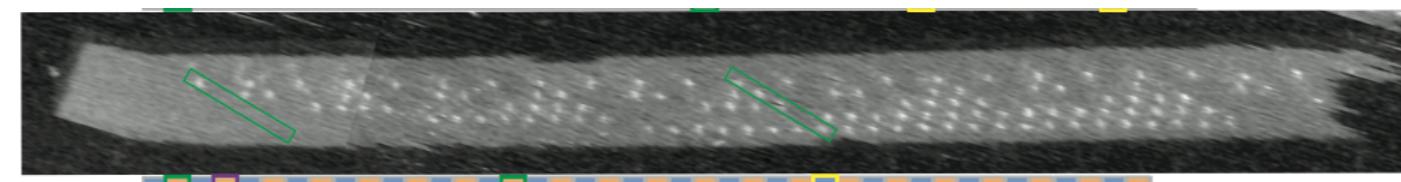
—~100 nm



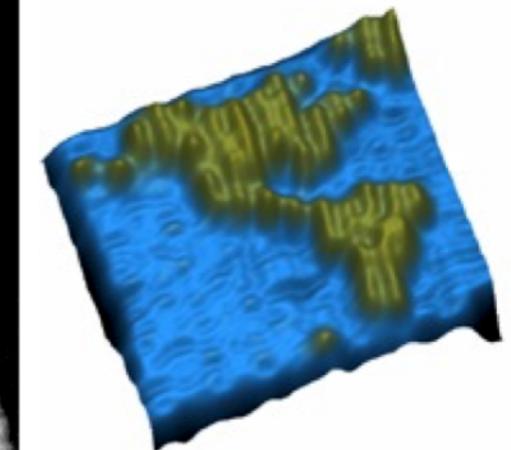
Andersen *et al*, 200



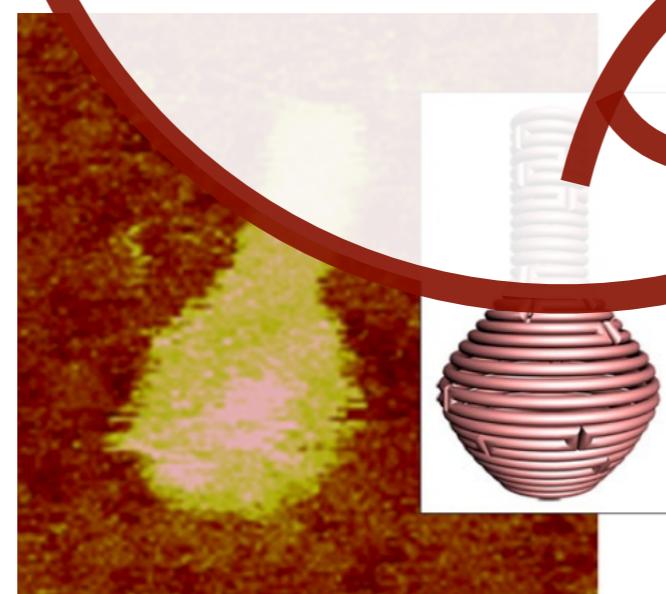
Fujibayashi *et al*, 2007



Constantine Evans, PhD Thesis, Caltech 2014



Rothenmund, Nature 2006

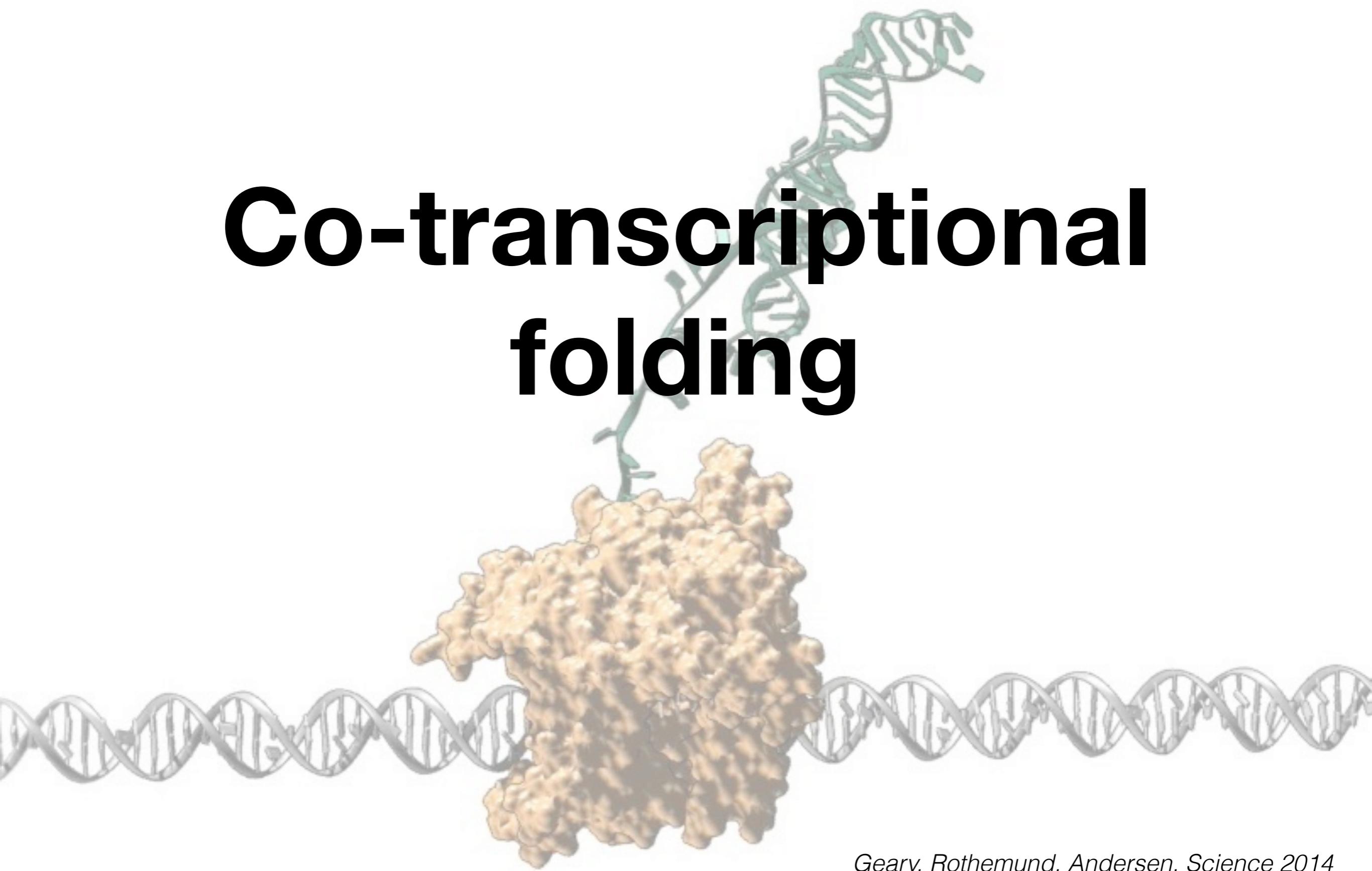


Han *et al*, Science 2011



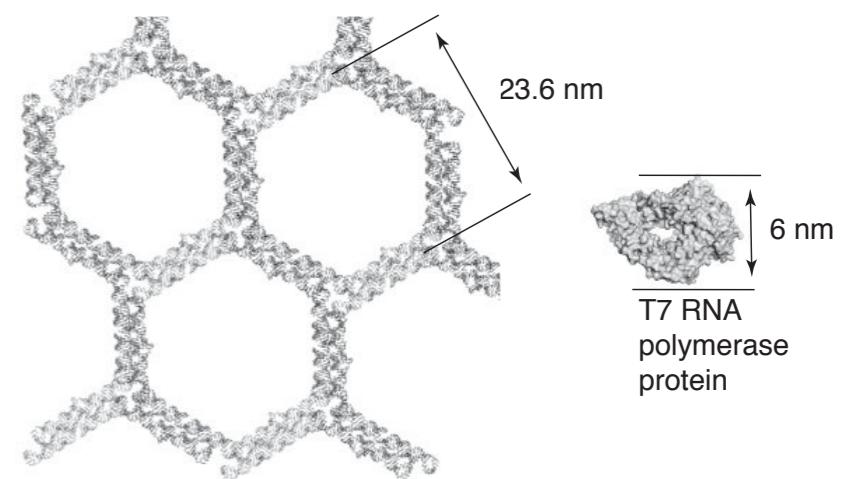
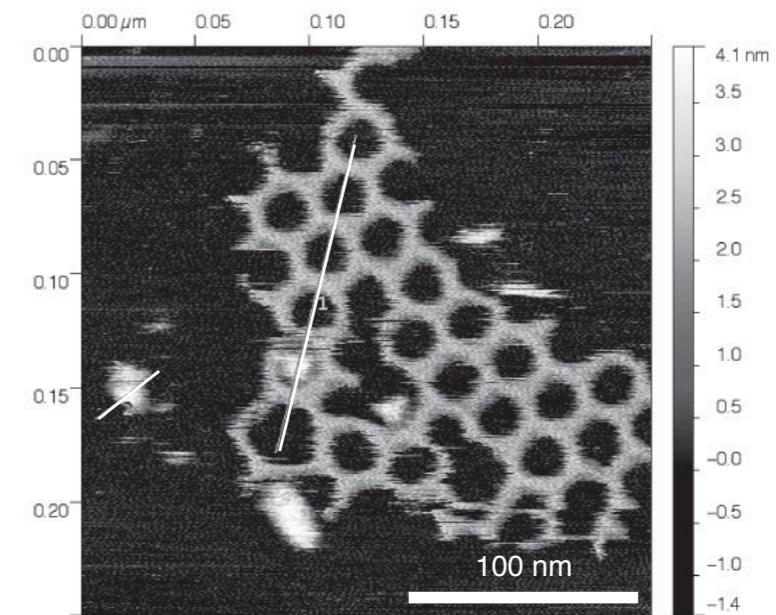
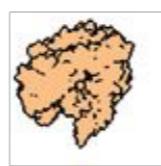
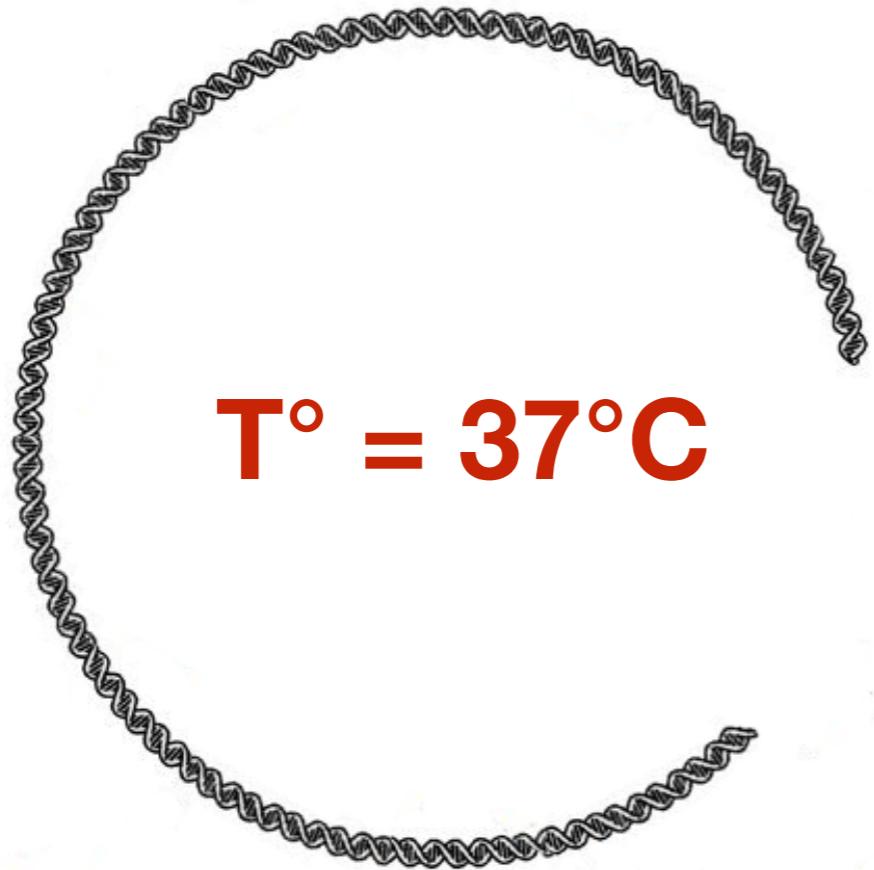
Wei, Dai, Yin, Nature 2013

Co-transcriptional folding



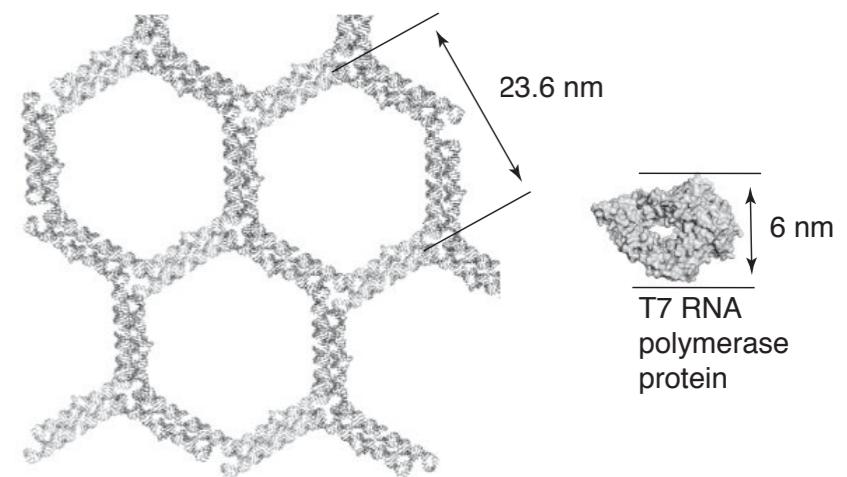
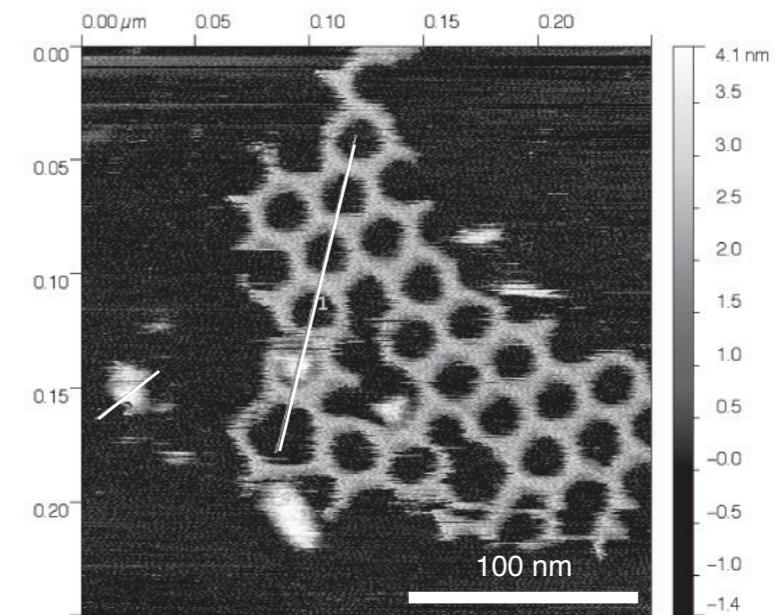
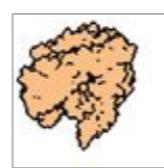
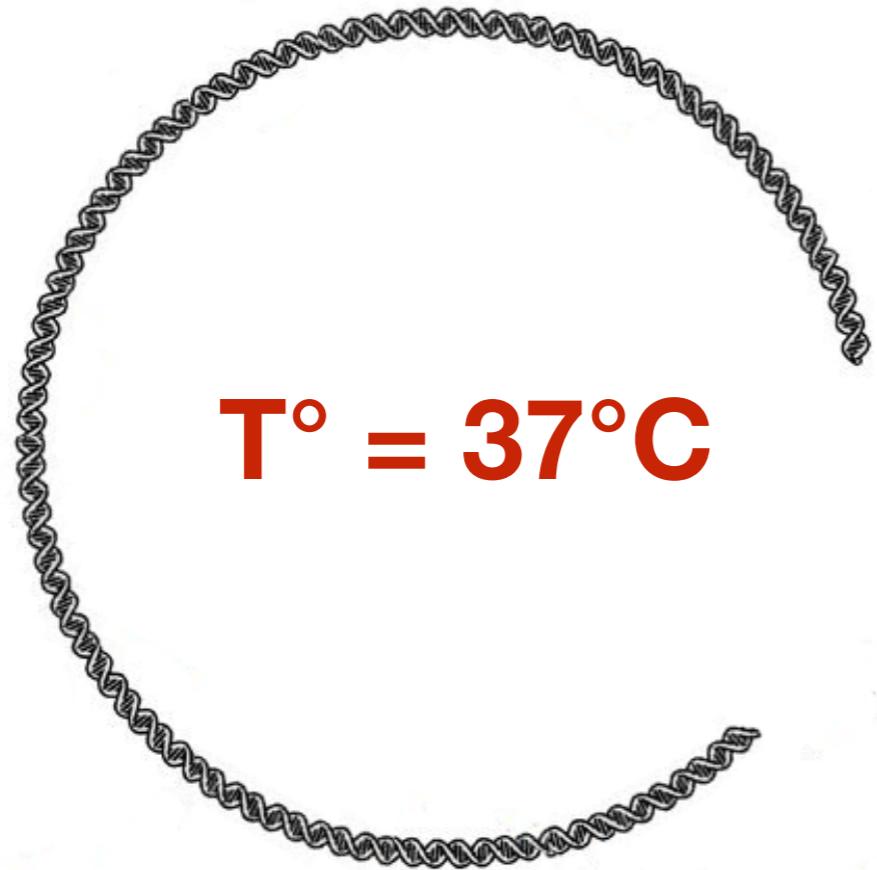
Geary, Rothenmund, Andersen, Science 2014

RNA co-transcriptional folding



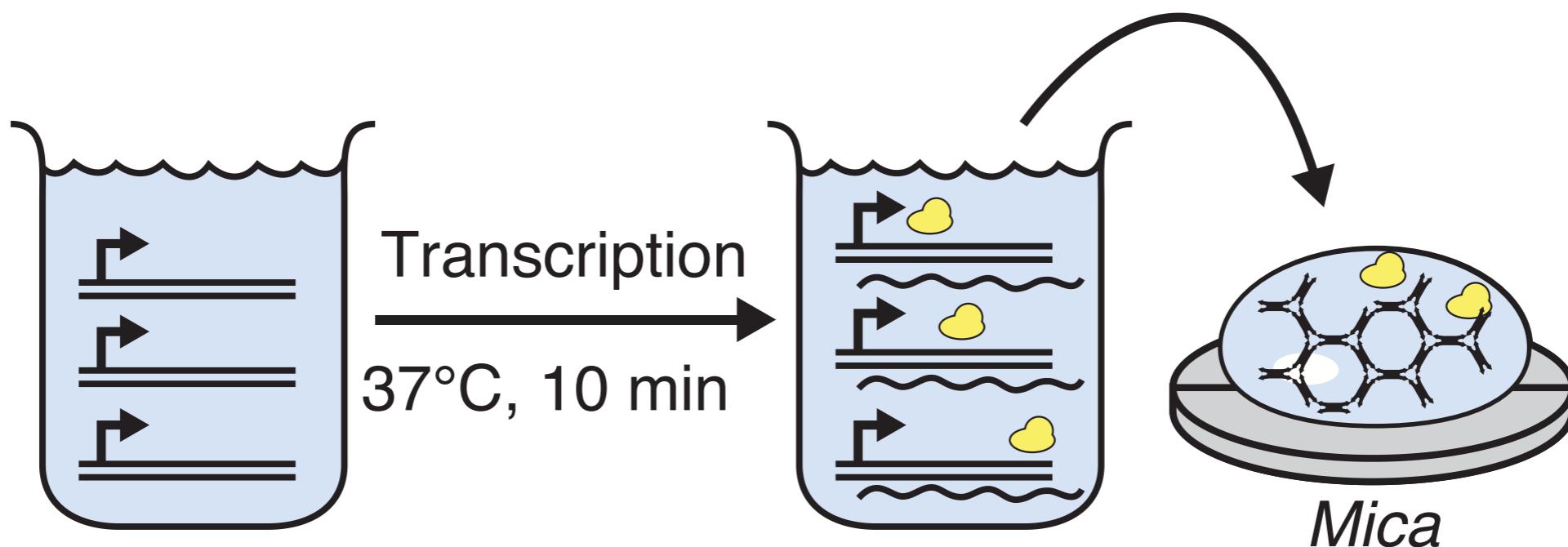
Geary, Rothemund, Andersen, Science 2014

RNA co-transcriptional folding

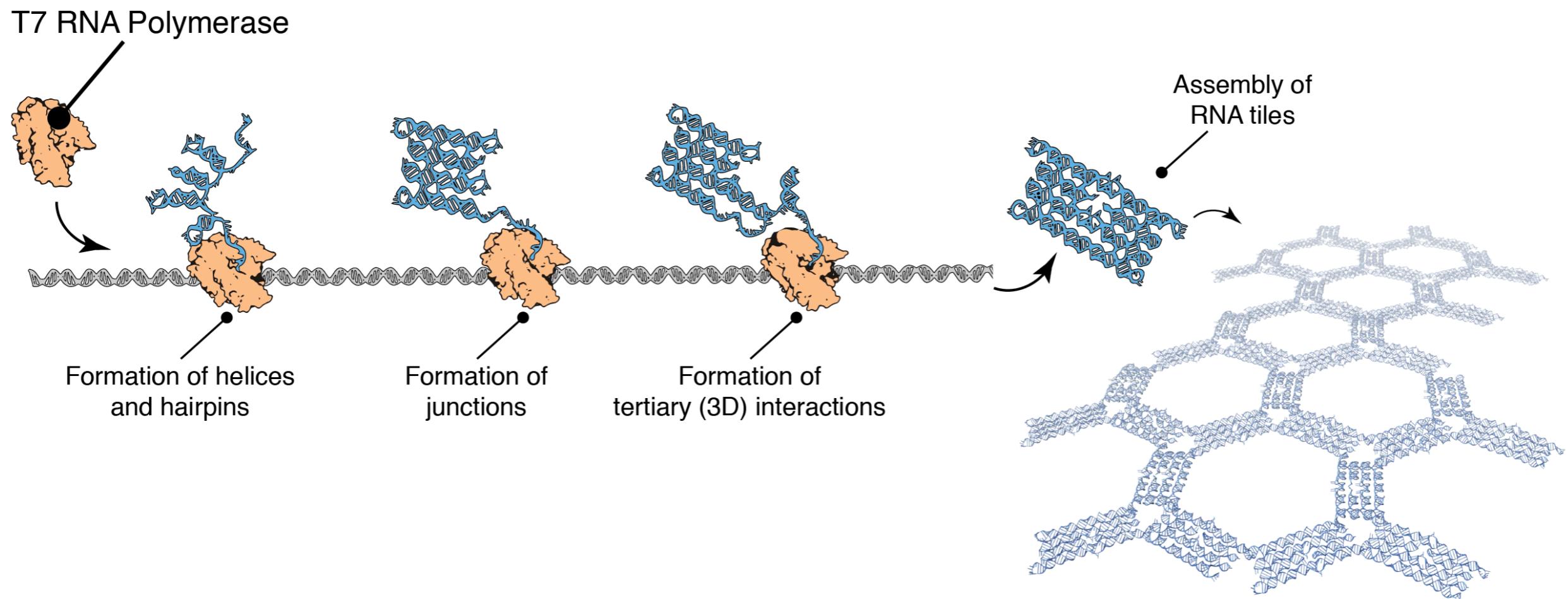


Geary, Rothemund, Andersen, Science 2014

Protocol



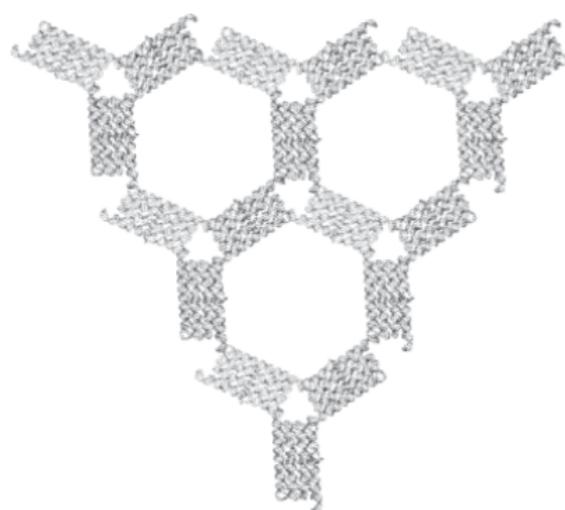
RNA Origami in Real Time



T7 RNA polymerase produces RNA directionally from 5' to 3', **at a rate much slower than the RNA folds up (few microseconds)**.

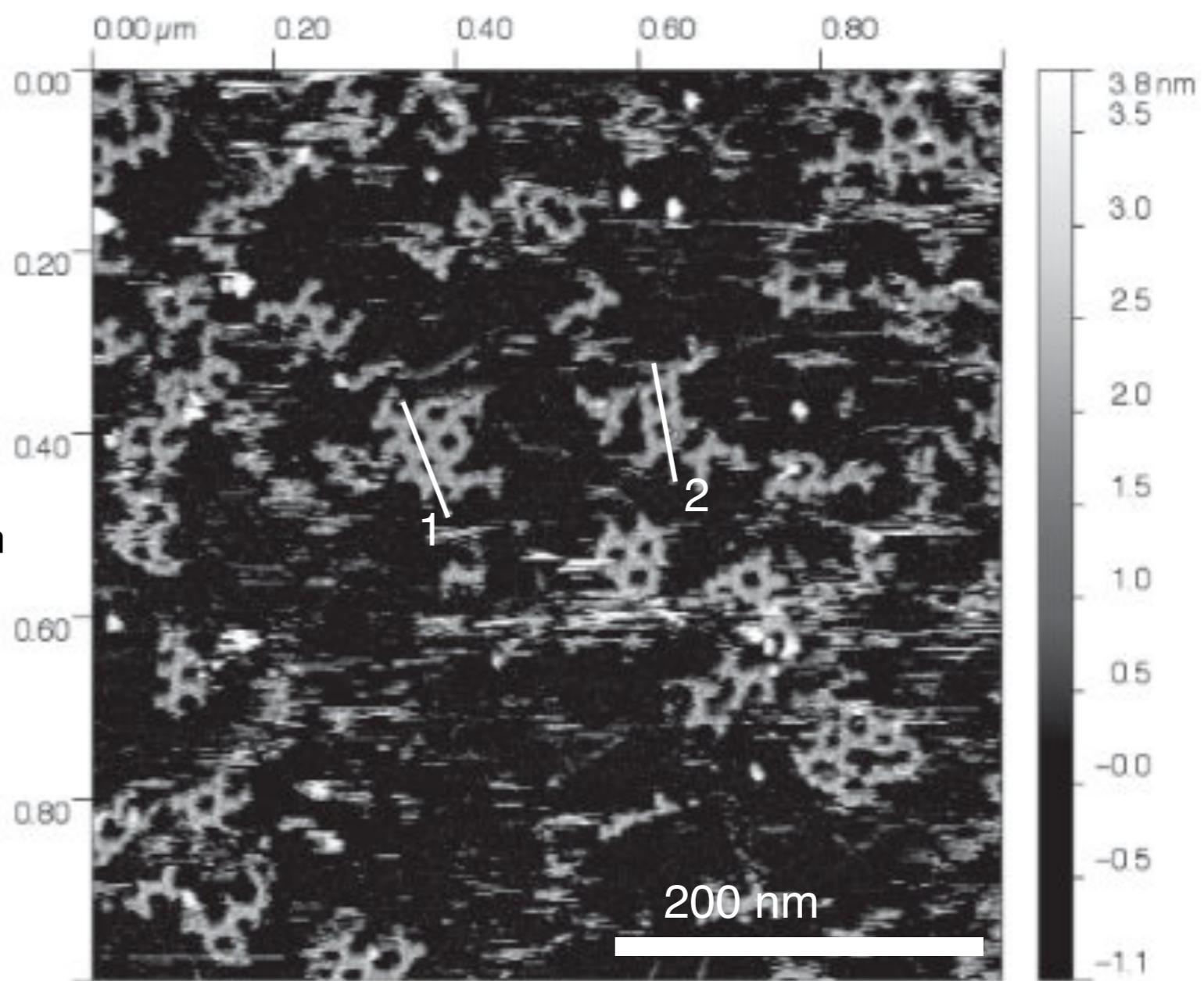
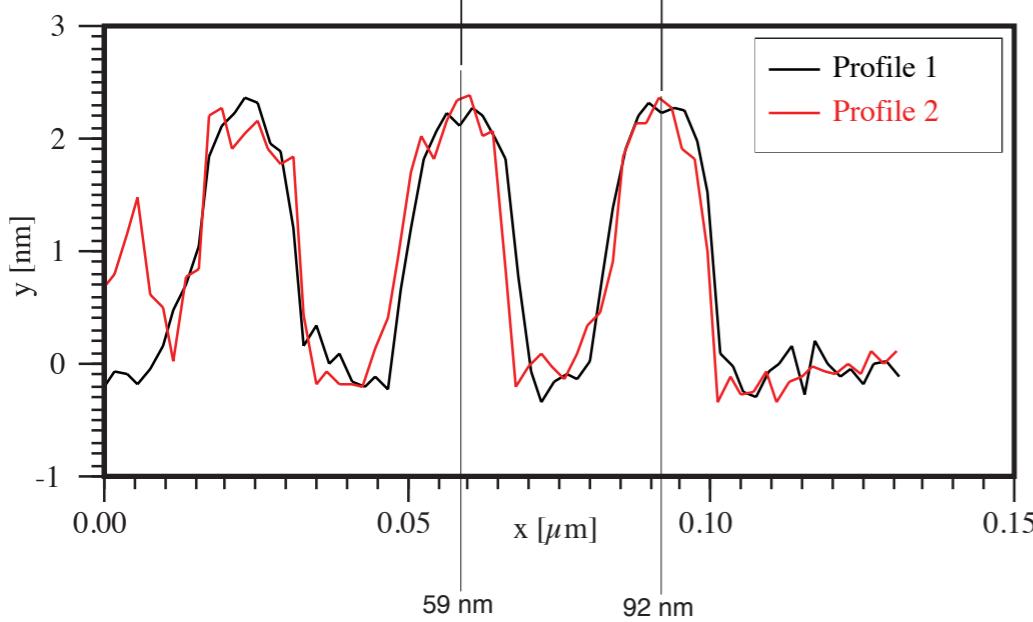
The polymerase reads the DNA gene, and becomes an RNA origami production factory, **synthesizing a new RNA origami roughly every 1 second**.

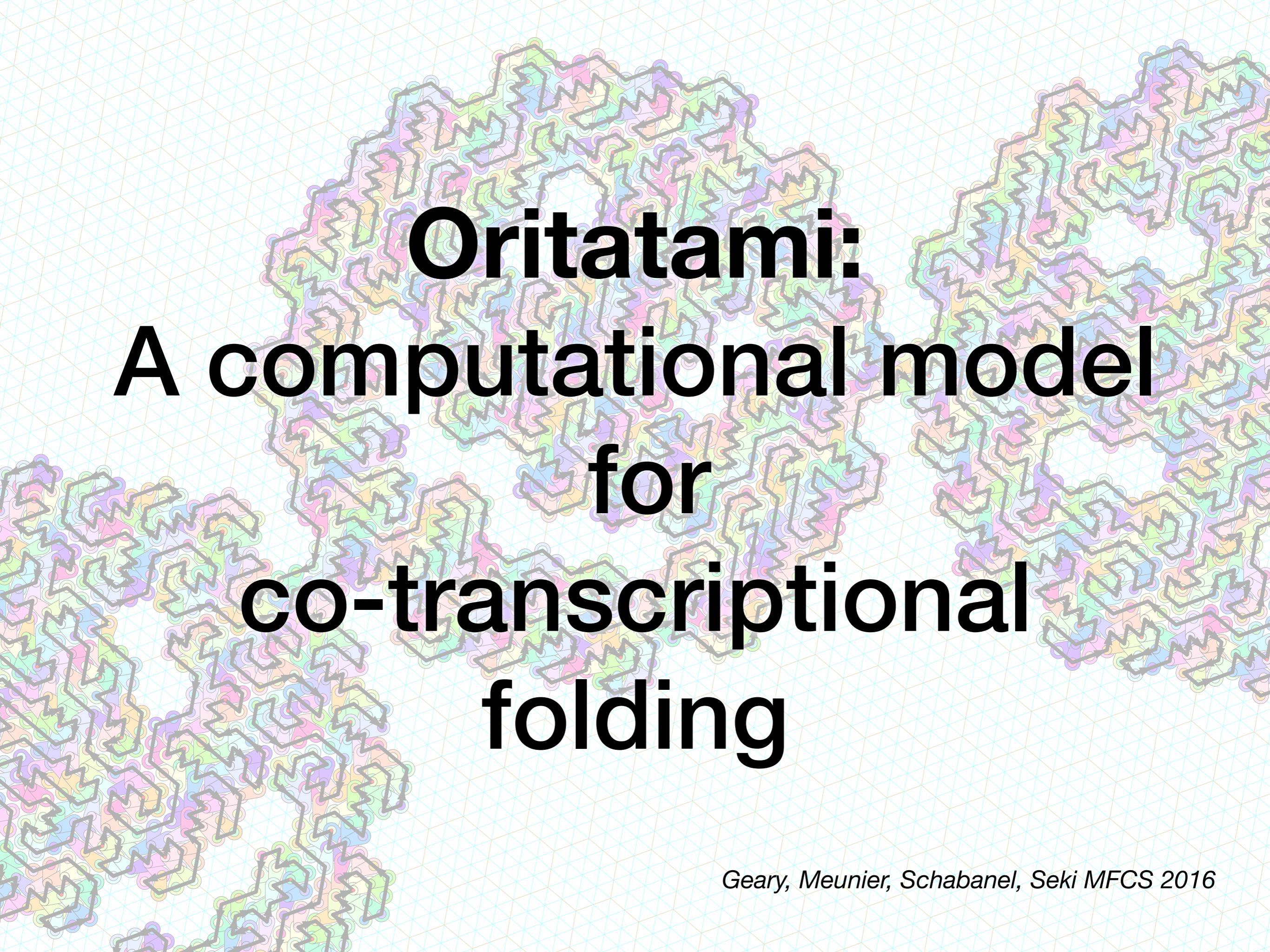
AFM imaging of 4H-AE co-transcriptional assembly



period = 33.0 nm

Note that the modeled spacing was 33.5nm



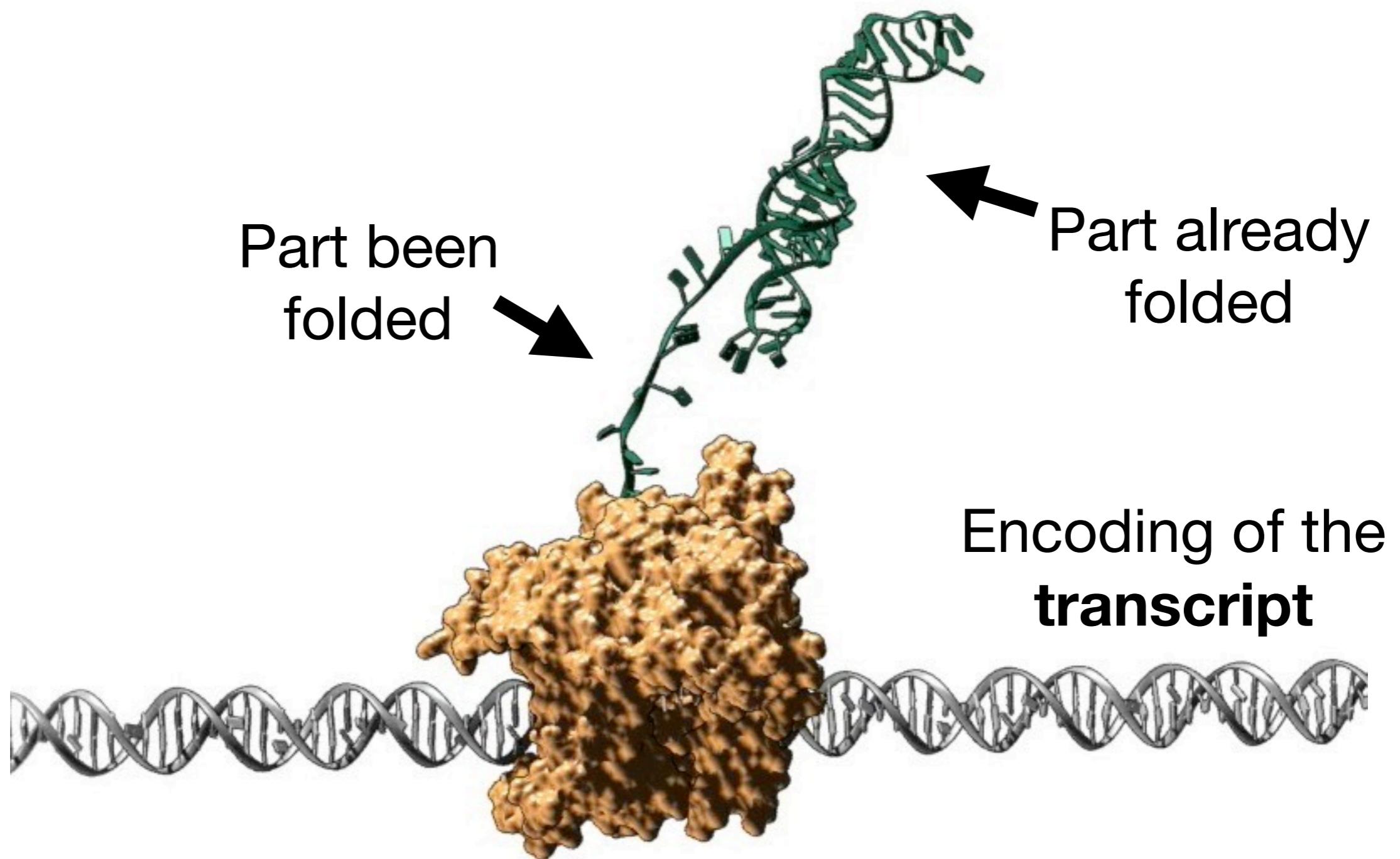


Oritatami: A computational model for co-transcriptional folding

Geary, Meunier, Schabanel, Seki MFCS 2016

RNA Folding

(Real time: ~1 second)



Oritatami: A model for co-transcriptional folding

The program:

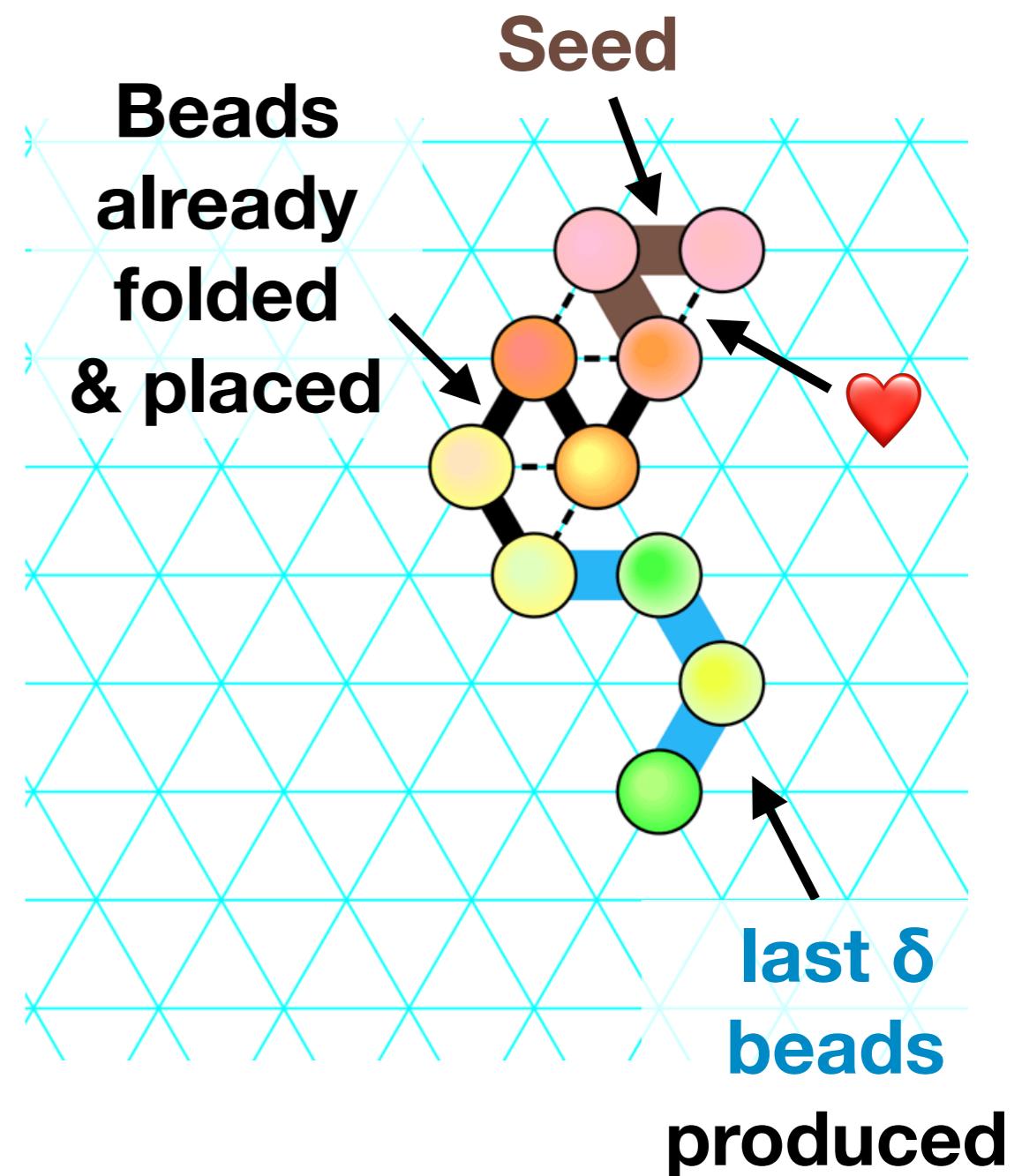
- a sequence of **bead types** (the **transcript**)

The instructions:

- the rule **a ❤ b** if bead types **a** and **b** attract each other

The input configuration:

- Some beads placed beforehand (the **seed**)

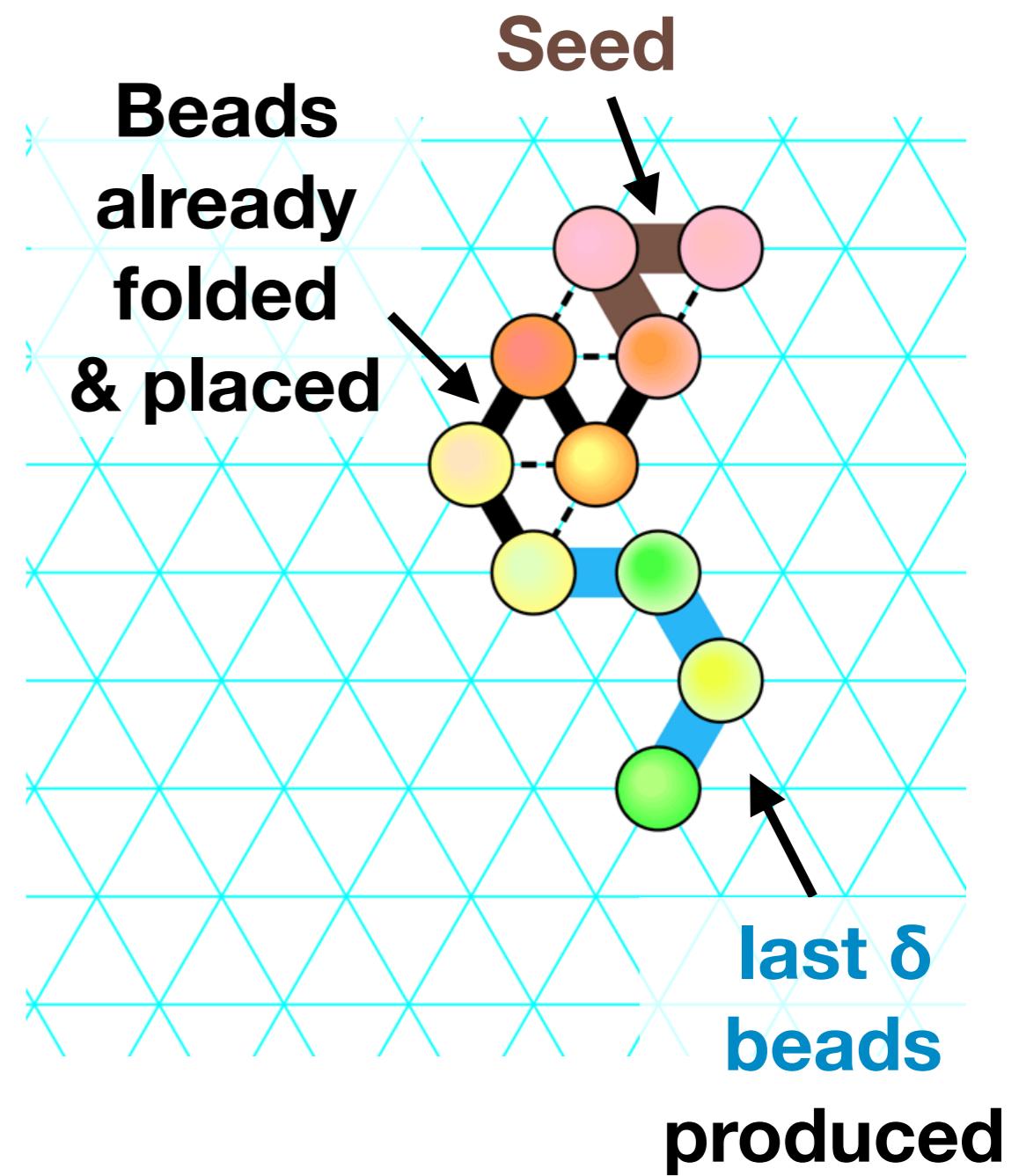


Oritatami: A model for co-transcriptional folding

The dynamics

- Starting from the seed, the sequence is *produced one bead at a time*
- **Only the δ last produced beads** are free to move and explore the accessible positions to settle in the ones **maximizing the number of bonds**
- All other beads remain in their last locations

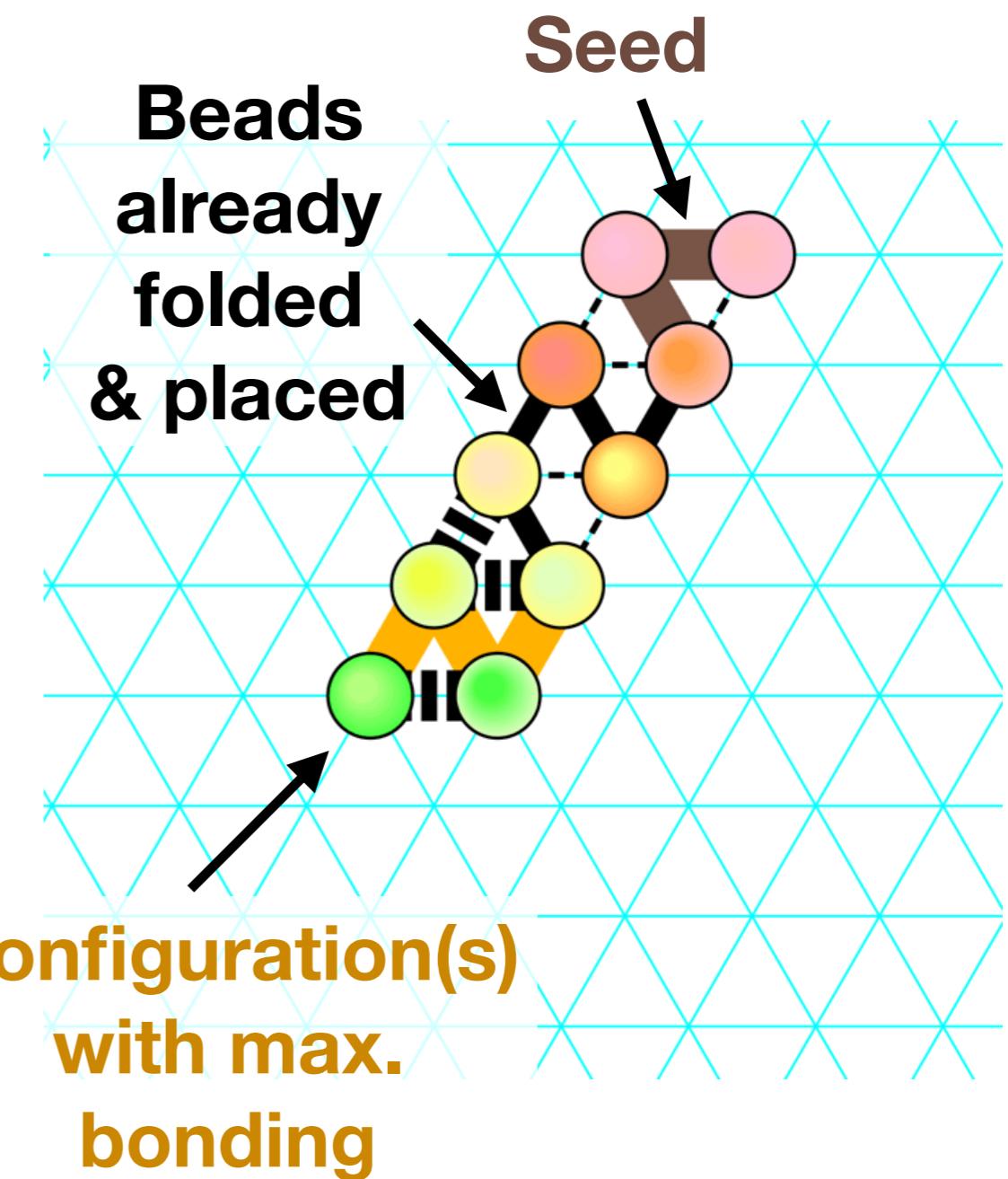
here, delay $\delta = 3$



Oritatami: A model for co-transcriptional folding

The dynamics.

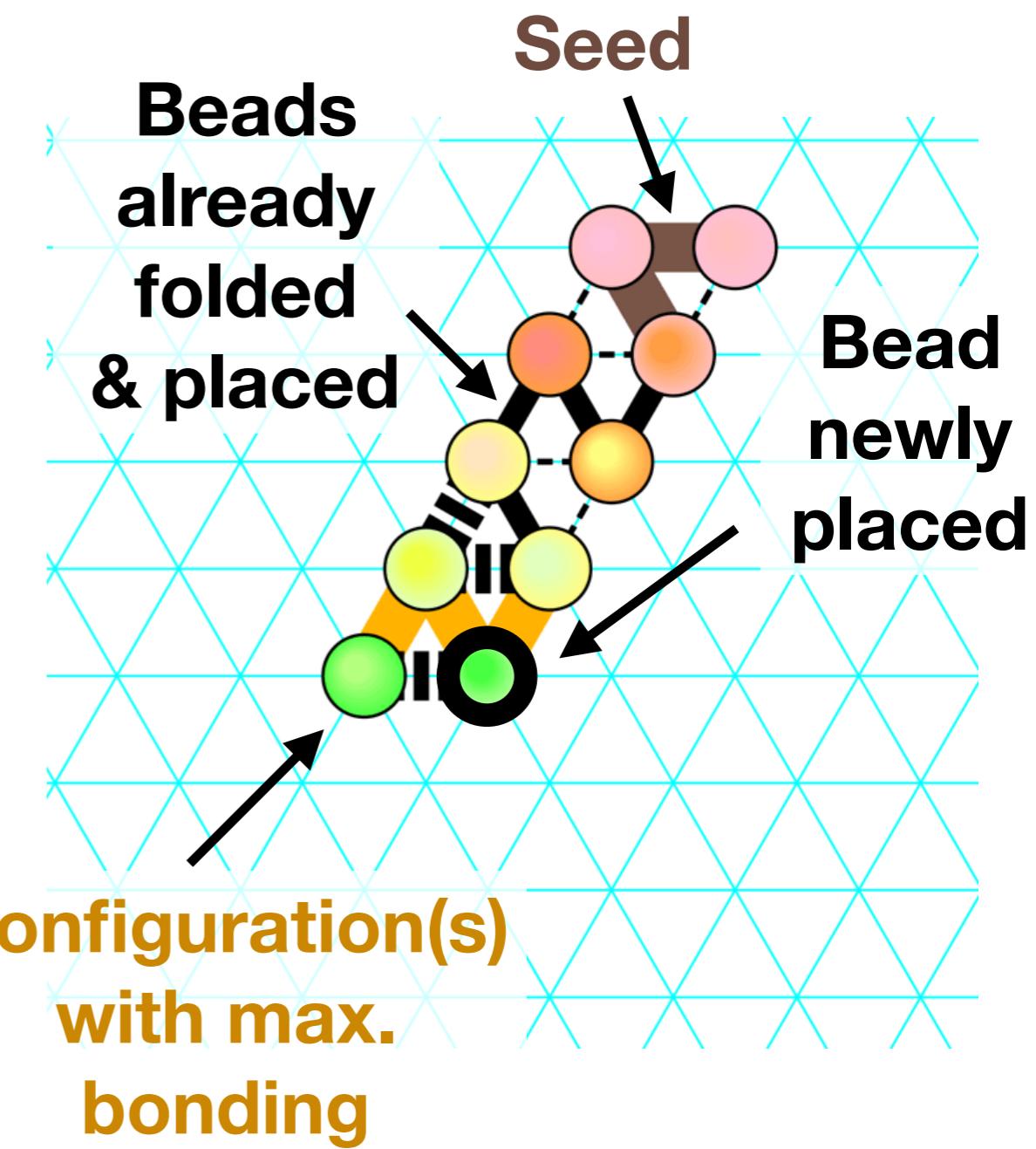
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Oritatami: A model for co-transcriptional folding

The dynamics.

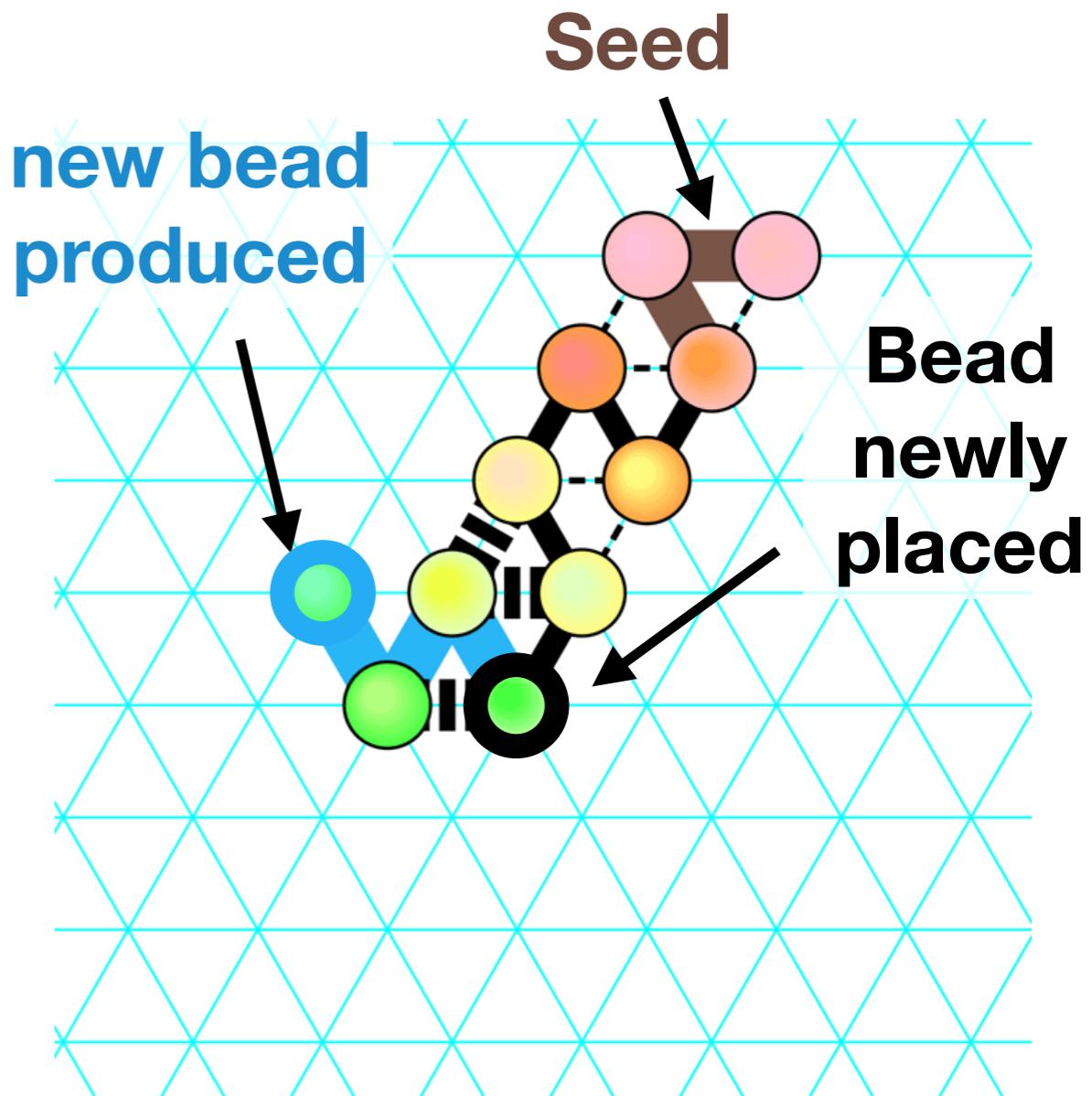
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Oritatami: A model for co-transcriptional folding

The dynamics.

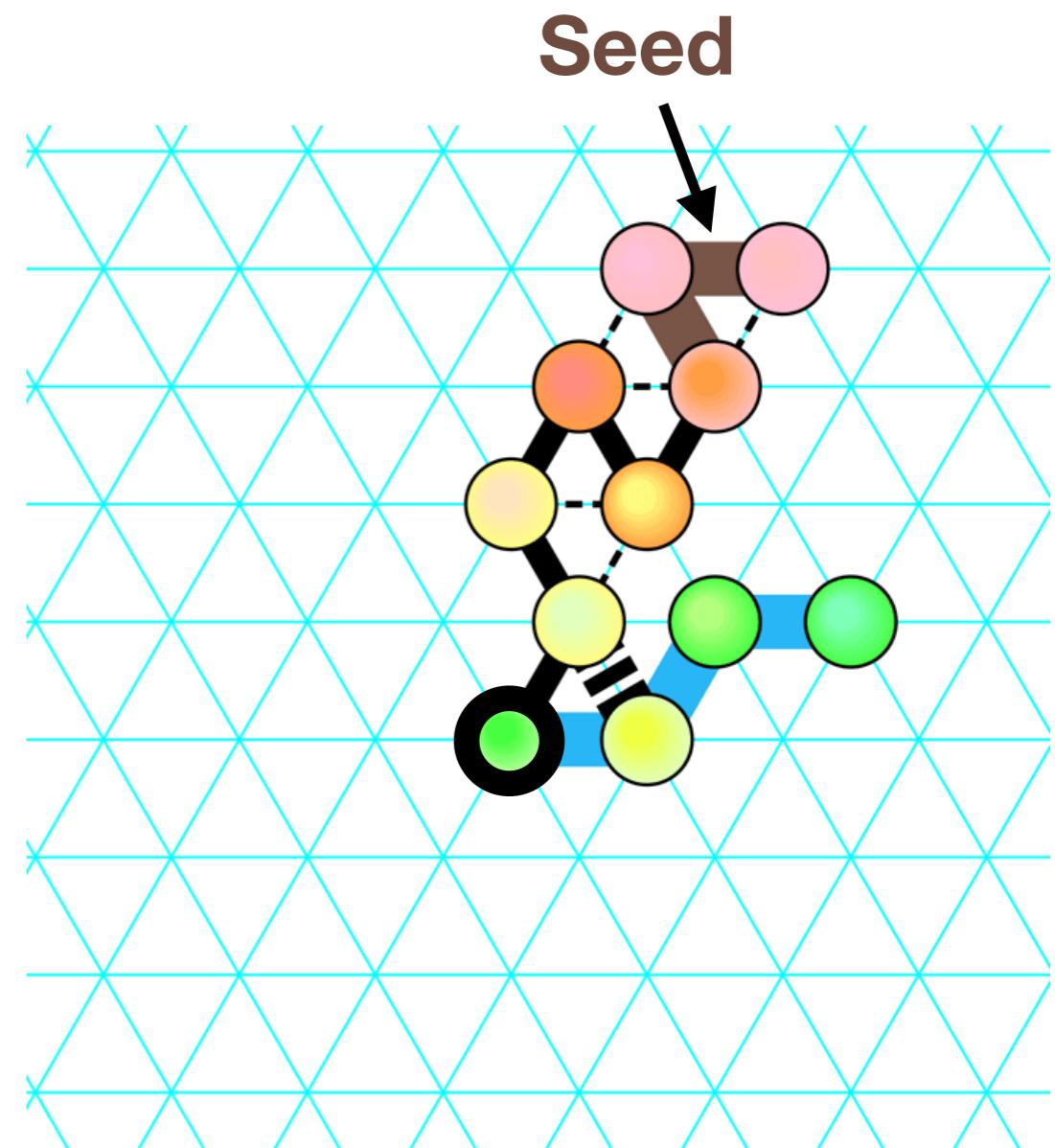
- Starting from the seed, the sequence is *produced one bead at a time*
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Oritatami: A model for co-transcriptional folding

The dynamics.

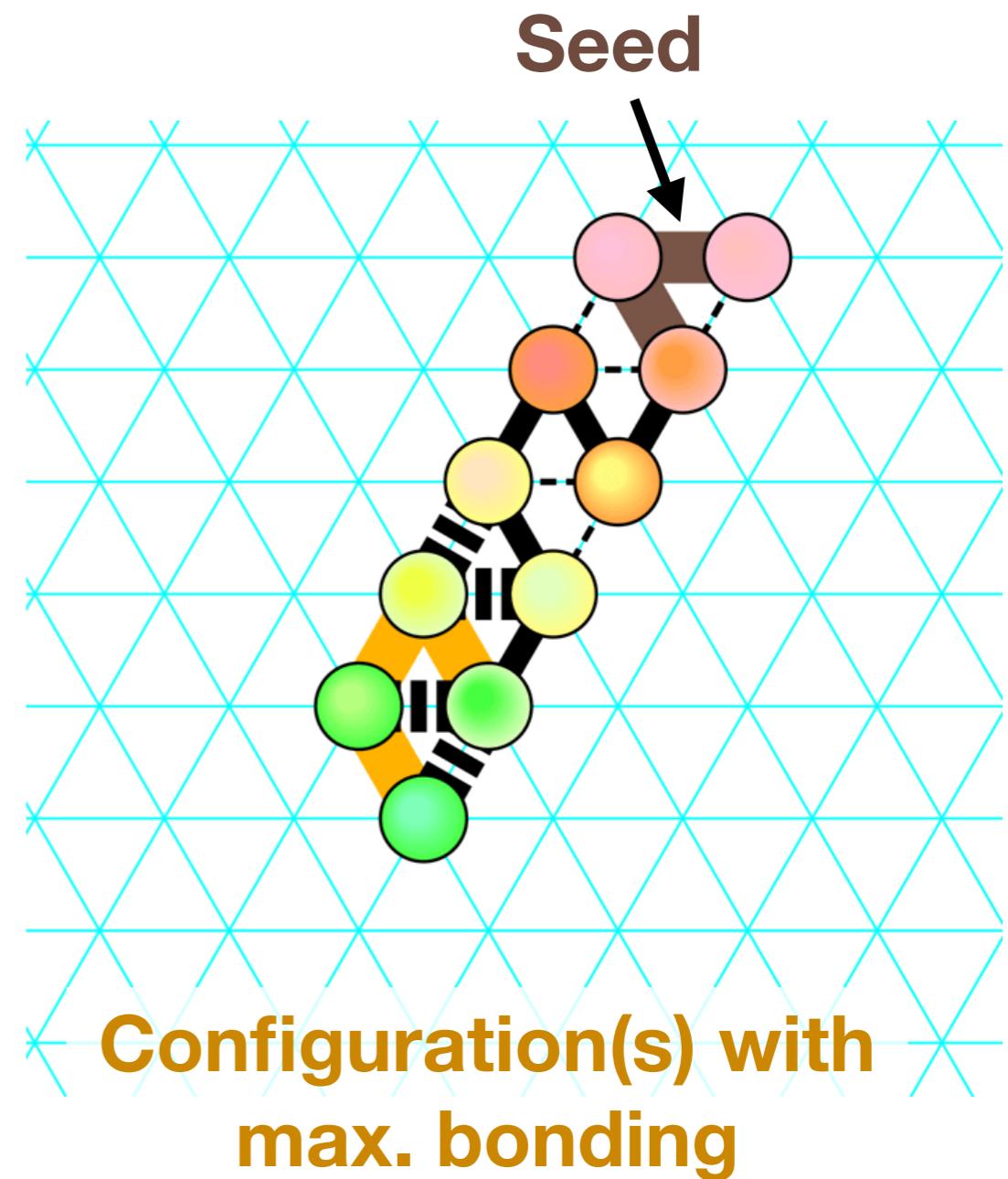
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Oritatami: A model for co-transcriptional folding

The dynamics.

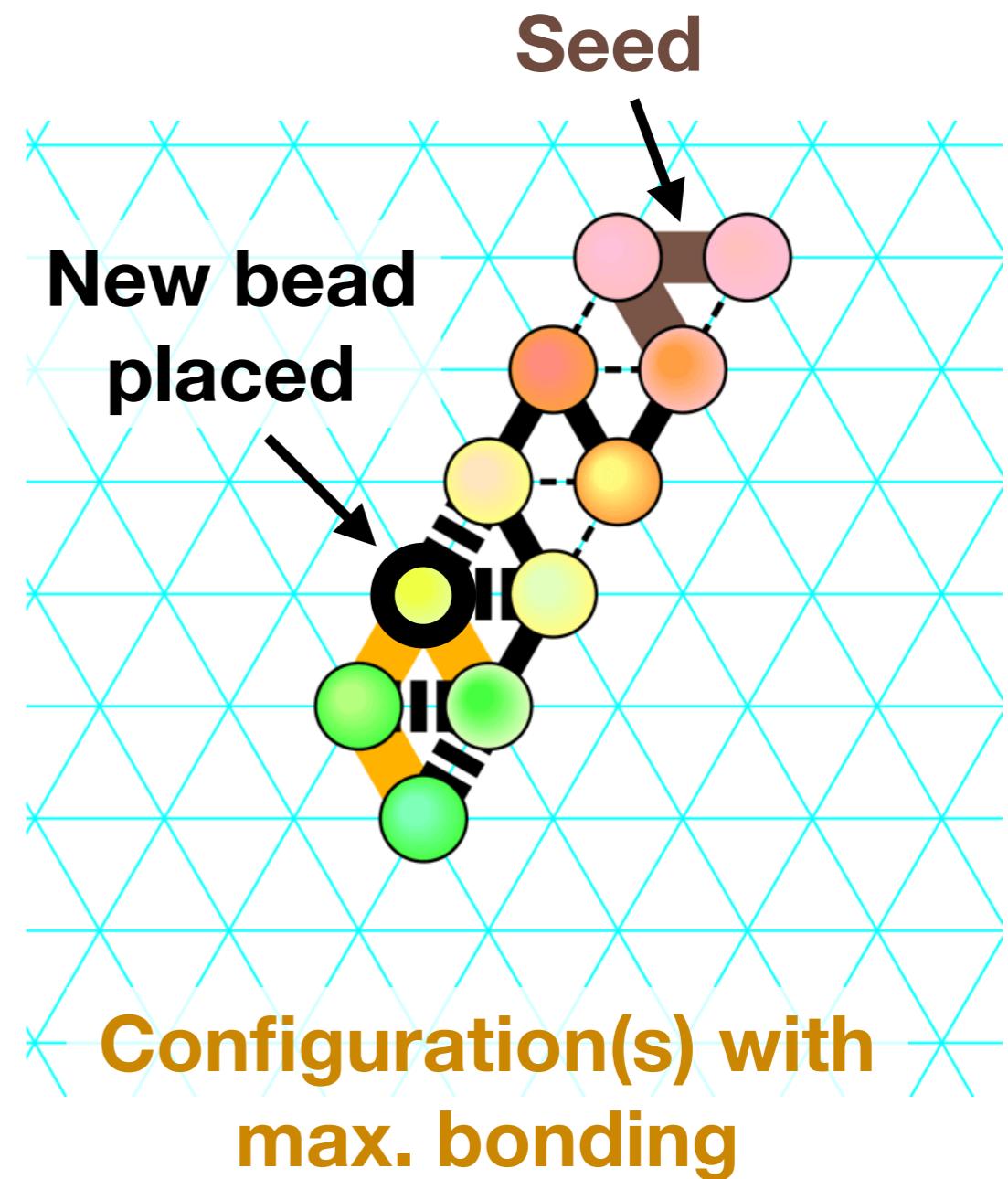
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Oritatami: A model for co-transcriptional folding

The dynamics.

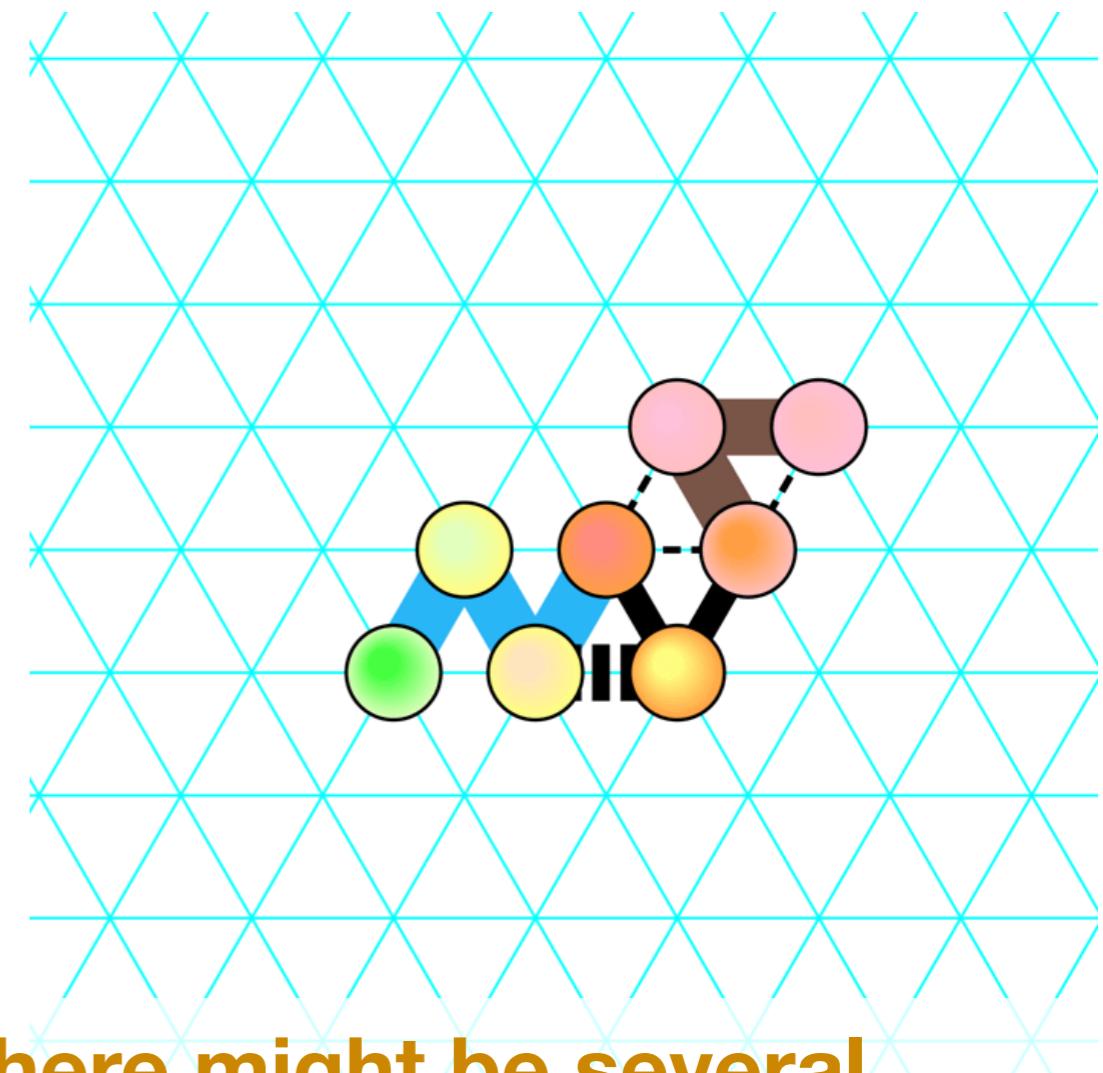
- Starting from the seed, the sequence is *produced one bead at a time*
- **Only the δ last produced beads** are free to move and explore the accessible positions to settle in the ones **maximizing the number of bonds**
- All other beads remain in their last locations



Oritatami: A model for co-transcriptional folding

The dynamics.

- Starting from the seed, the sequence is *produced one bead at a time*
- **Only the δ last produced beads** are free to move and explore the accessible positions to settle in the ones **maximizing the number of bonds**
- All other beads remain in their last locations

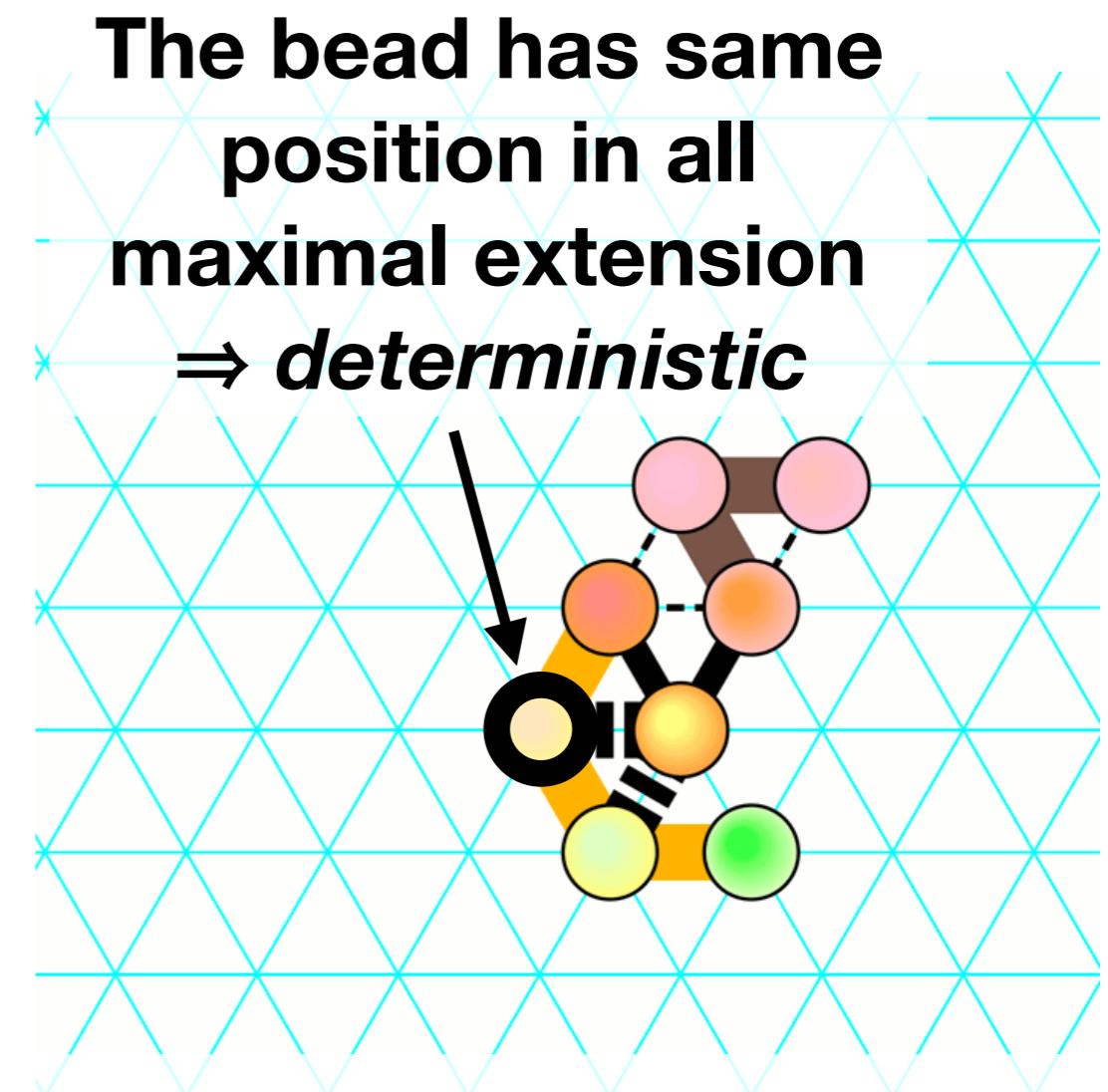


There might be several configurations with max. bonding

Oritatami: A model for co-transcriptional folding

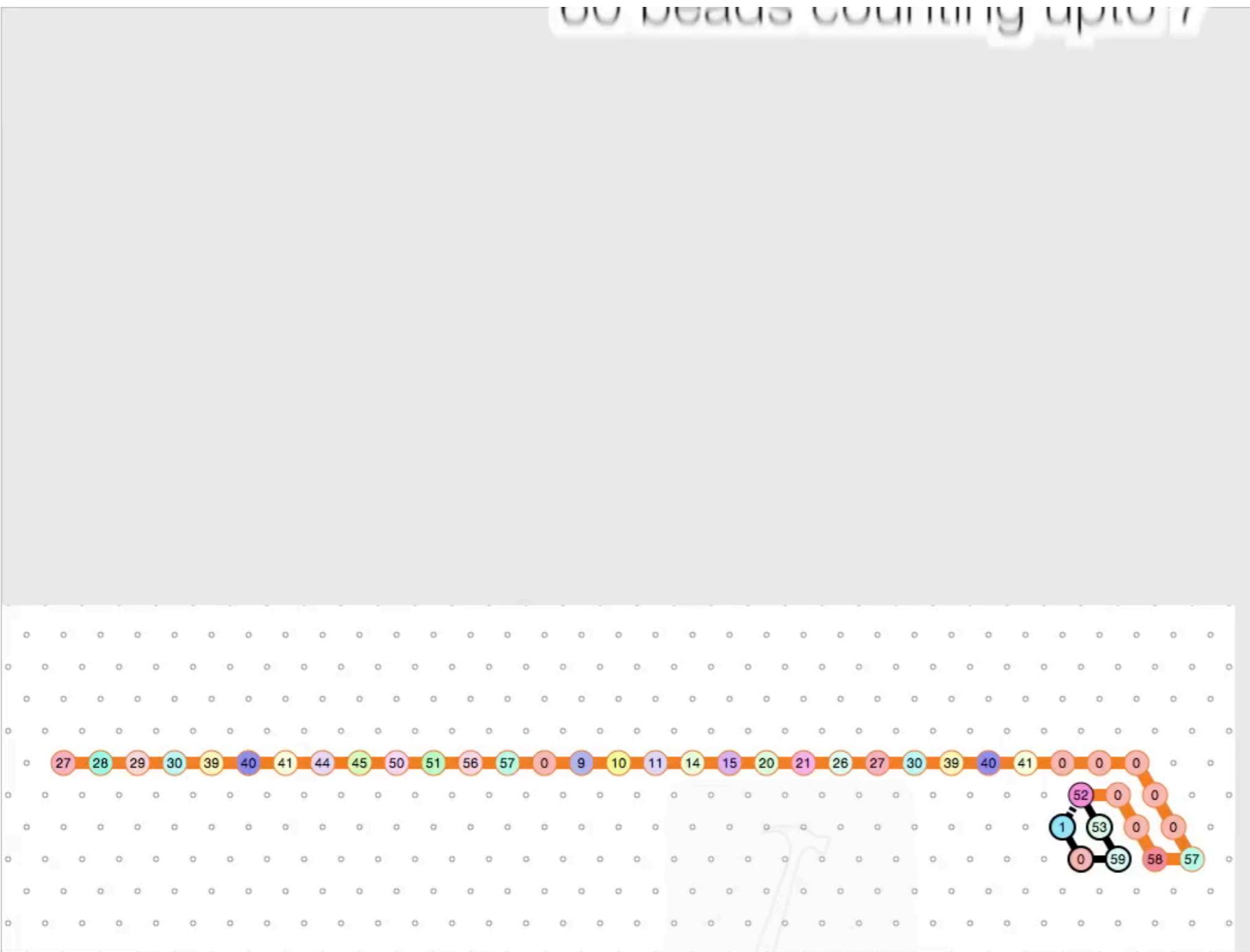
The dynamics.

- Starting from the seed, the sequence is *produced one bead at a time*
- **Only the δ last produced beads** are free to move and explore the accessible positions to settle in the ones **maximizing the number of bonds**
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Oritatami

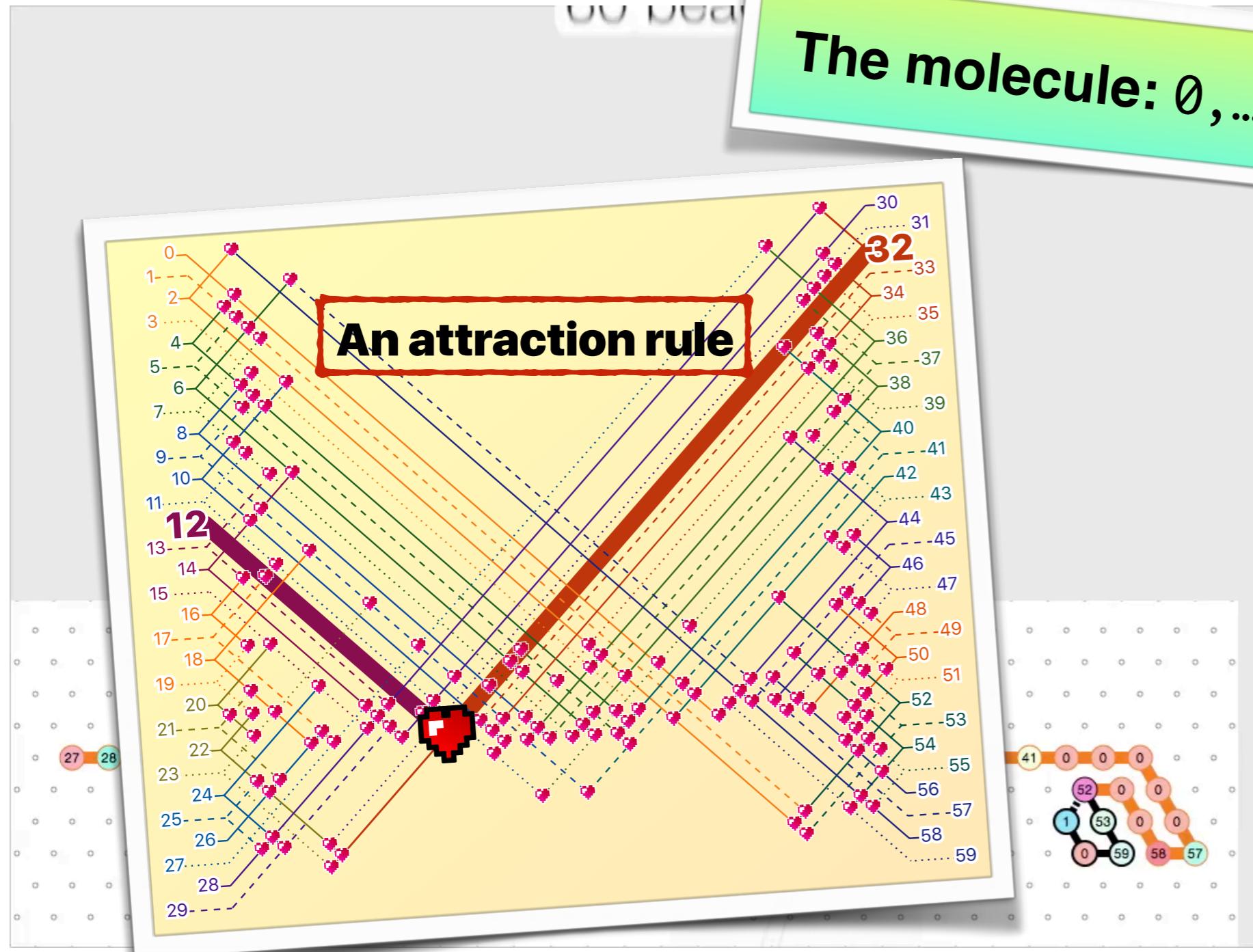
A first example



A binary counter made of a **single** 60-beads periodic molecule folding upon itself

Oritatami

A first example

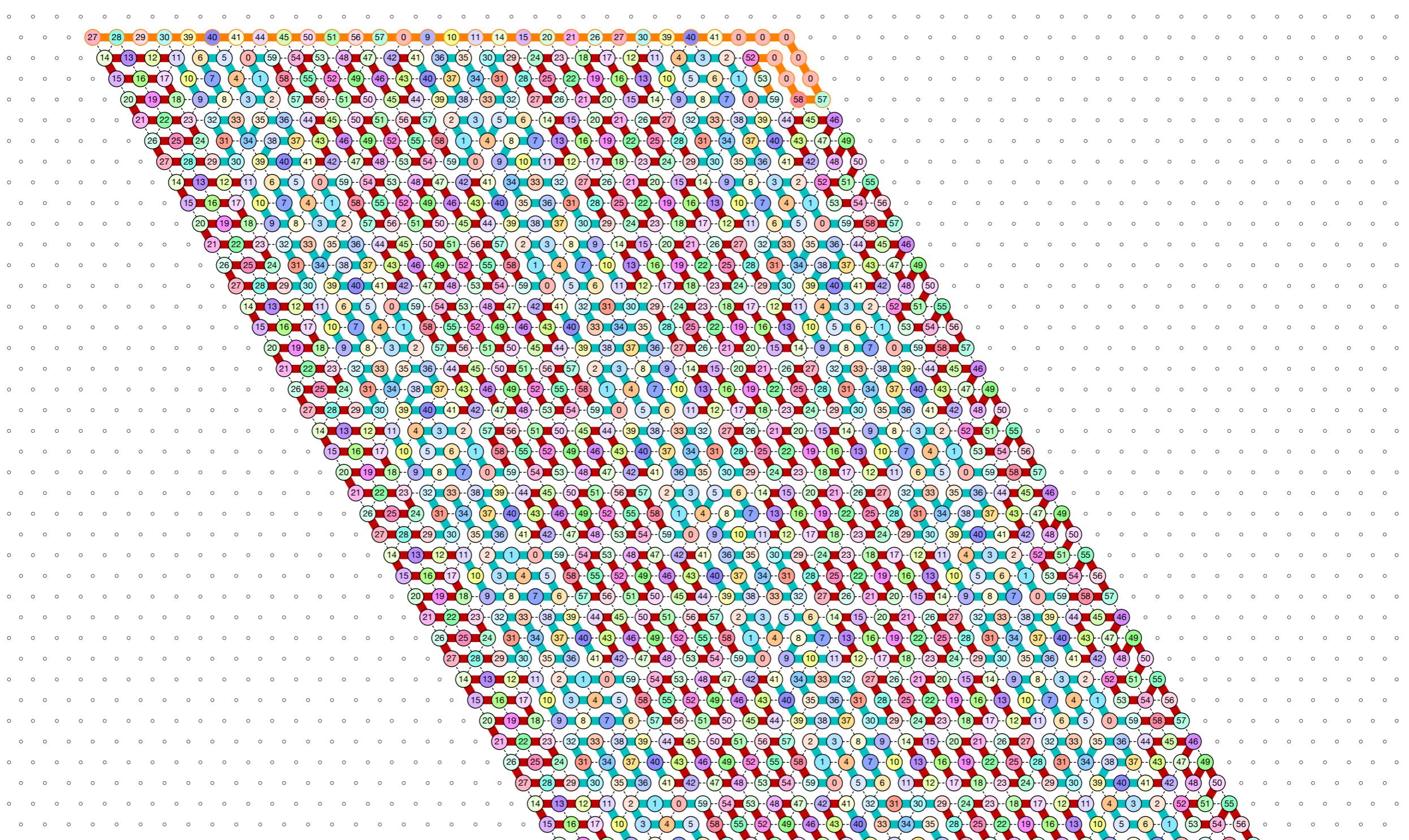


The molecule: $0, \dots, 59, 0, \dots, 59, 0, \dots$

of a **single** ∞
beads
periodic
molecule
folding upon
itself

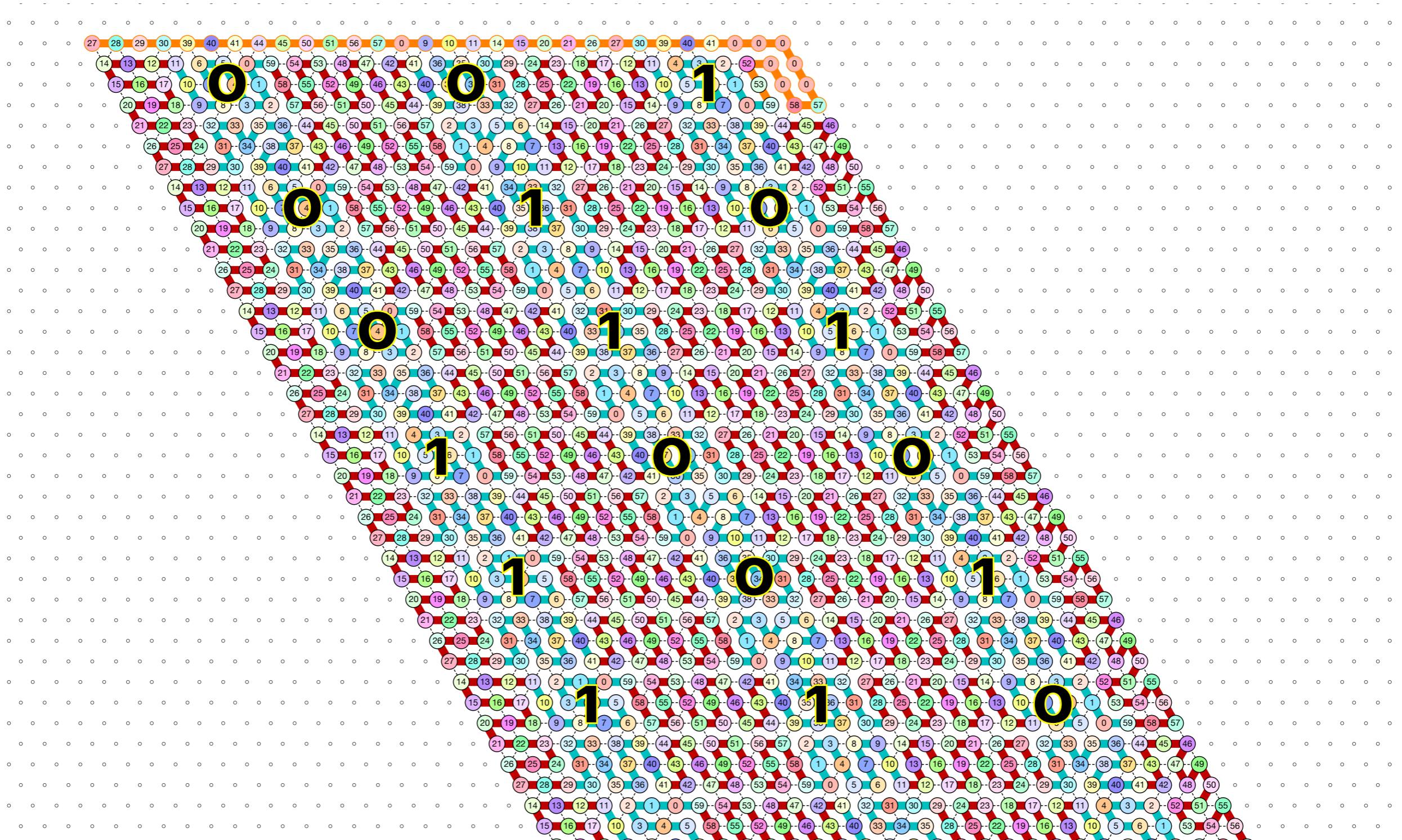
Oritatami. A binary counter

Information is encoded in the geometry



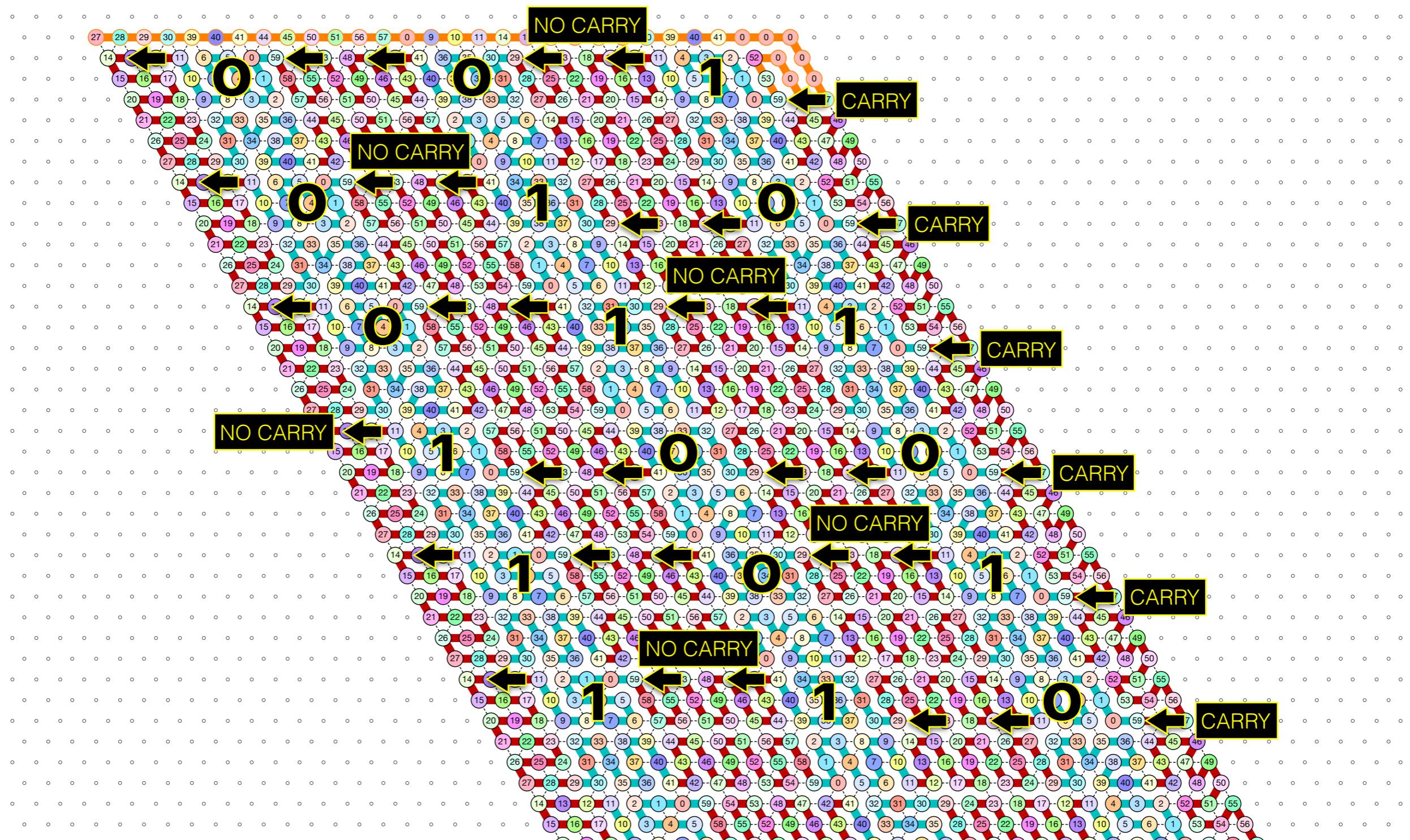
Oritatami. A binary counter

Information is encoded in the geometry



Oritatami. A binary counter

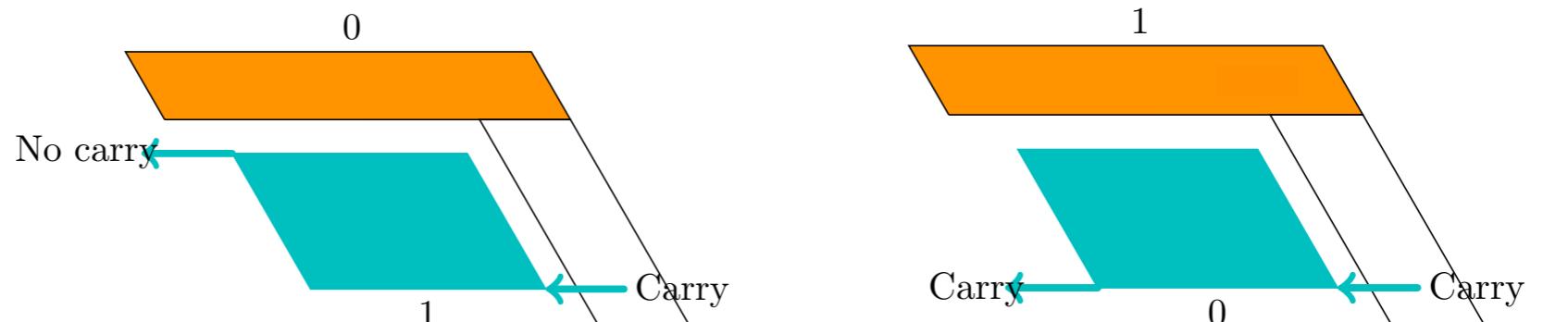
Information is encoded in the geometry



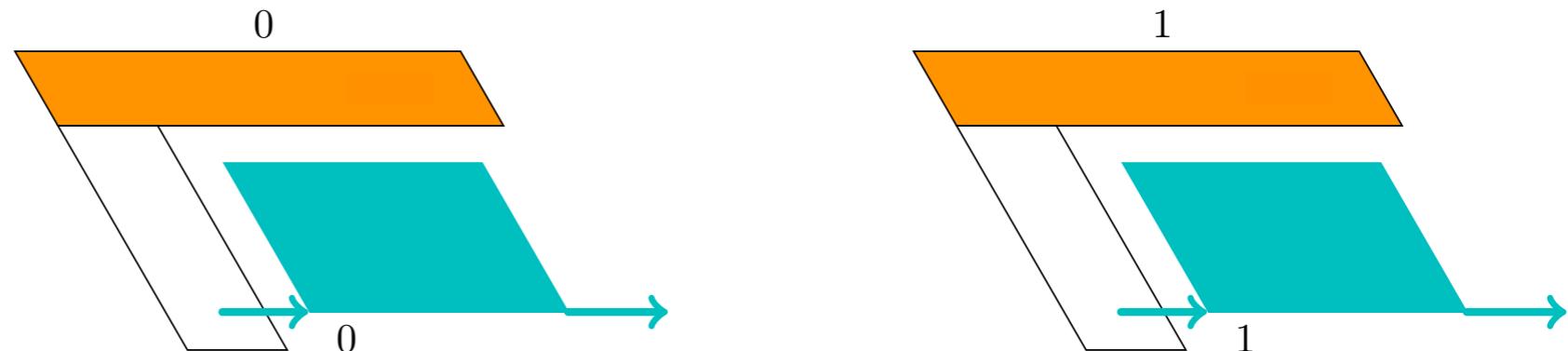
Oritatami. A binary counter

Information is encoded in the geometry

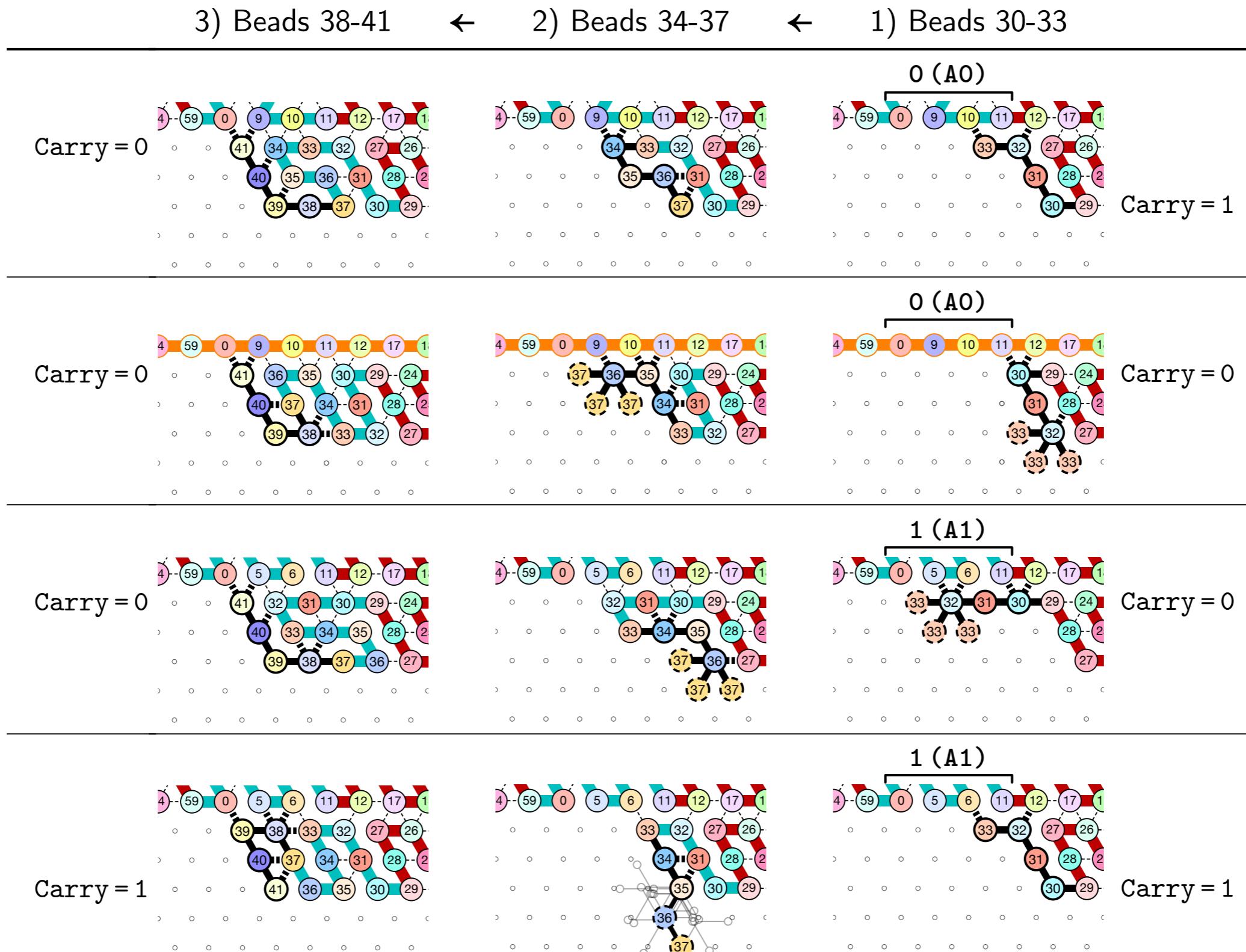
Carry
propagation



Line feed



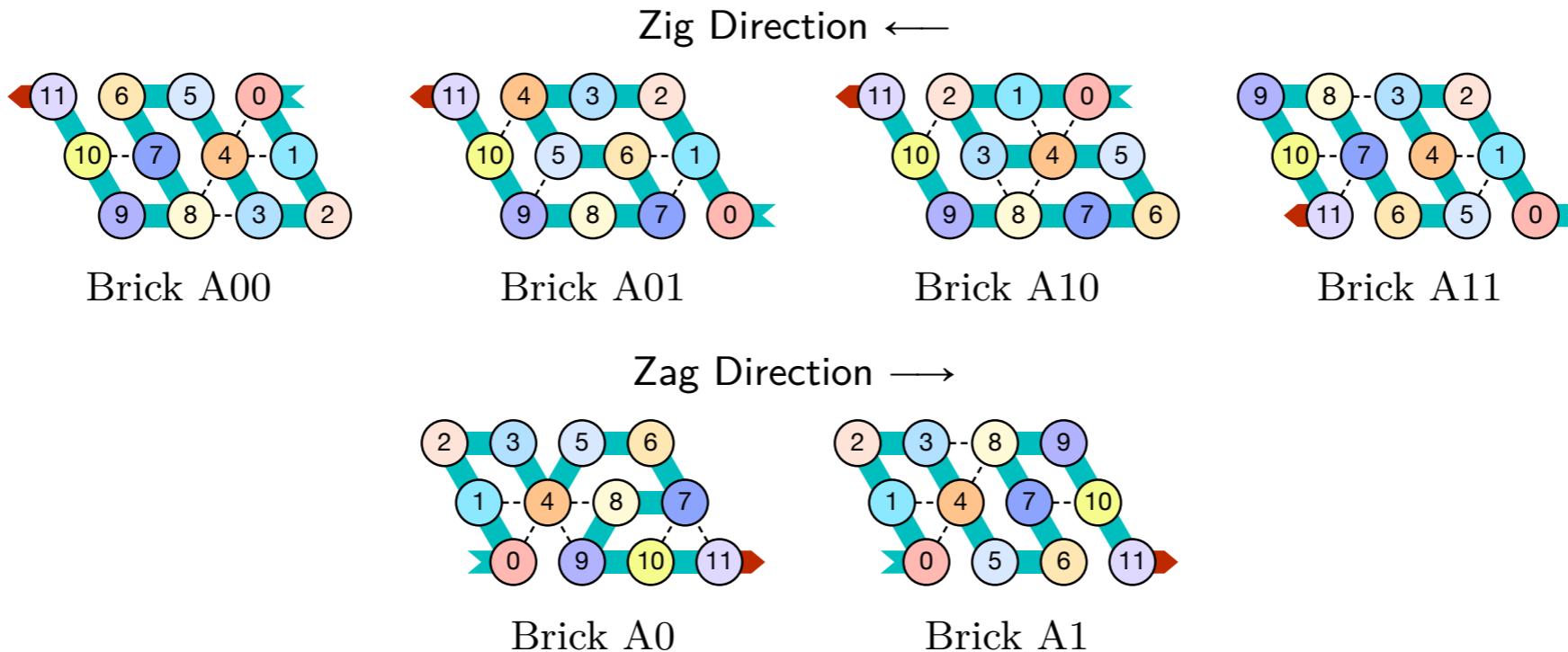
How does computation work?



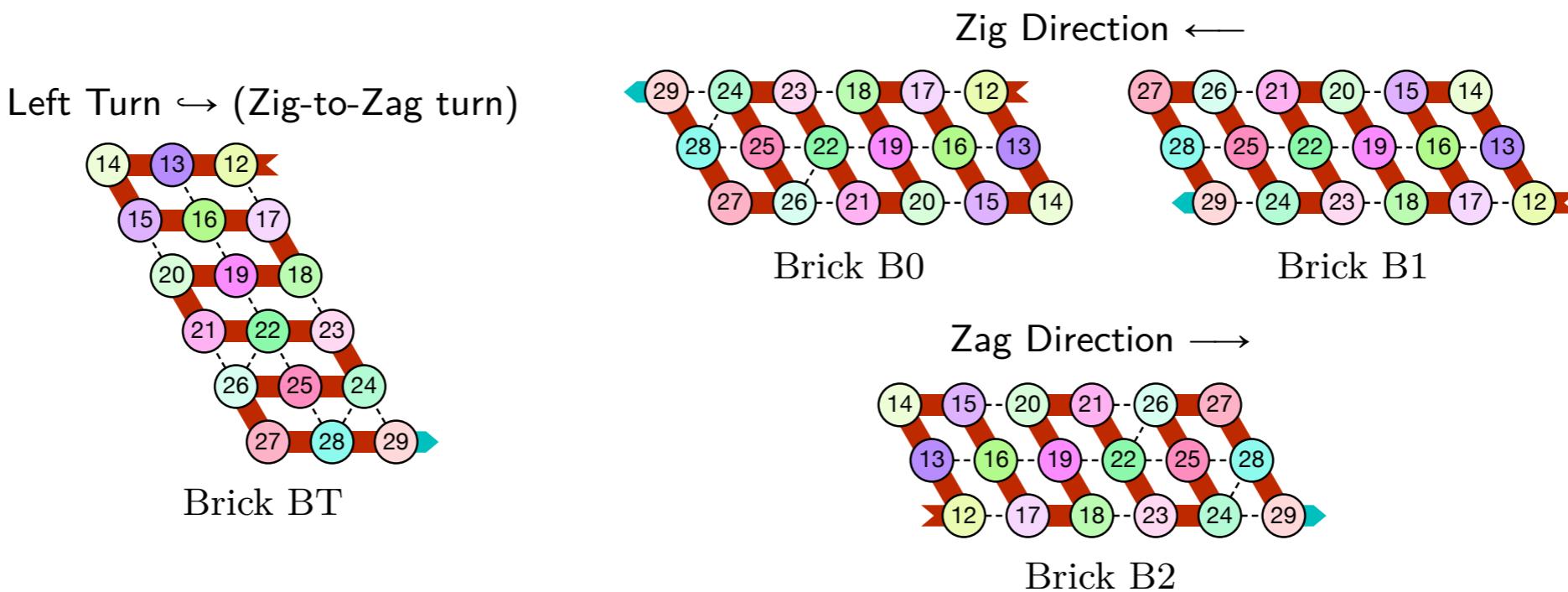
Proving the binary counter:

First, define the *bricks*

- Module A, First Half-Adder (beads 0–11):



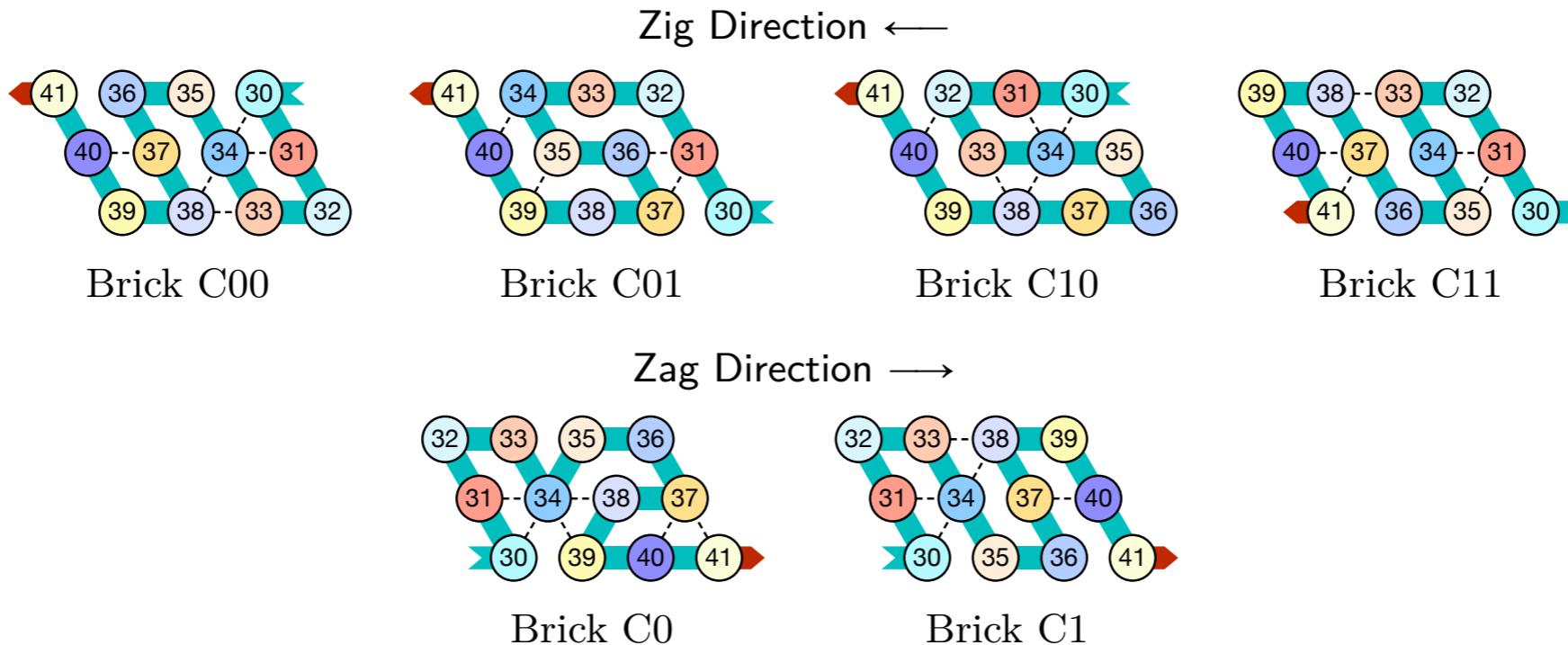
- Module B, Left-Turn module (beads 12–29)



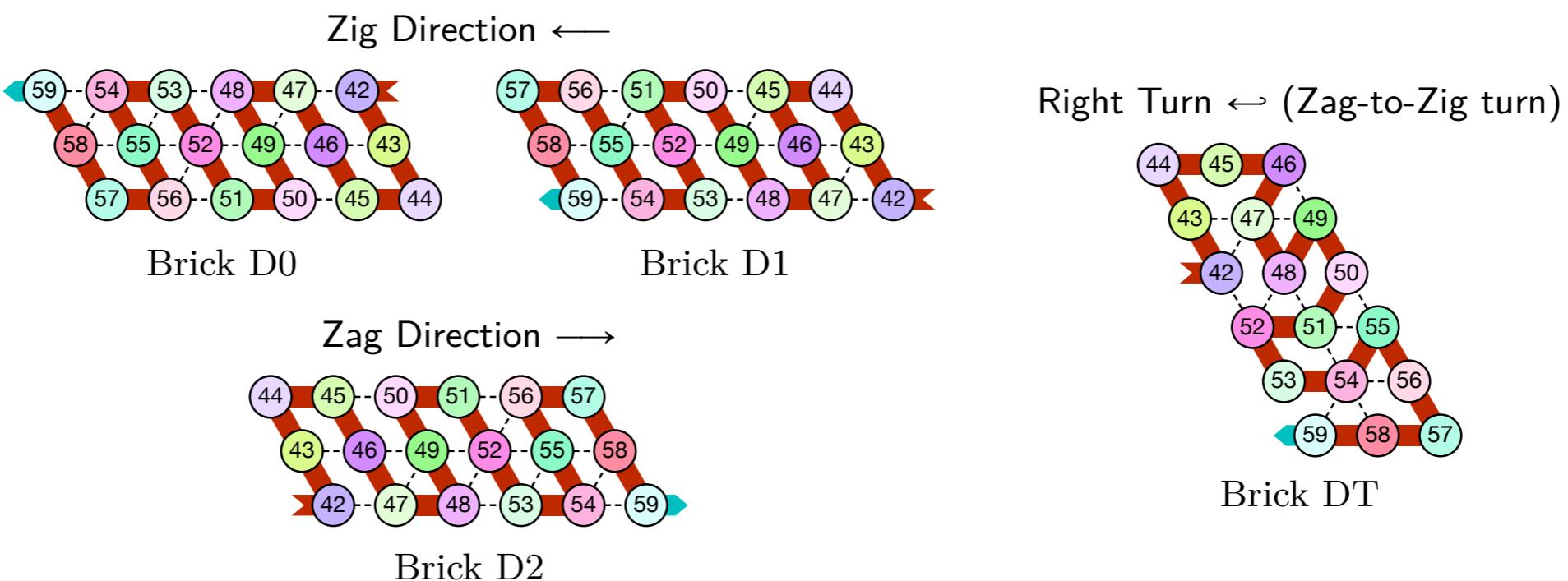
Proving the binary counter:

First, define the *bricks*

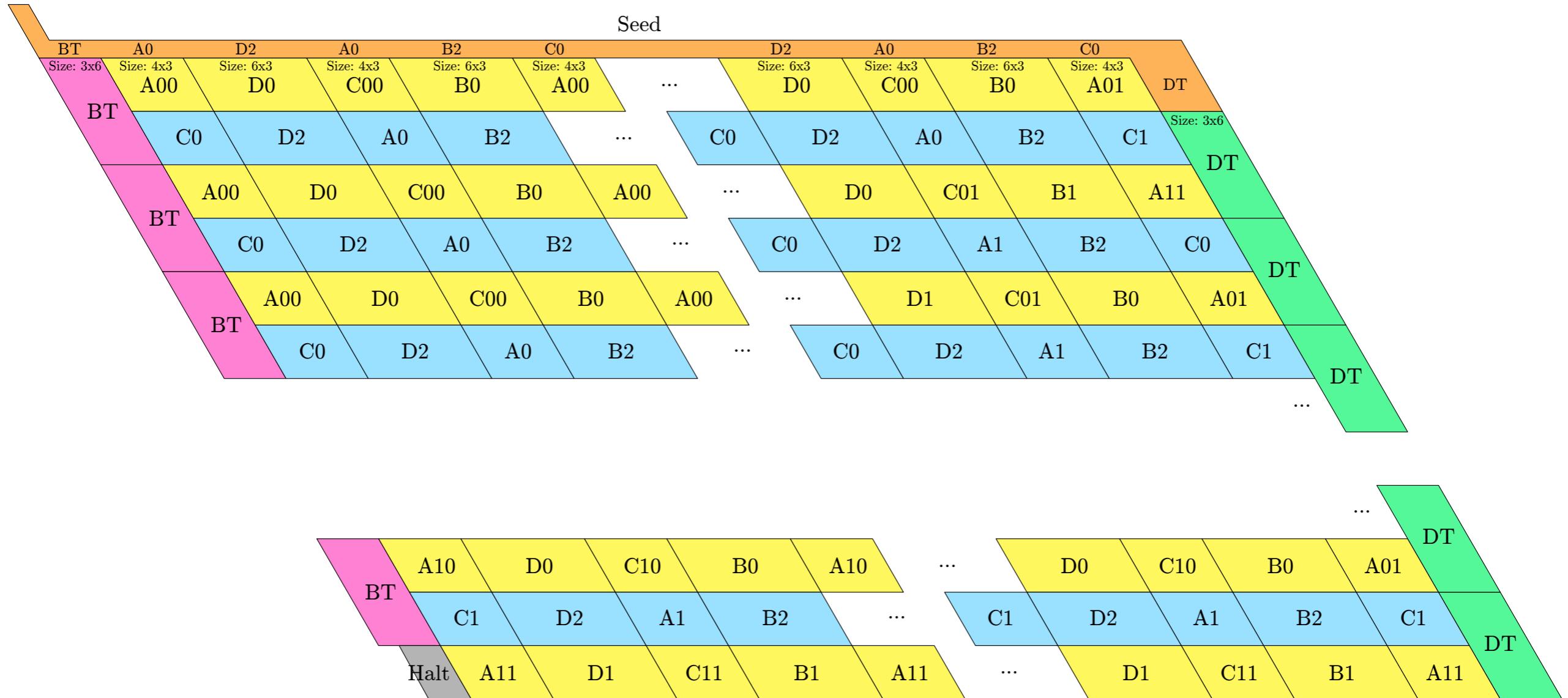
- Module *C*, Second Half-Adder (beads 30–41)



- Module *D*, Right-Turn module (beads 42–59)

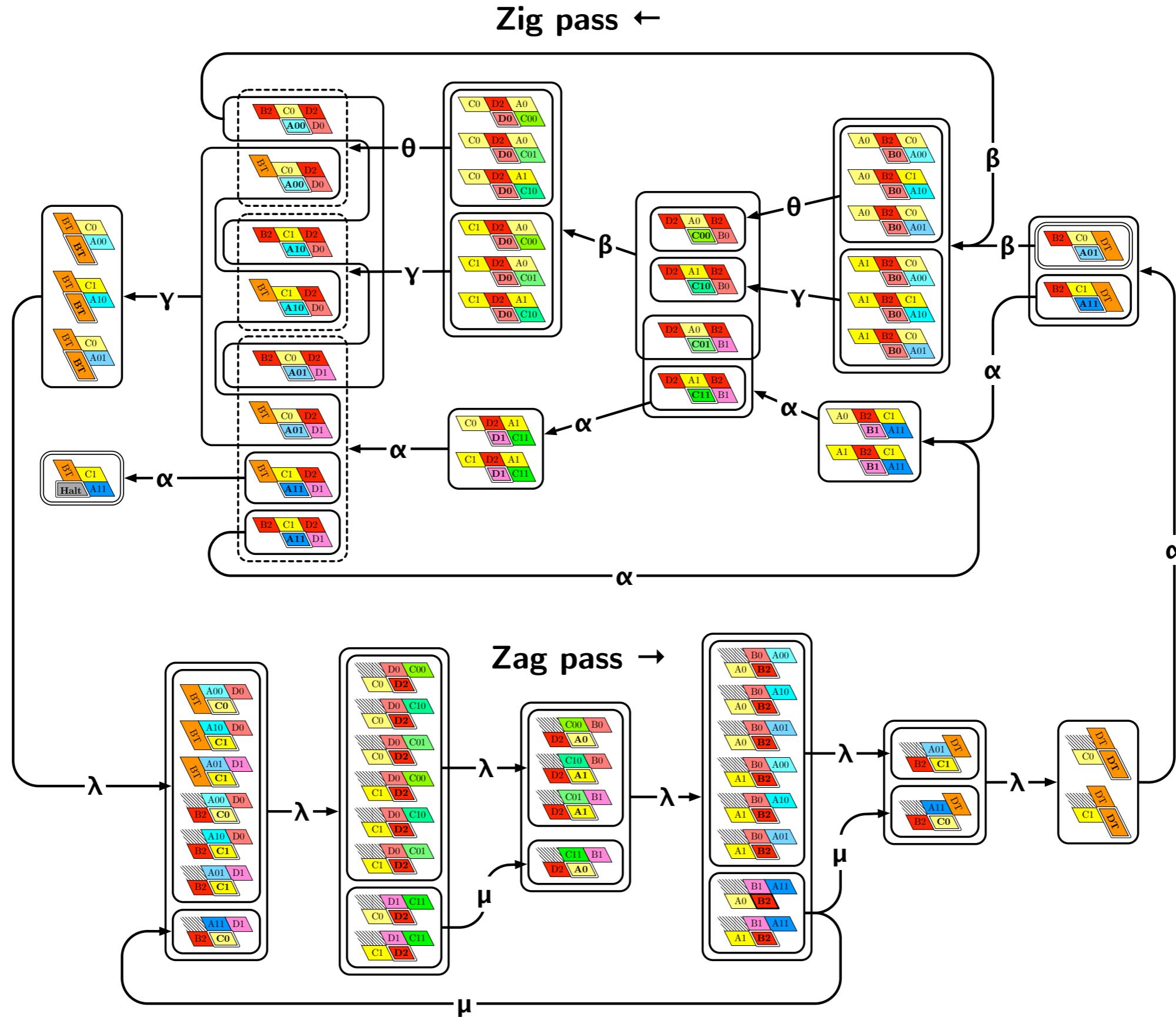


2nd, describe the final folding

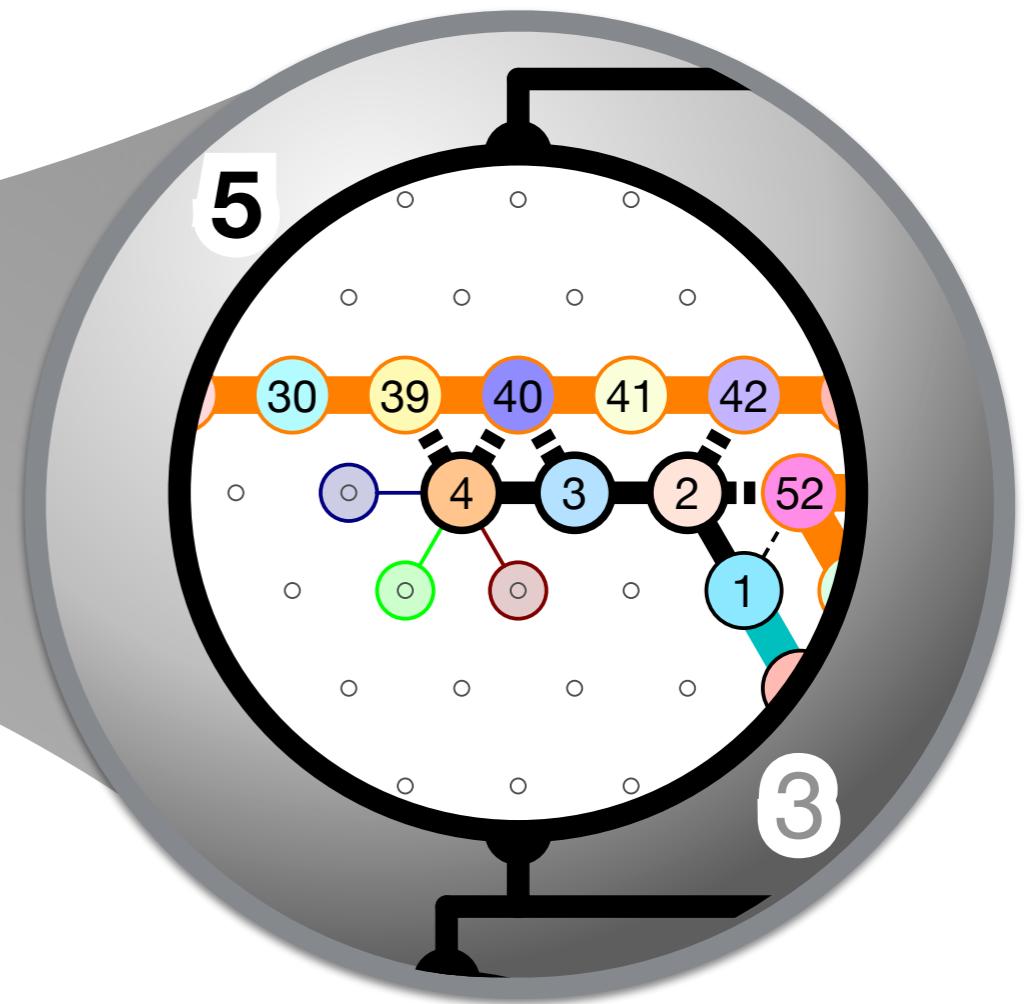
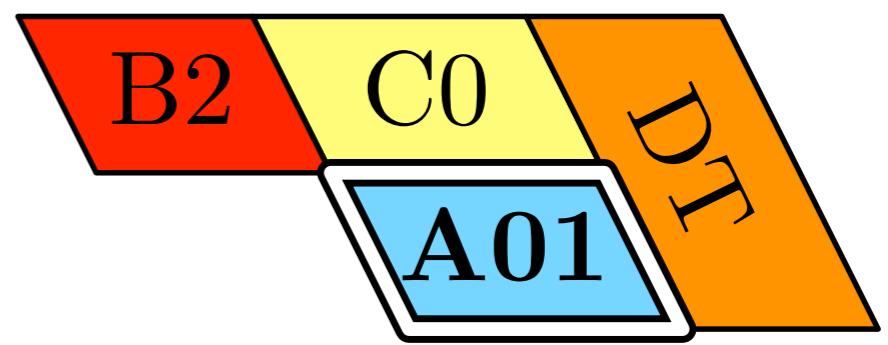
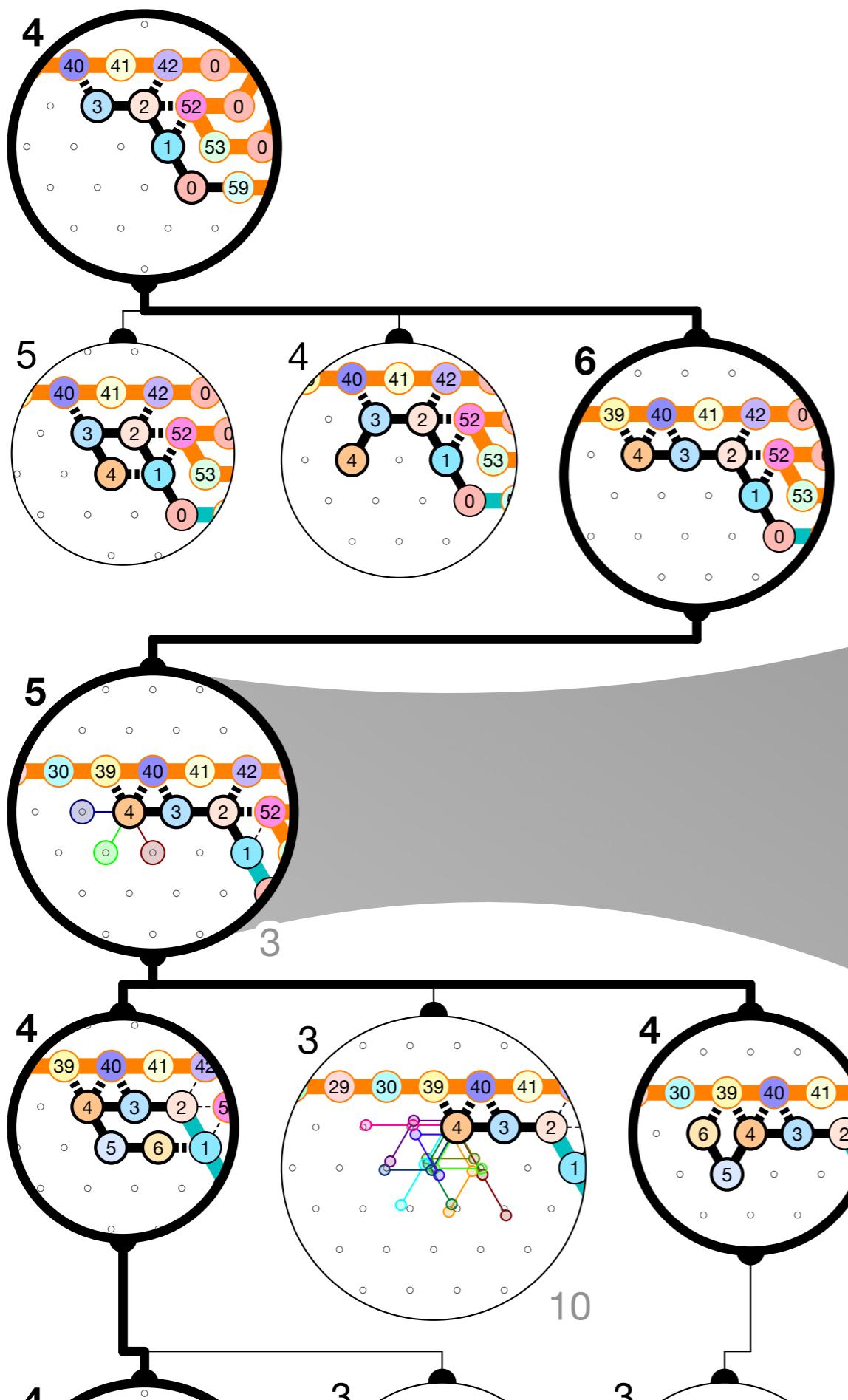


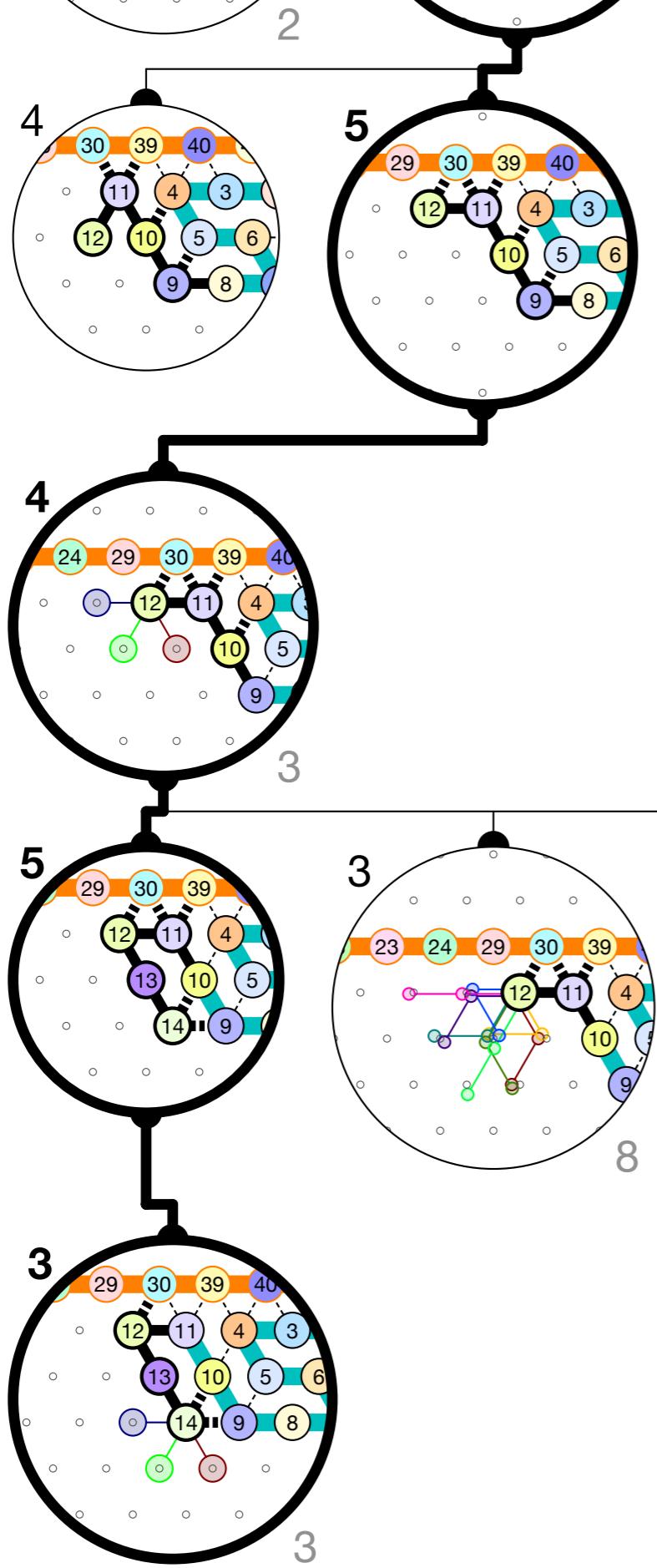
We prove that the molecule folds like this by induction

3rd, enumerate all the environments for each brick

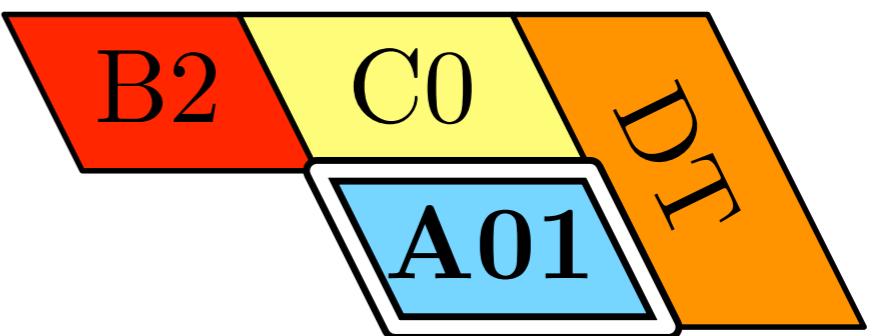


4th, prove the folding for each brick



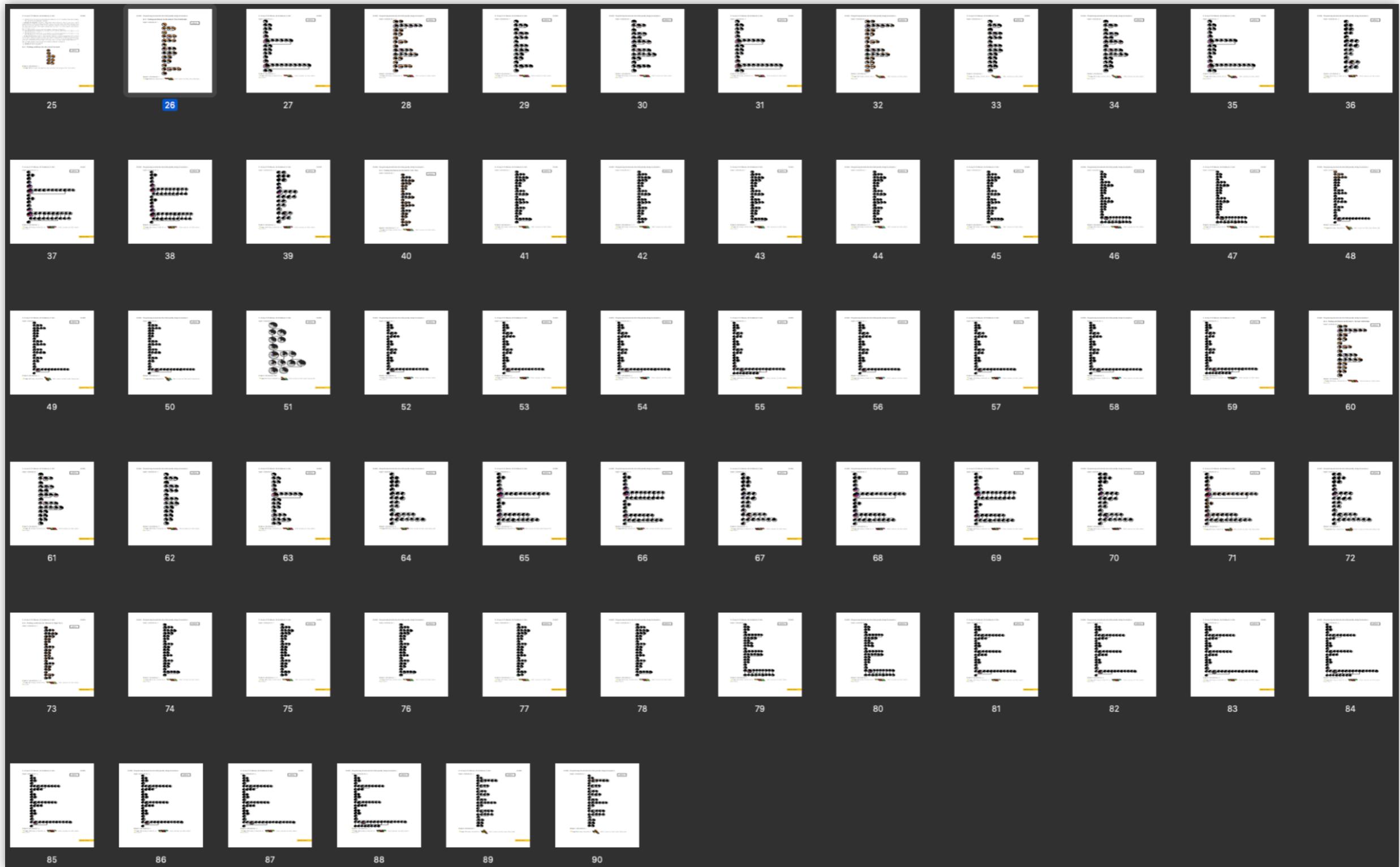


**4th, prove the folding
for each brick**

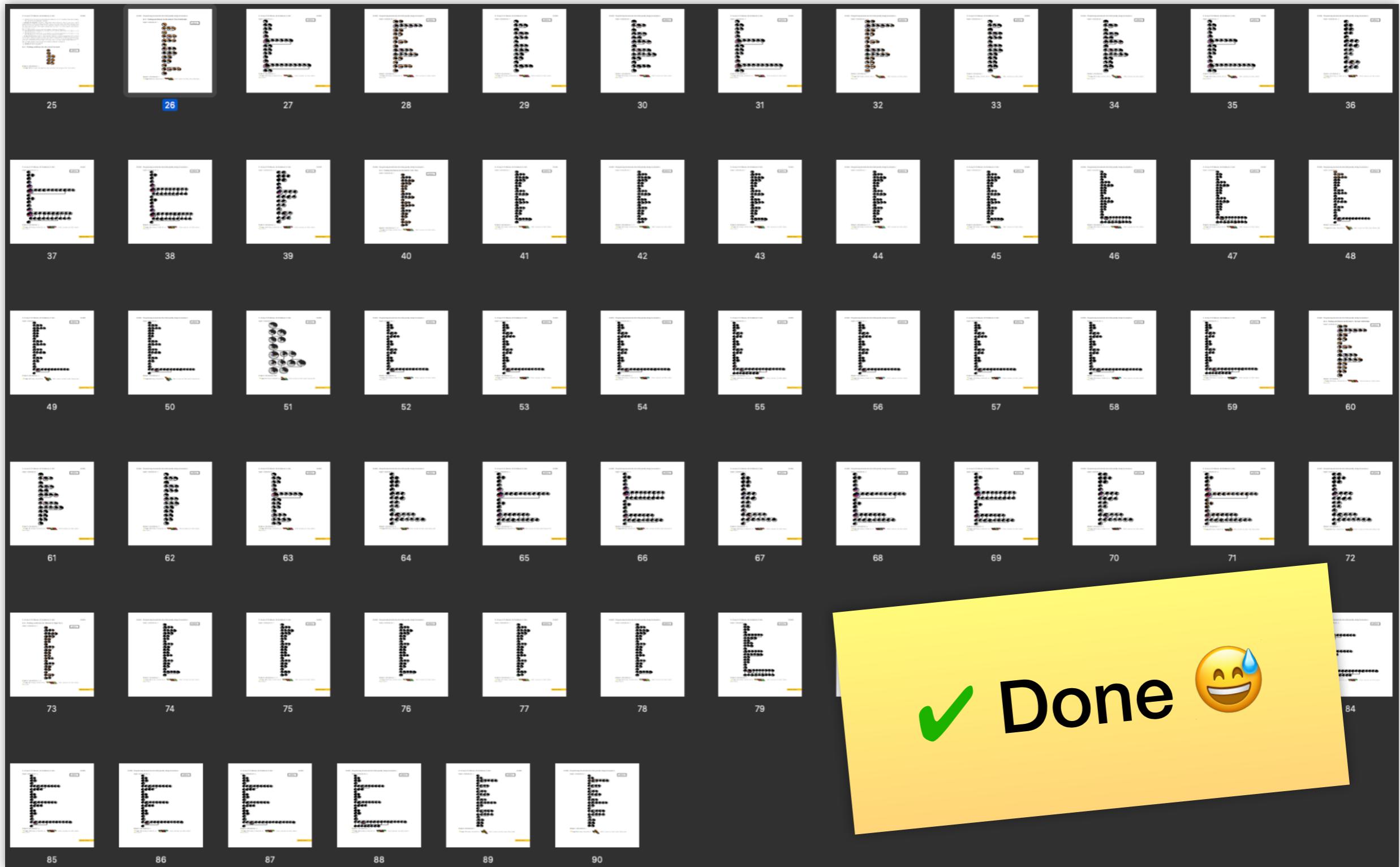


**Its folding is
correct !**

Repeat for each brick in each environment



Repeat for each brick in each environment

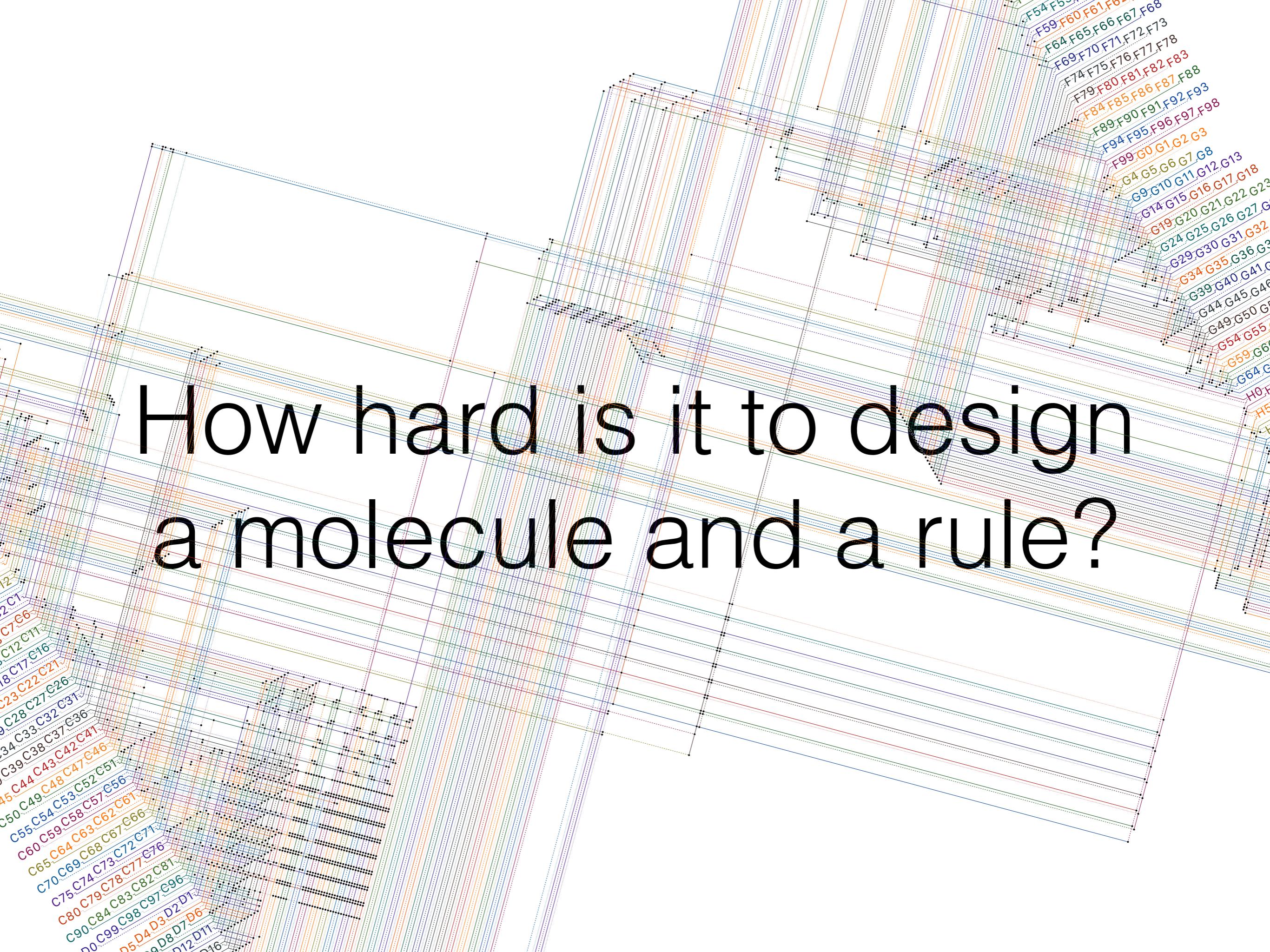


Binary counter: conclusion

- **Theorem.** There is a 60-periodic molecule that simulates a binary counter using 60 bead types and delay 3.

Back to general oritatami

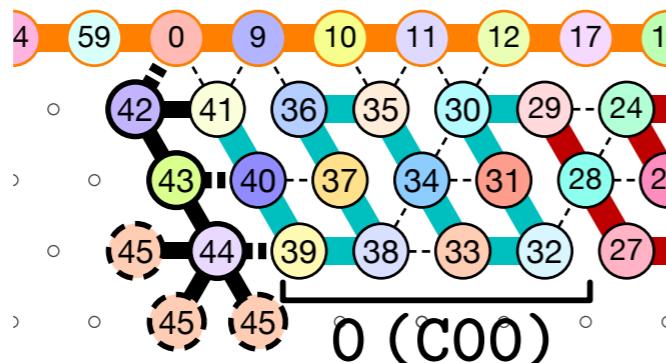
- How hard is it to design a rule?
 - NP-hard... but FPT, thus feasible!
- What can it compute?
 - Simulates any Turing Machine... *efficiently!*



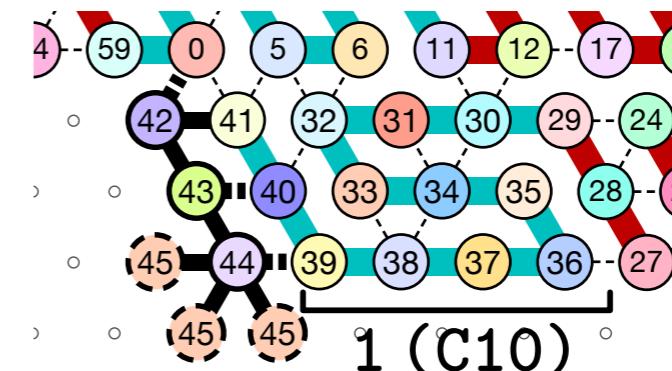
How hard is it to design
a molecule and a rule?

The first challenge: Designing the desired shapes

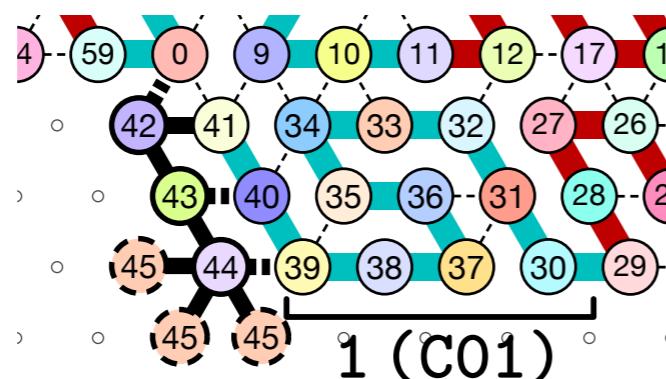
- Design shapes for which a **common** rule ❤ exists



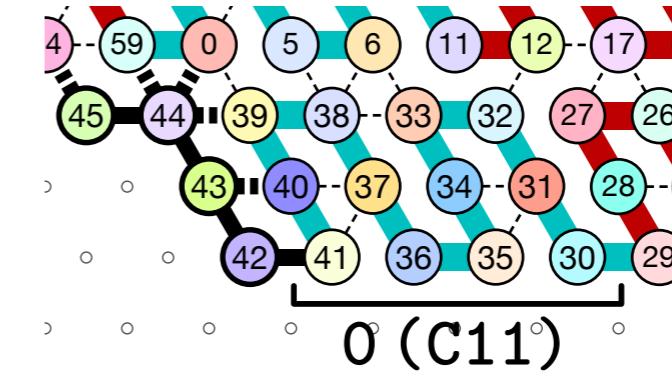
$$0+0 = 0 + \text{no C}$$



$$1+0 = 1 + \text{no C}$$



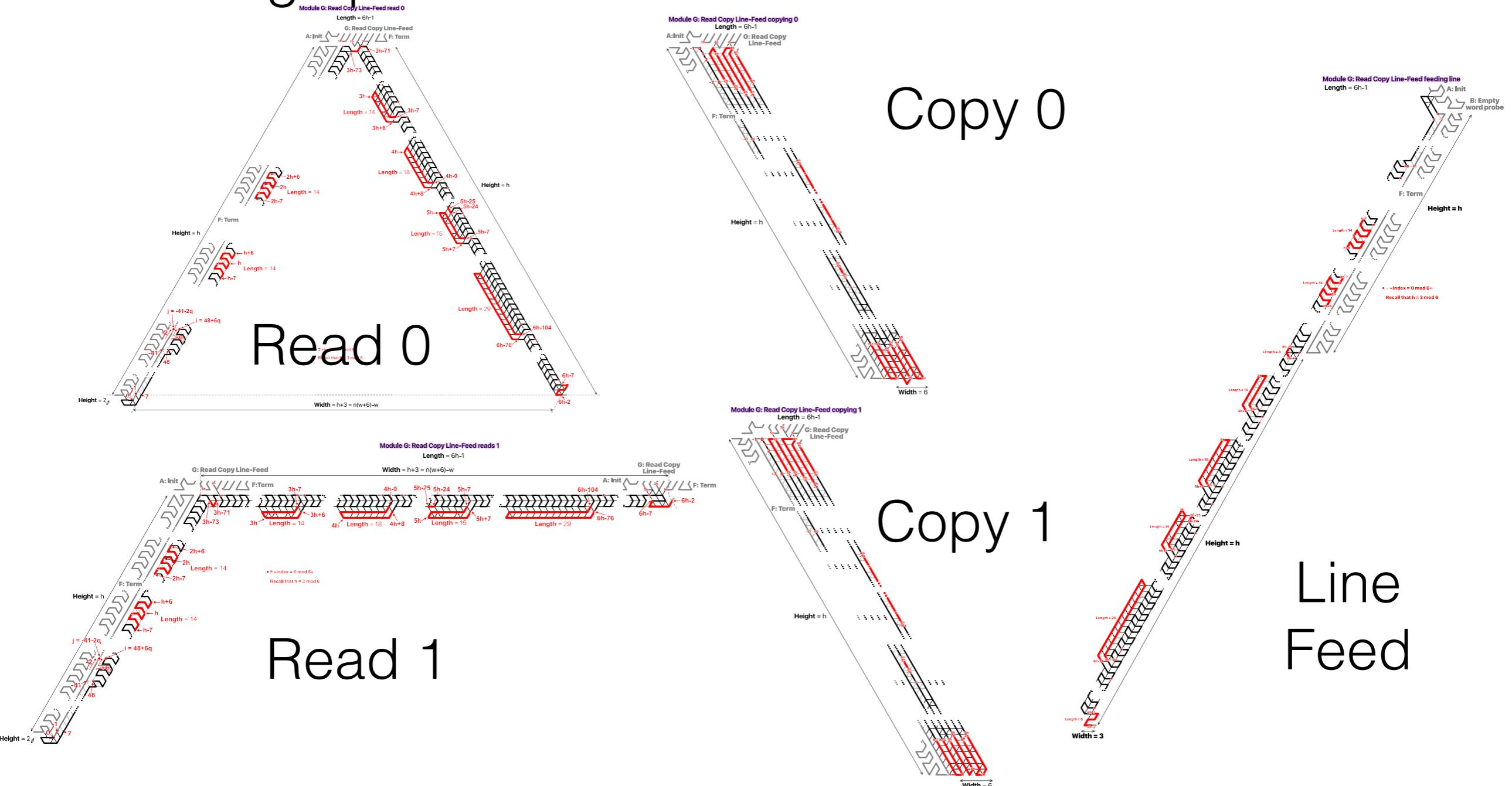
$$0+1 = 1 + \text{no C}$$



$$1+1 = 0 + \text{C}$$

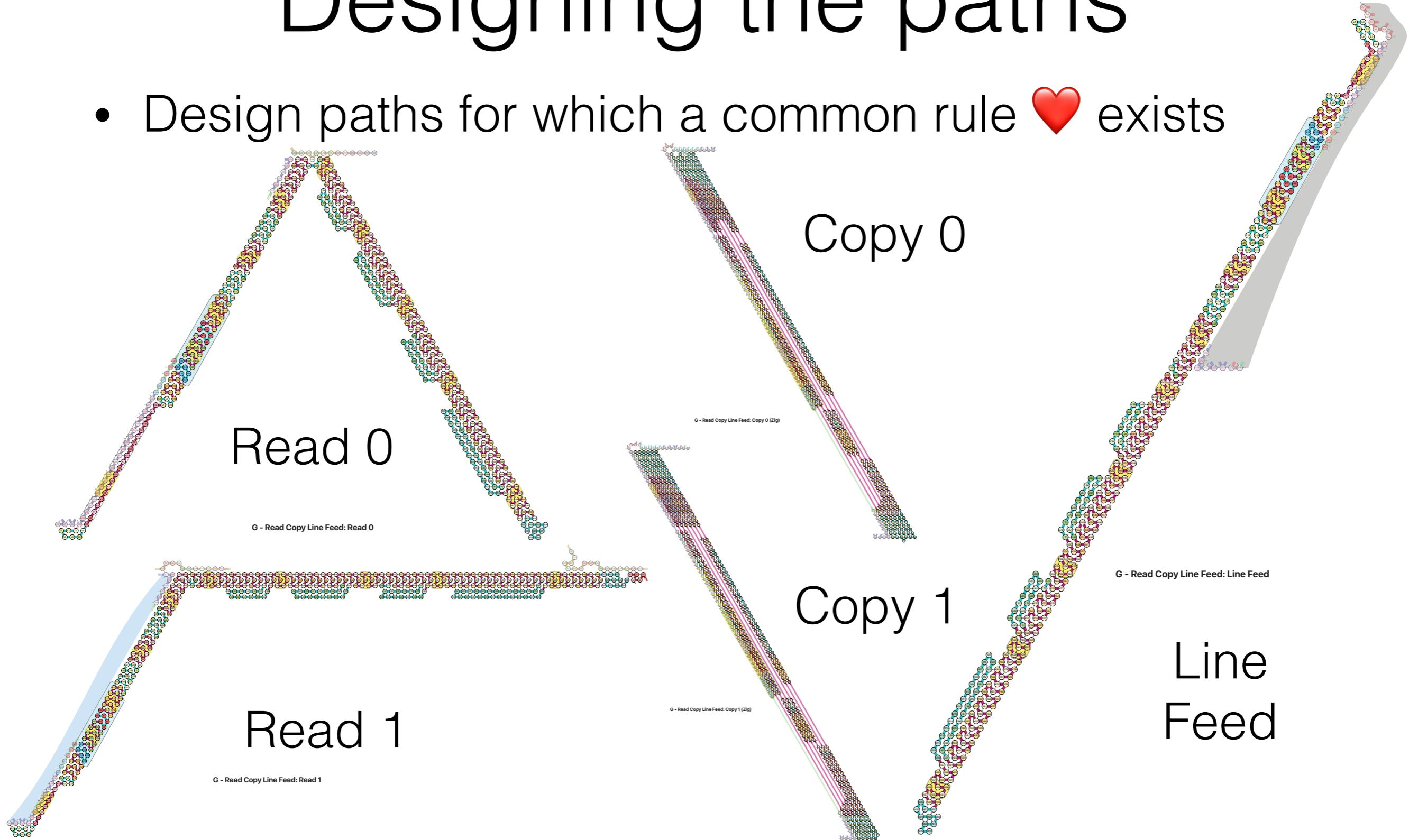
The first challenge: Designing the desired paths

- Design paths for which a **common** rule ❤ exists



The first challenge: Designing the paths

- Design paths for which a common rule ❤ exists

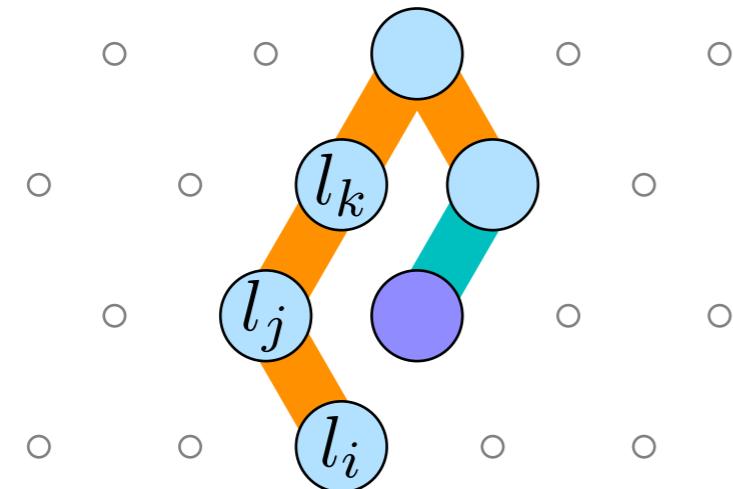


Oritatami design is NP-hard

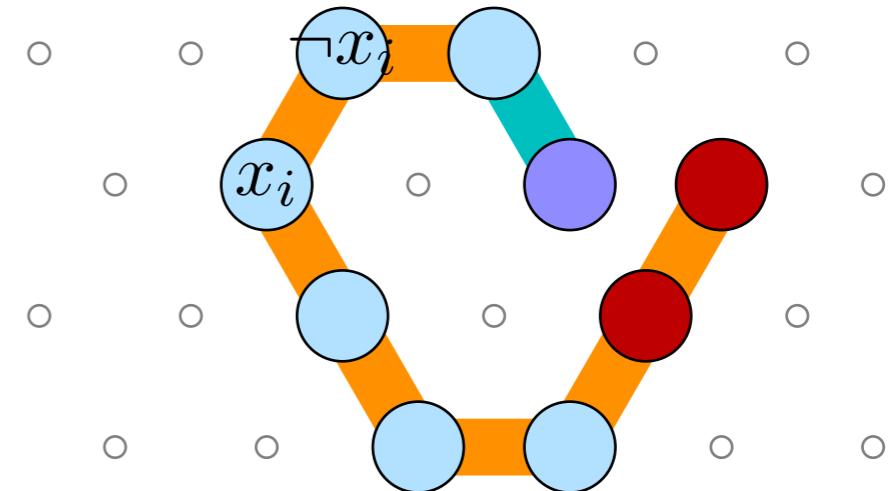
INPUT:	a delay time δ , a list of $n > 0$ seeds $\sigma_1, \sigma_2, \dots, \sigma_n$, and a list of n conformations c_1, c_2, \dots, c_n of the same length l
OUTPUT:	an attraction rule \heartsuit such that for all $i \in \{1, 2, \dots, n\}$, Oritatami system $\mathcal{O}_i = (s, \sigma_i, \heartsuit, \delta)$ deterministically folds into conformation c_i , where s is the sequence of length l such that for all $i \in \{1, 2, \dots, l\}$, $s_i = i$.

The reduction ($\text{length}=1$, δ arbitrary)

Ensures it binds to at least one literal in $l_i \vee l_j \vee l_k$



Ensures it binds to at most one of x_i and $\neg x_i$



The second challenge: Designing the rule ❤

Theorem. There is a **FPT algorithm** with respect to L that designs **in linear time in L** (but exponential in k and δ) a **rule** ❤ that folds the sequence $1, \dots, L$ of length L into k prescribed conformations when folded in k prescribed environments.

Proof. • **Locality:** each bead only sees a bounded number (exponential in δ) of other beads when folded.

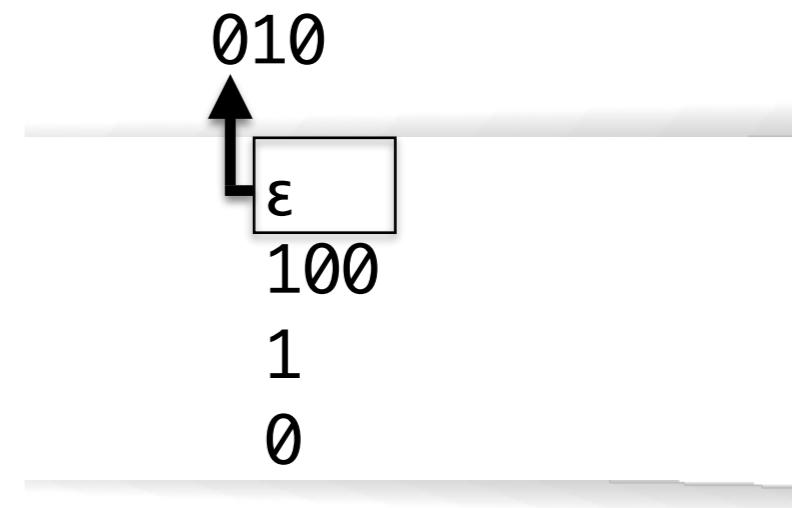
- Then, compute all valid local rules for each of these neighborhoods
- And use dynamic programming to decide whether there is a global rule compatible with at least one of the local rule for each environment.

Oritatami is
Turing complete

Skipping Cyclic Tag Systems

- A finite **cyclic sequence** of finite binary **code words** with a pointer p to one of them
- An initial binary **tape word** (the input)
- **Dynamics:**
 - *If the tape word is empty (ϵ): halt*
 - *If the 1st letter of the tape word is 0:* delete the 0 and increment the pointer p
 - *If the 1st letter of the tape word is 1:* delete the 1, append to the tape word the code word at position $p+1$ and increase p by +2

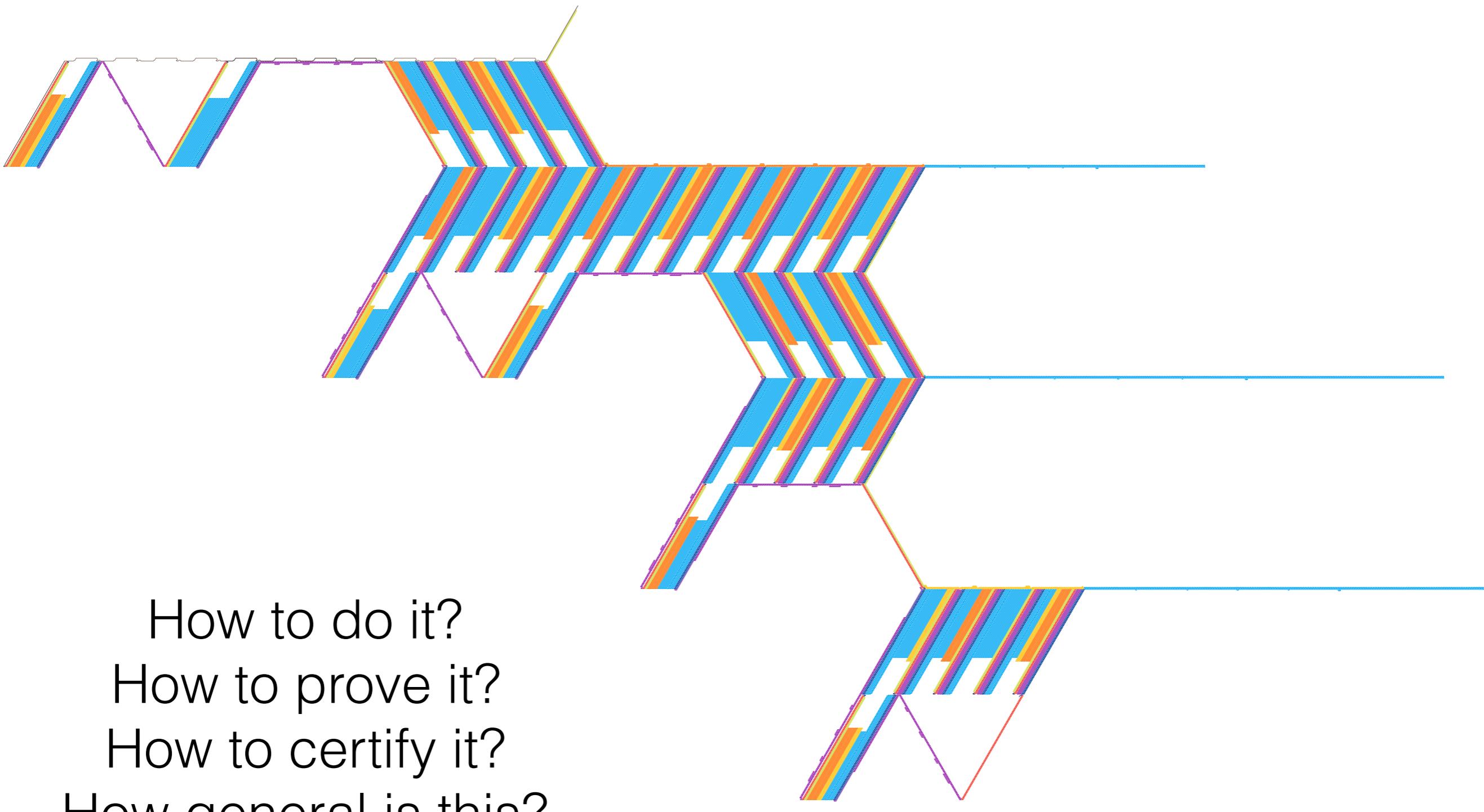
Example.



Skipping Cyclic Tag Systems

- A finite **cyclic sequence** of finite binary **code words** with a pointer p to one of them
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- **Theorem** [Neary, Woods, 2006]
Cyclic tag systems simulate any Turing machine with only a **quadratic** slow down

The simulation



A general programming framework

Abstract
Level

Blocks

Modules

Functions

Bricks

Bricks

Bricks

Bricks

Beads

Beads

Beads

Beads

Assembly
Level

A general programming framework

Prove here correctness of
algorithm

Abstract
Level

Blocks

Modules

Functions

Bricks

Bricks

Bricks

Beads

Beads

Assembly
Level

Certify here correctness
of implementation

General programming tools

State

Area entry point

Position in Molecule

Logic

Sliding shapes

Bouncing gliders

Geometry

Expanding shapes

Goto

Offsets

Socks

Exponential coloring

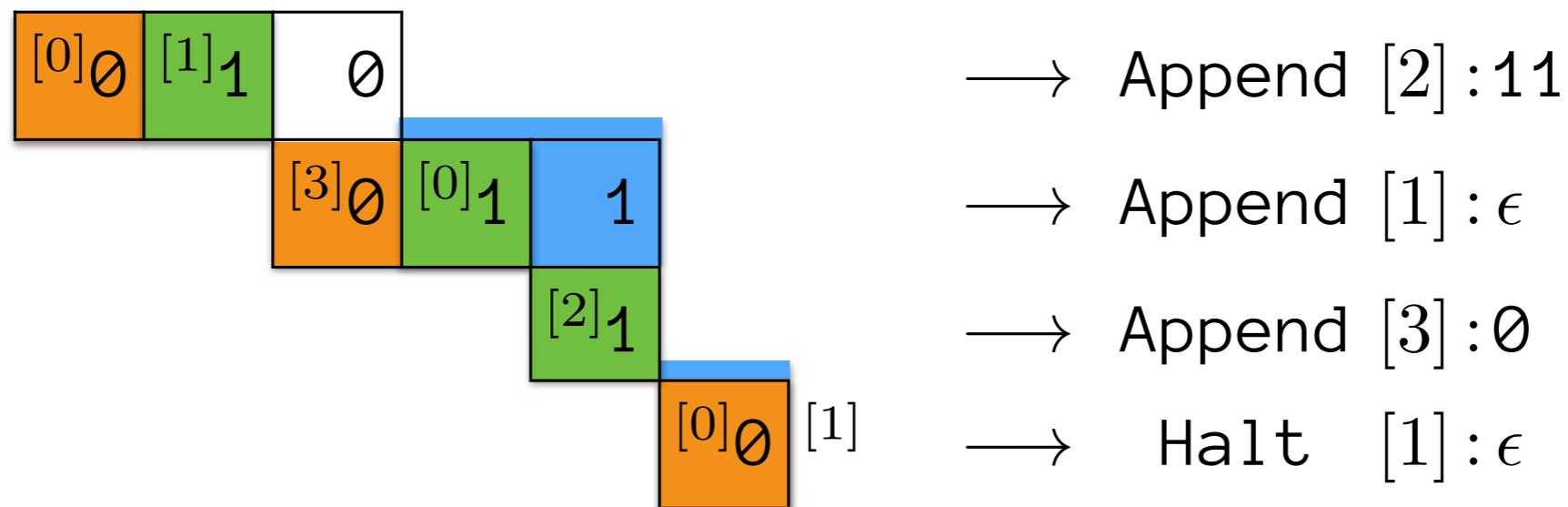
Hiding

Back to our simulation

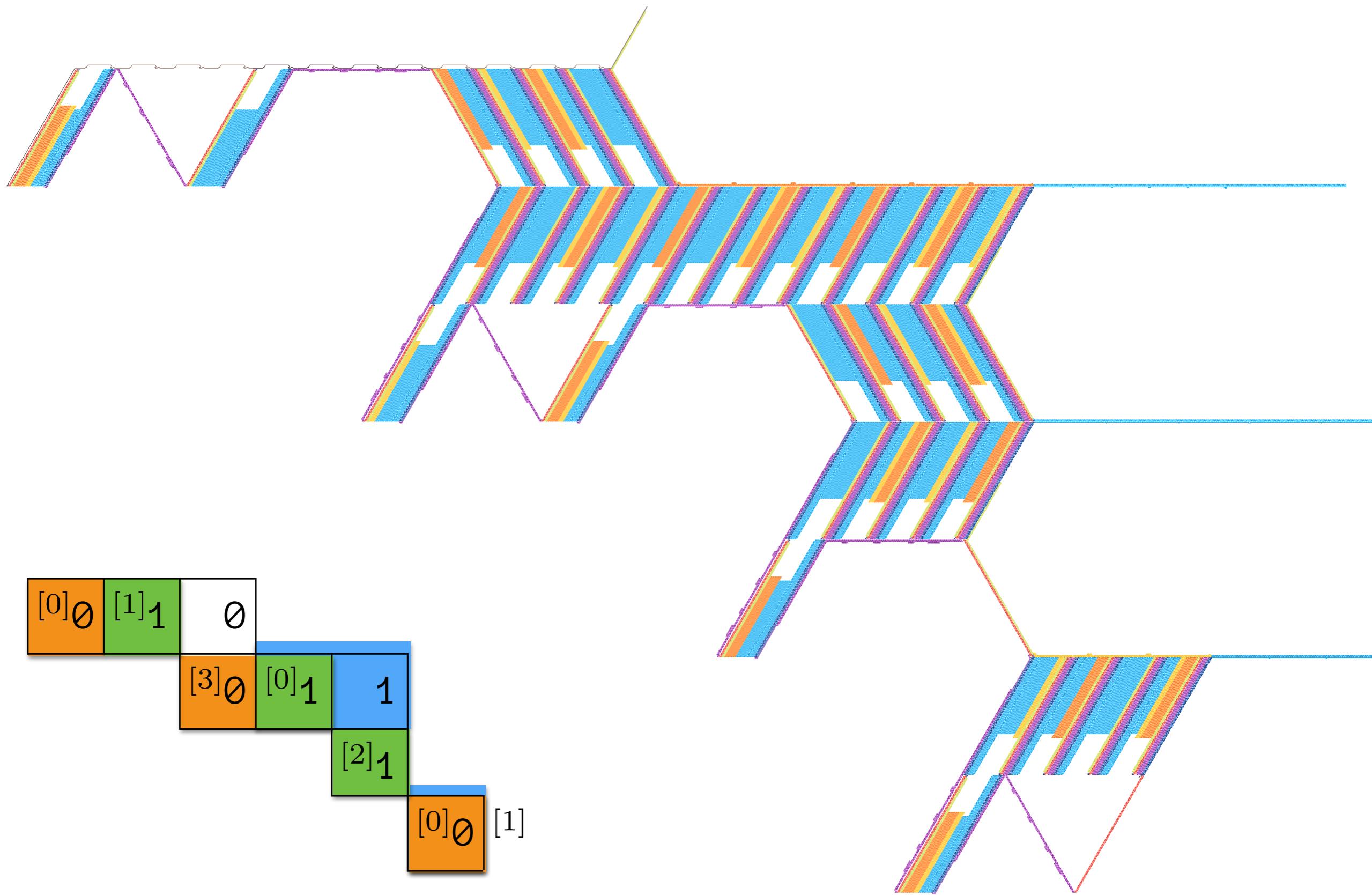
Trimmed space-time diagram

Consider the following productions: $p = \langle [0]110, \epsilon, [1]11, [2]:[3]\rangle$

$$[0]010 \rightarrow [1]10 \xrightarrow{\text{Append } [2]:11} [3]011 \rightarrow [0]11 \xrightarrow{\text{Append } [1]:\epsilon} [2]1 \xrightarrow{\text{Append } [3]:0} [0]\emptyset \rightarrow [1] \text{ Halt}$$



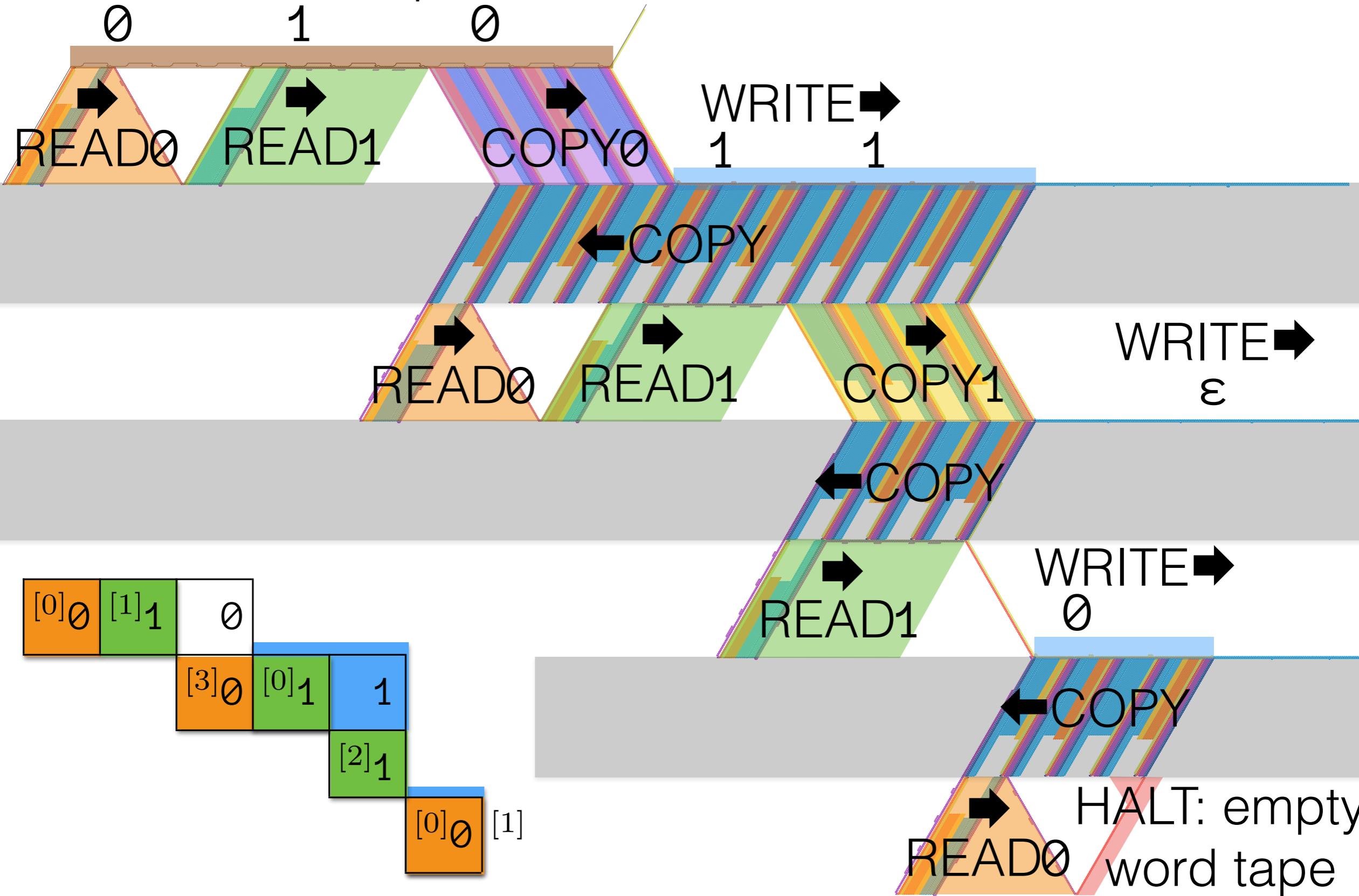
The simulation



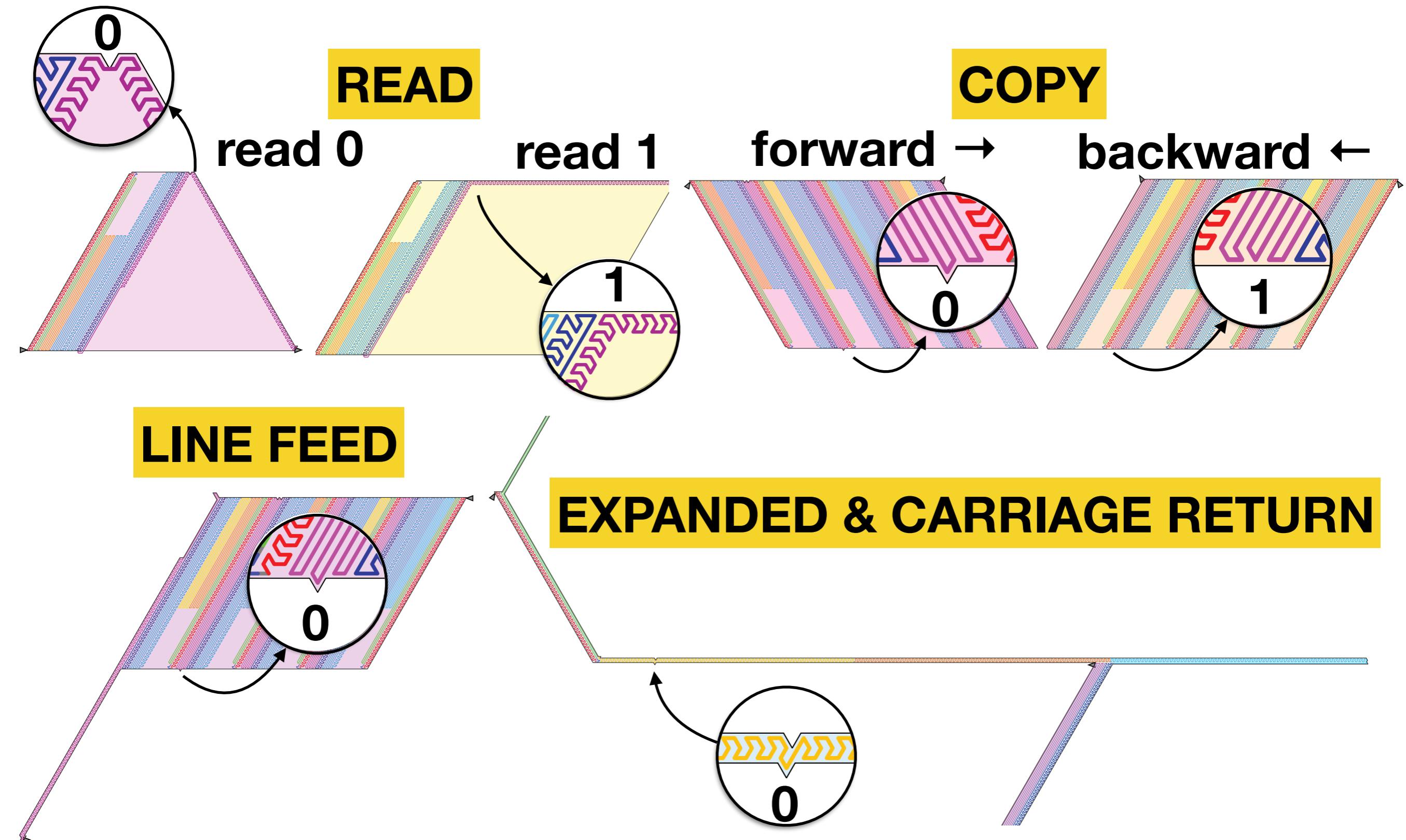
The simulation

Initial word tape:

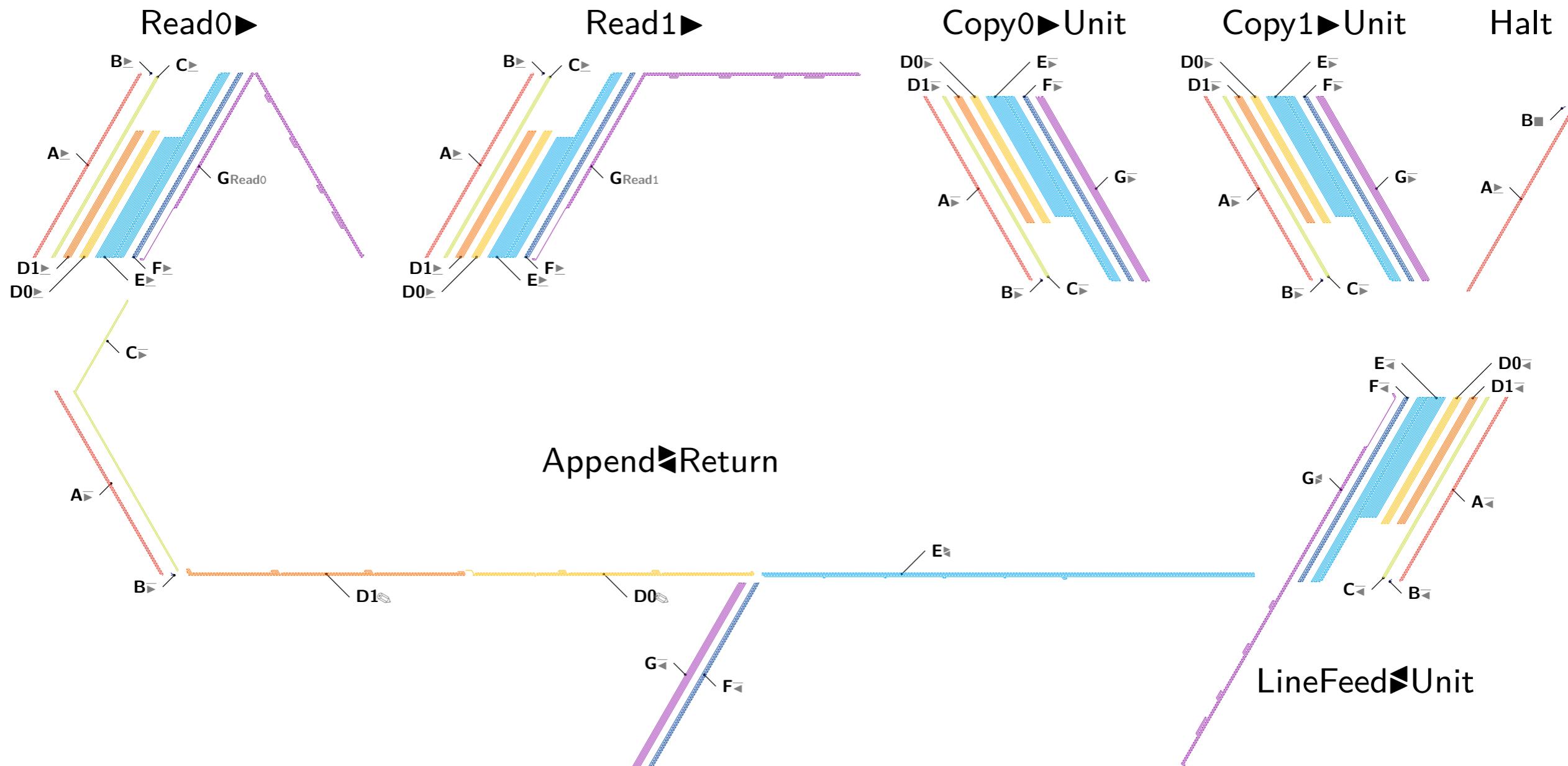
0 1 0



The blocks



The bricks inside each block



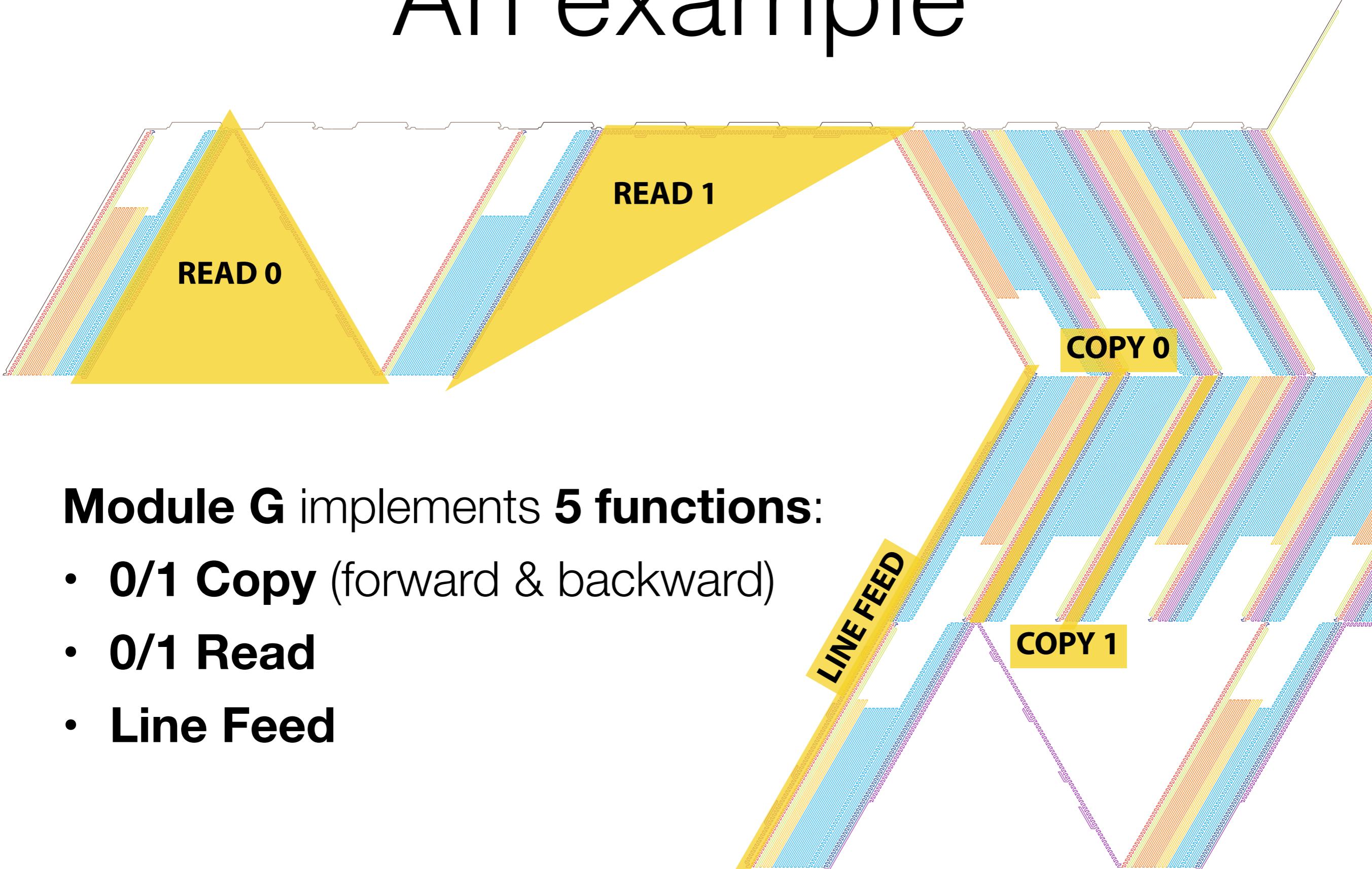
How do we implement
several functions
(i.e. folding into different bricks)
in a given module?

An example

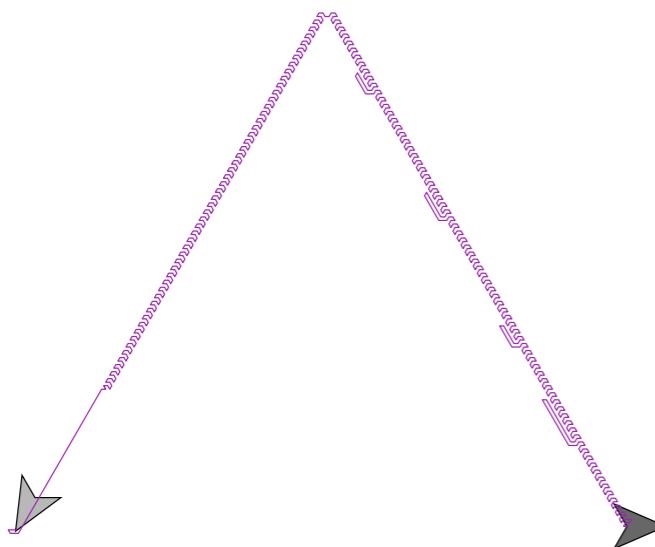
Module G implements 5 functions:

- **0/1 Copy** (forward & backward)
- **0/1 Read**
- **Line Feed**

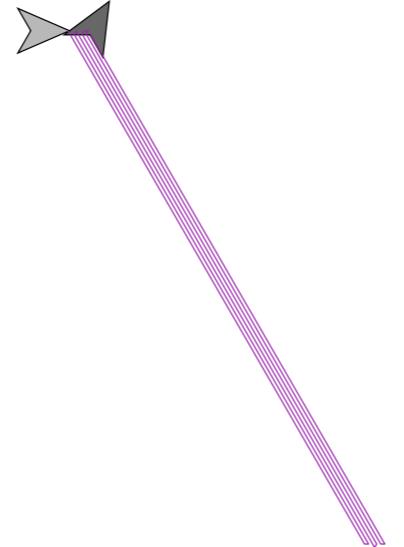
An example



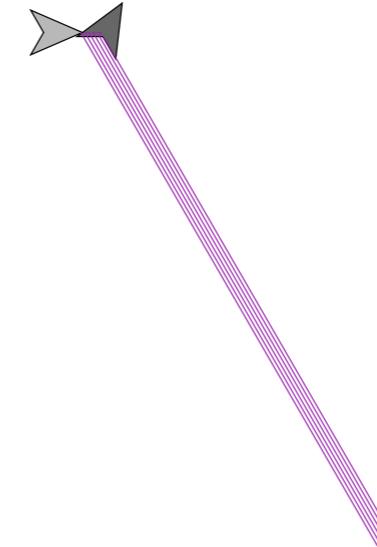
The various bricks for module G



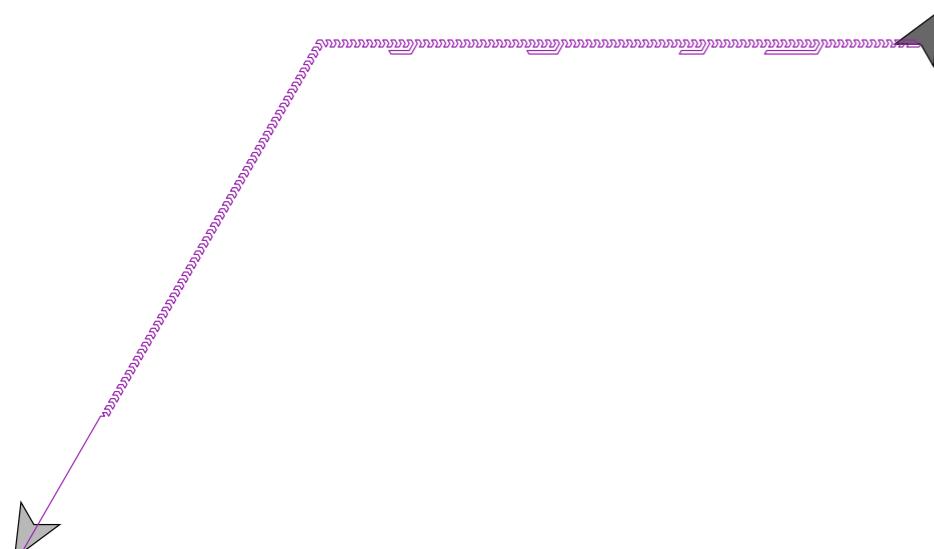
(a) The brick `G>Read0`.



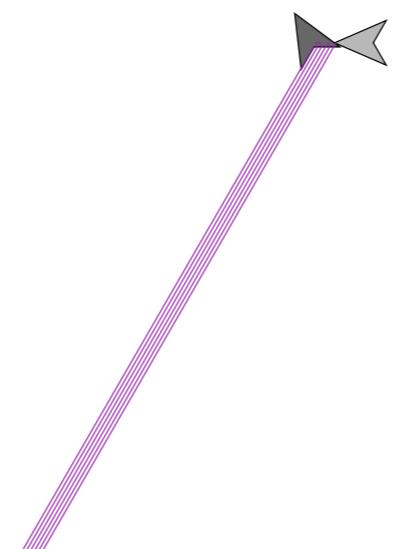
(a) The brick `G>Copy0`.



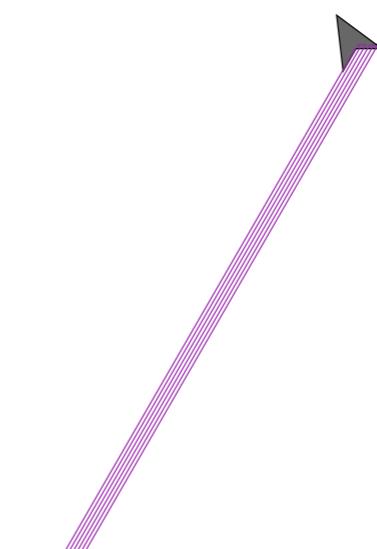
(b) The brick `G>Copy1`.



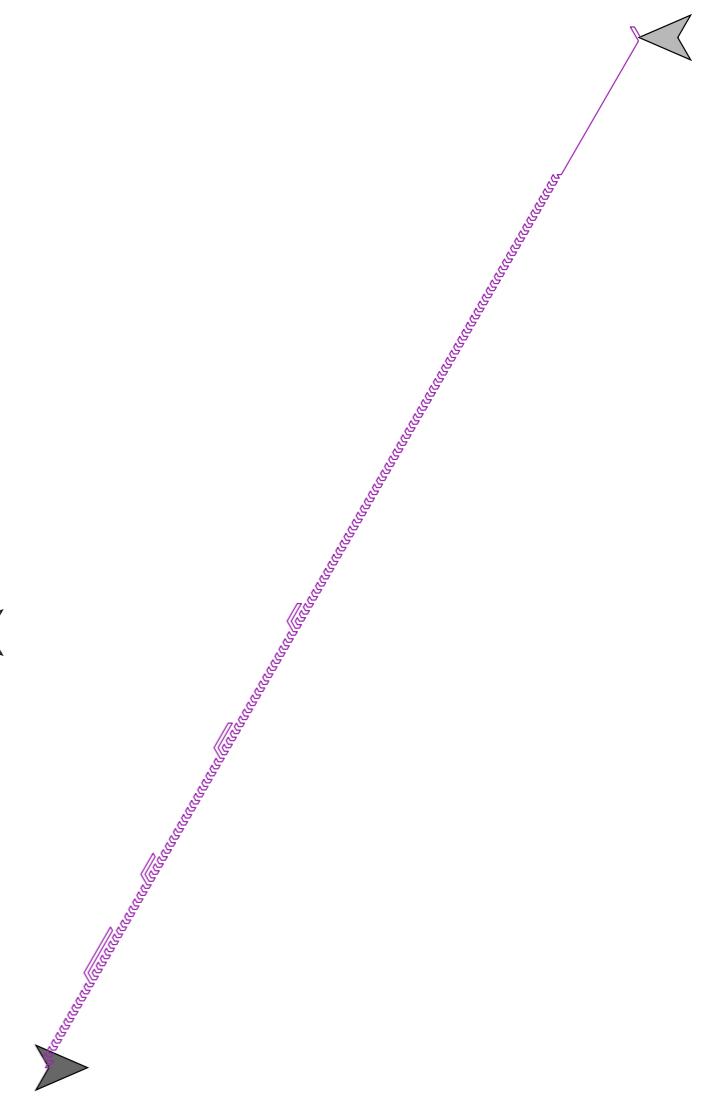
(b) The brick `G>Read1`.



(c) The brick `G<Copy0`.

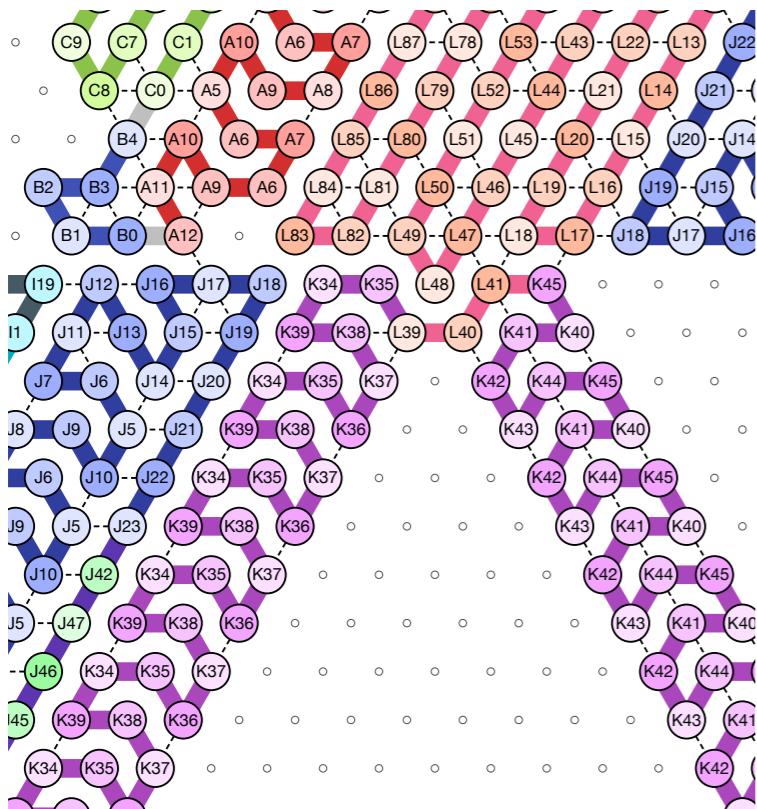


(d) The brick `G<Copy1`.

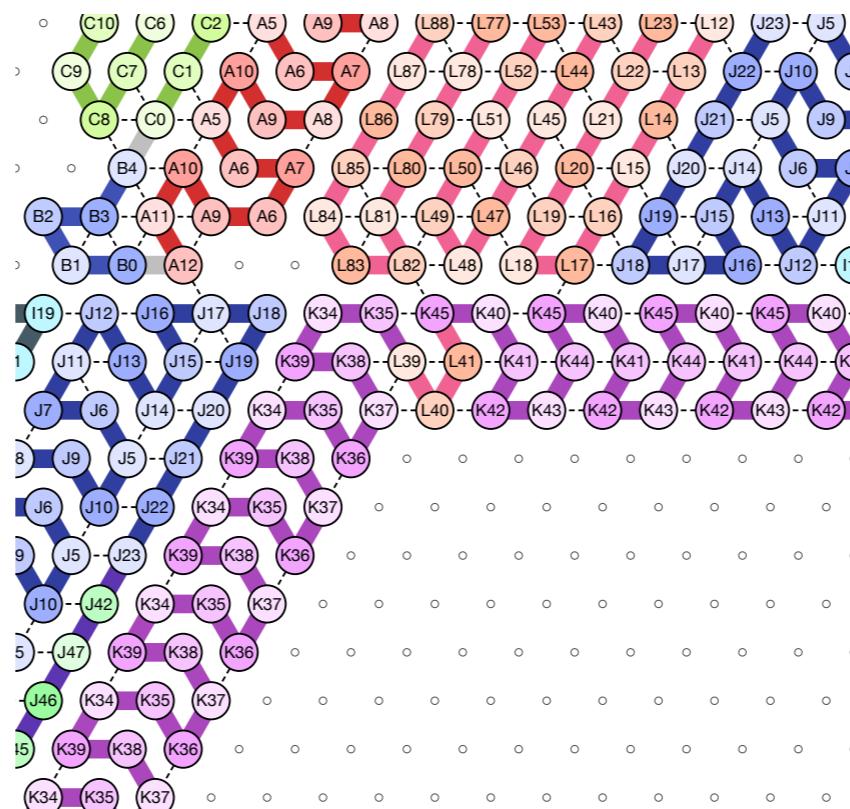


(a) The brick `G#LineFeed`.

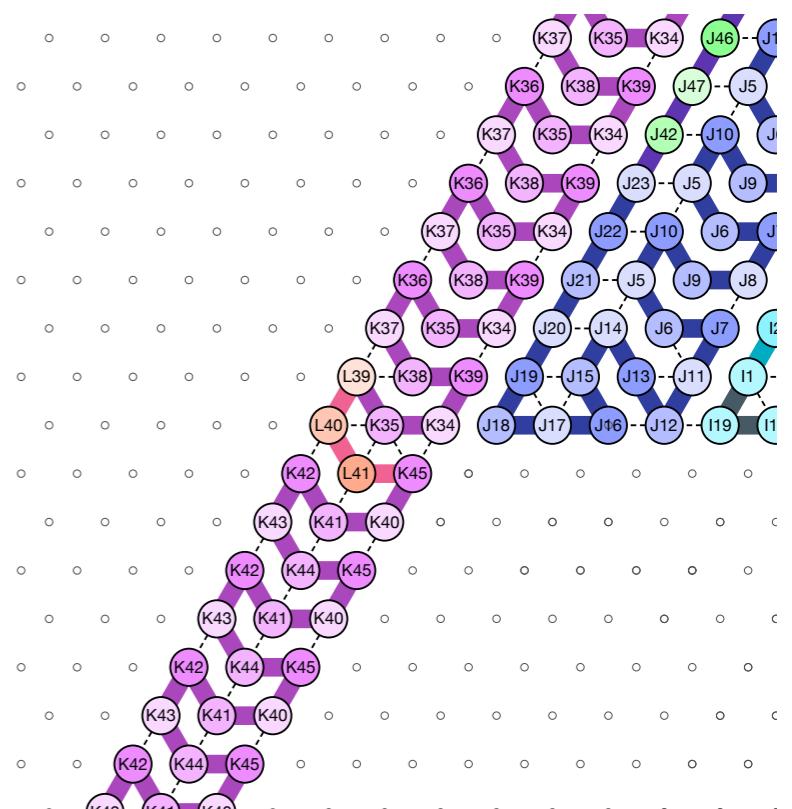
Glider turns



(a) **G** bounces southeastward in presence of a spike encoding a 0 and folds into **G ▶ Read0**.



(b) **G** bounces eastward on a flat surface encoding a 1, and folds into **G ▶ Read1**.

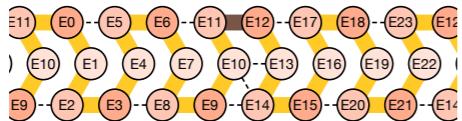


(c) **G** goes straight southwestward in absence of obstacle, and folds into **G ▶ LineFeed**.

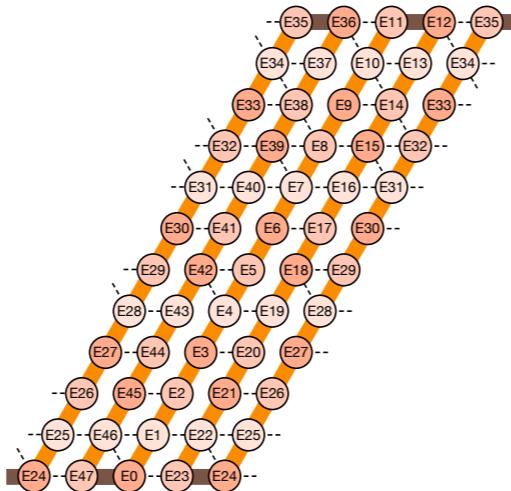
Some programming paradigms

- Switchback expanding in Gliders
- Offset
- Exponential coloring
- Socks

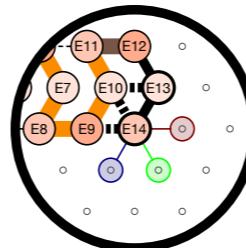
Switchback expanding into gliders



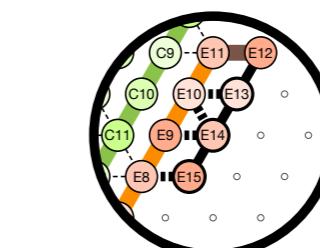
(a) Glider



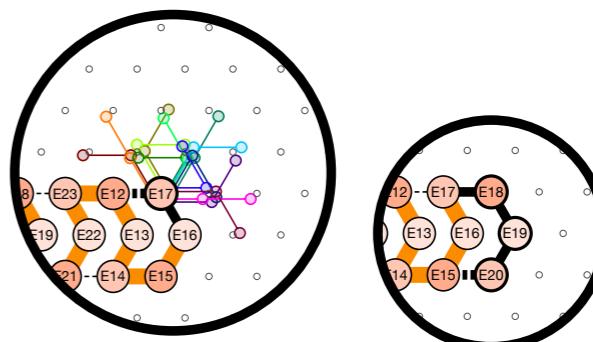
(b) Switchback



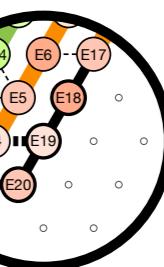
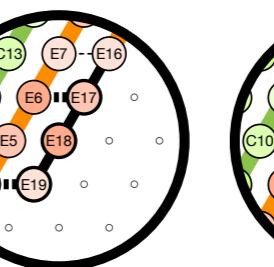
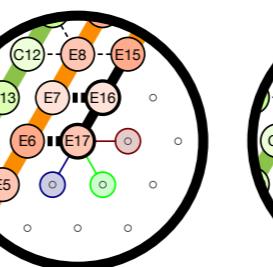
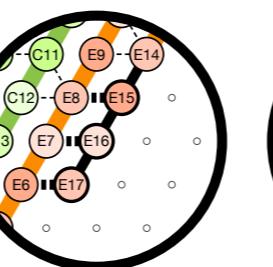
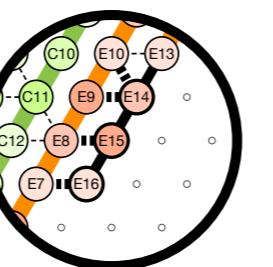
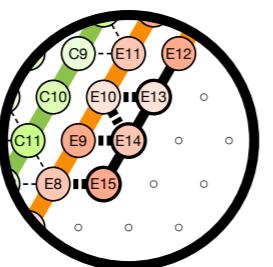
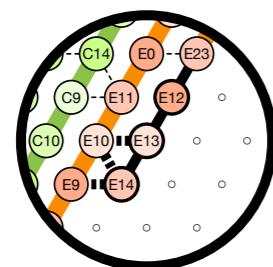
(c) Glider/Switchback turn folding compatibility.



(d) from left to right: the folding of the subsequence as a glider.

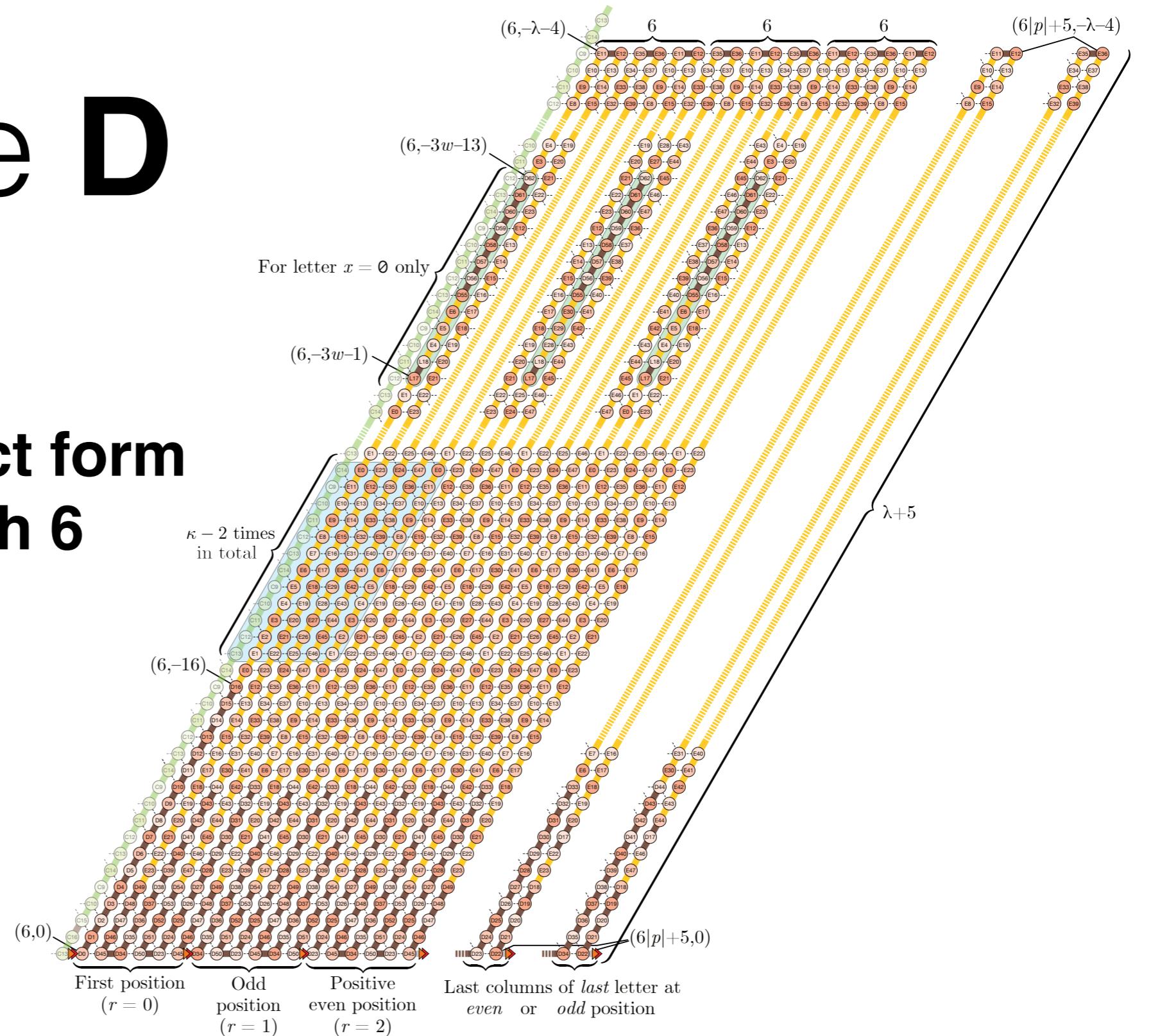


(e) from left to right: the folding of the subsequence as a switchback.

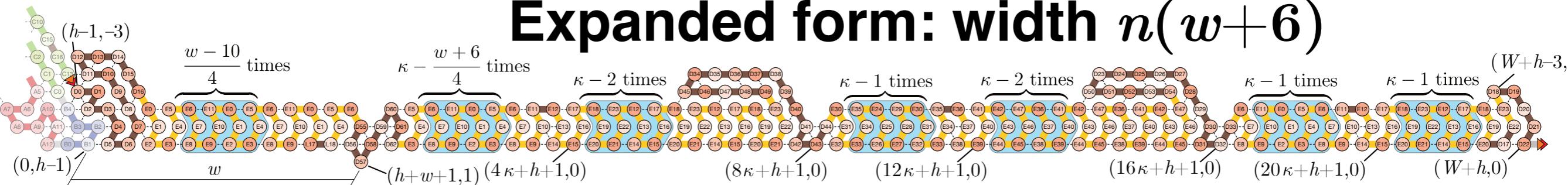


Module D

**Compact form
width 6**



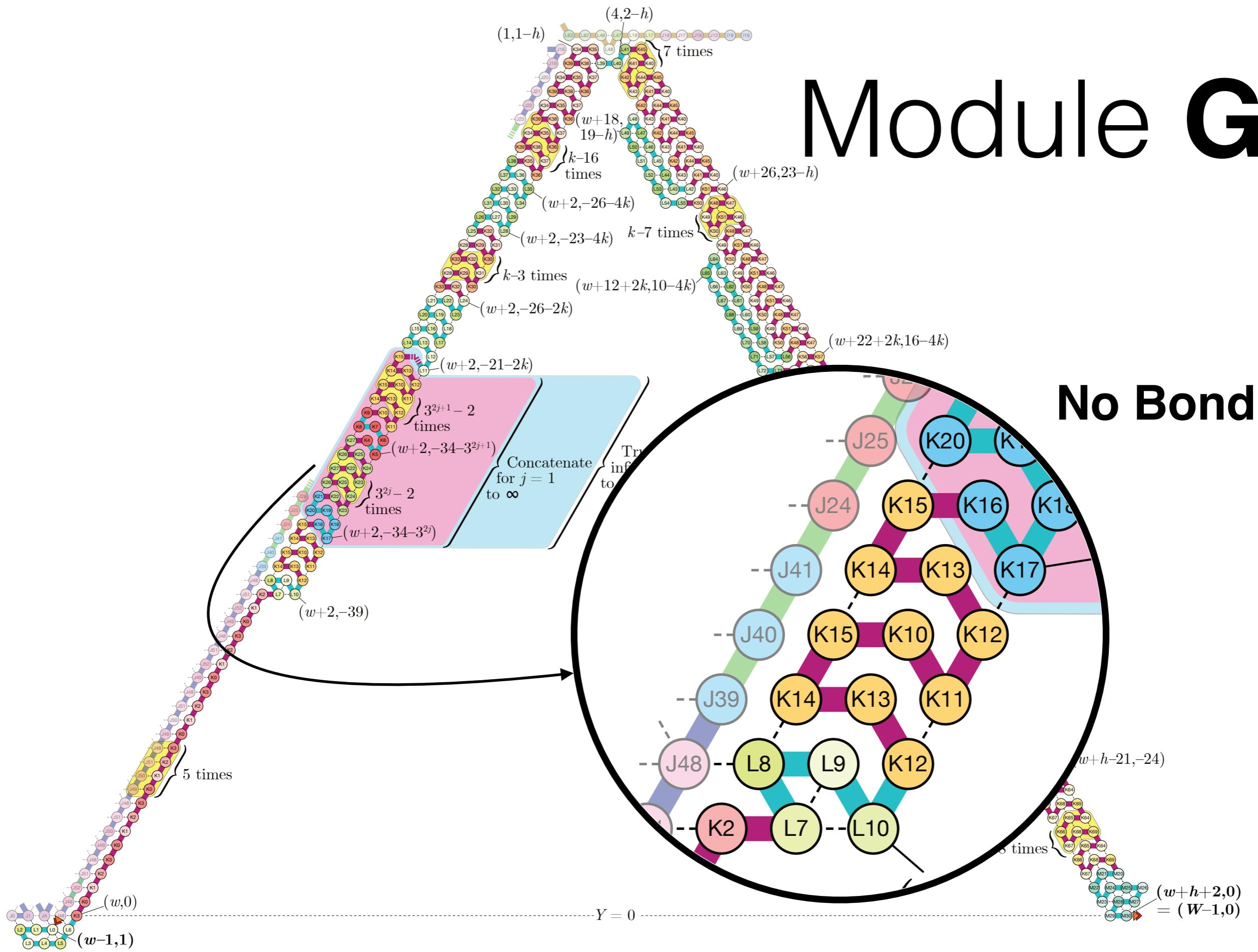
Expanded form: width $n(w+6)$



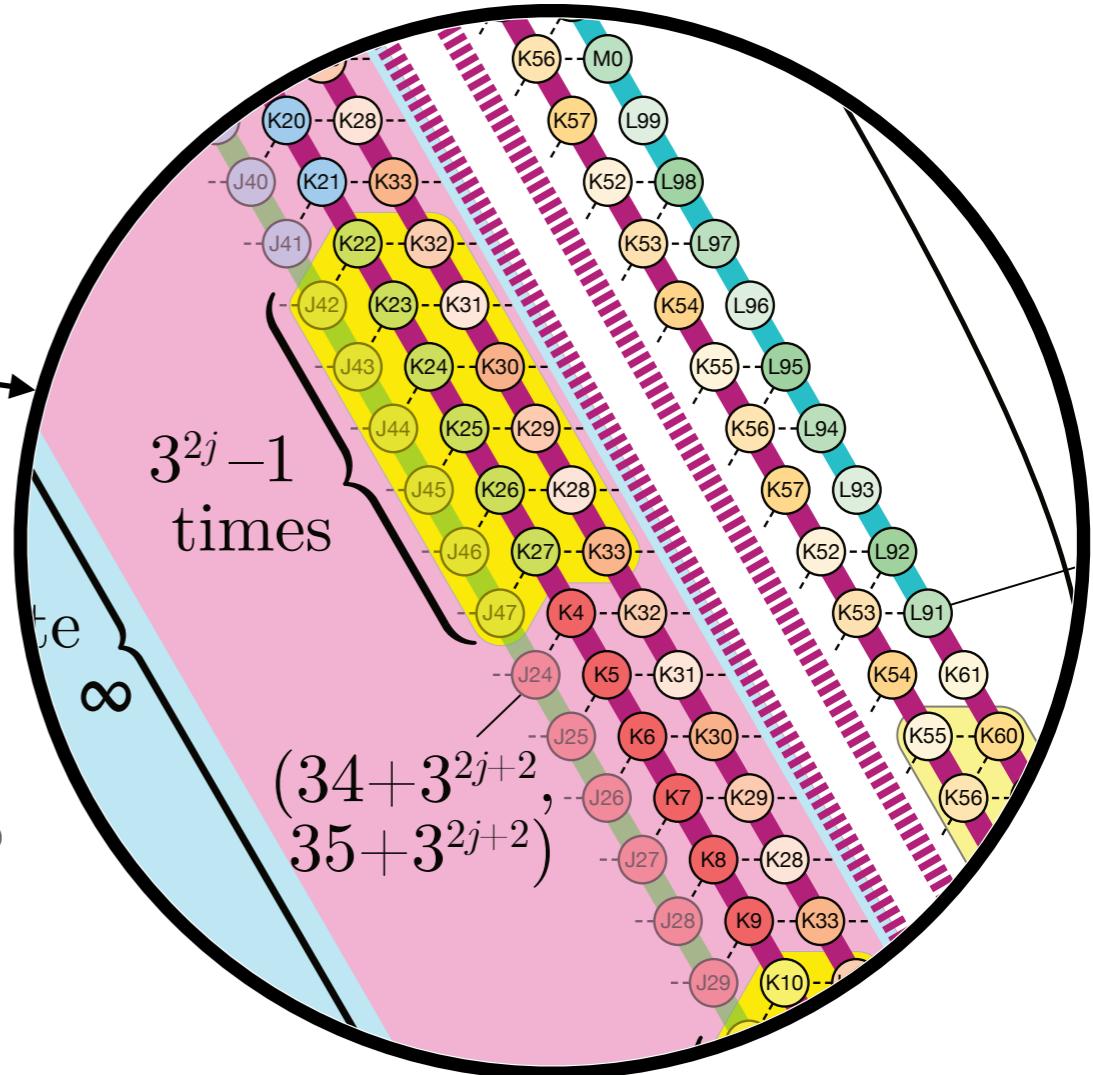
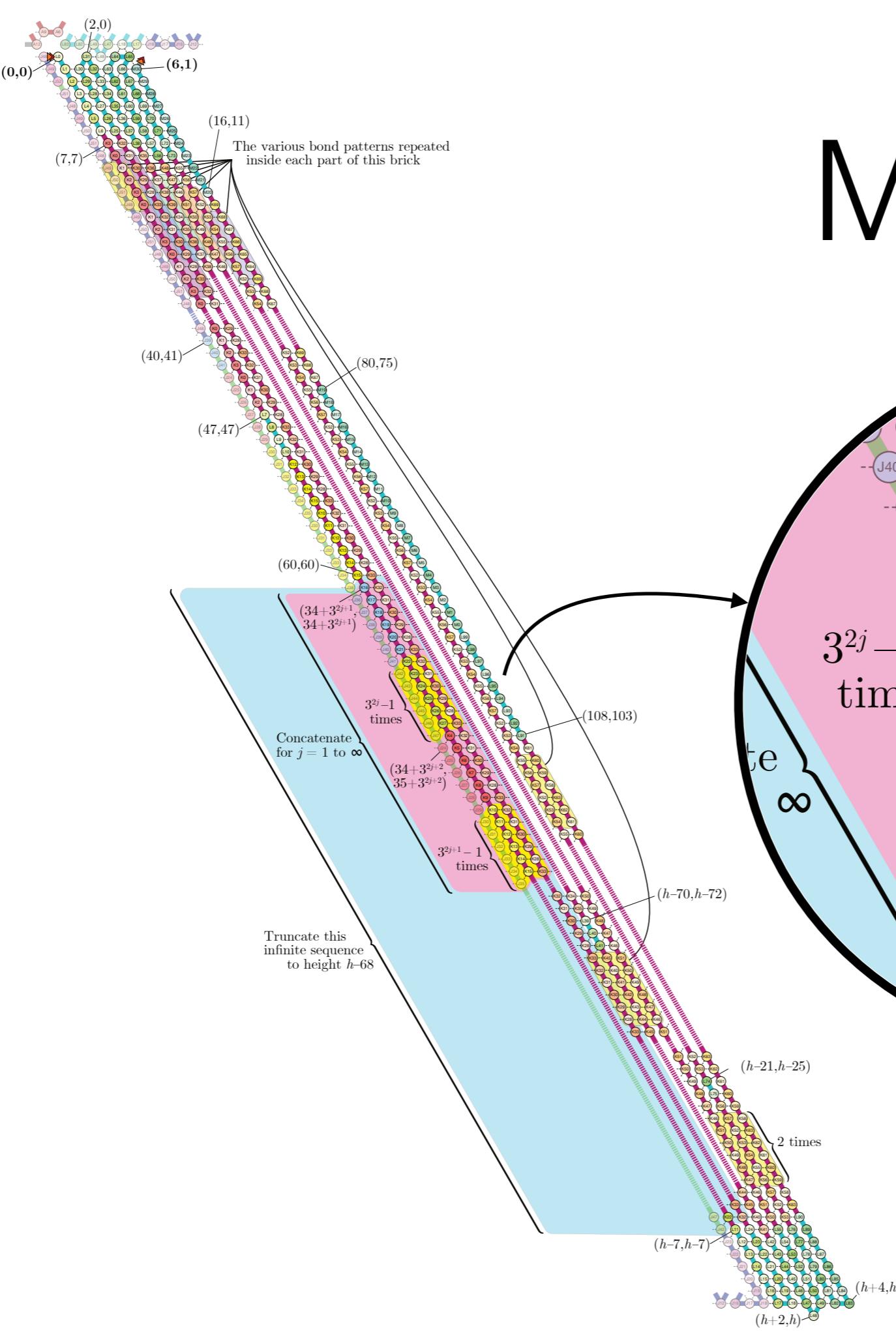
Exponential coloring

- Bonds everywhere if unshifted and then adopt switchback form
- Bonds nowhere if shifter and then adopt glider form

Module G

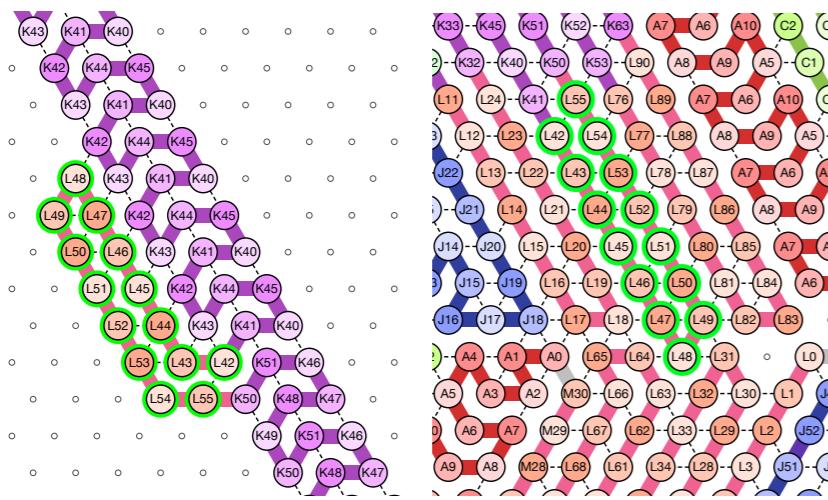


Module G

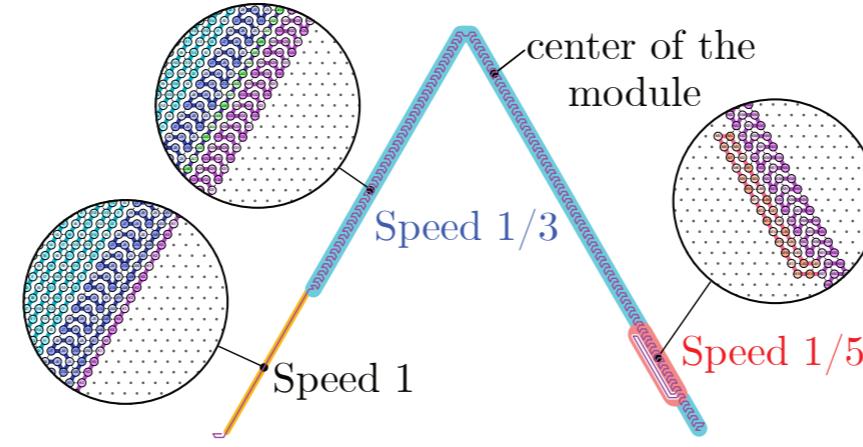


Bonds
everywhere

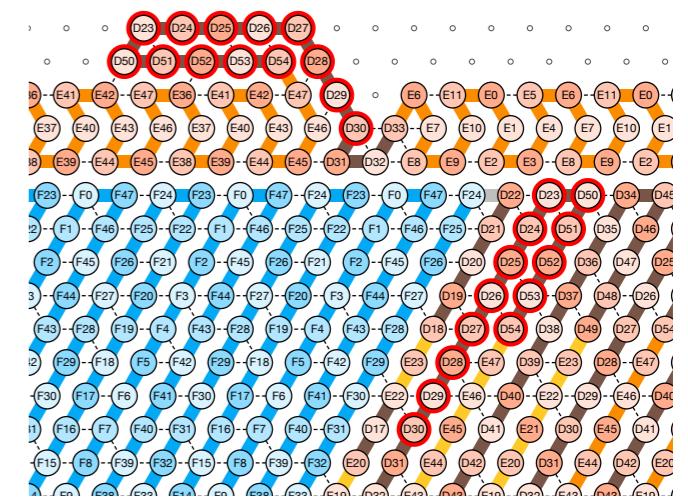
Socks



(a) Easier bond design



(b) Delaying gliders



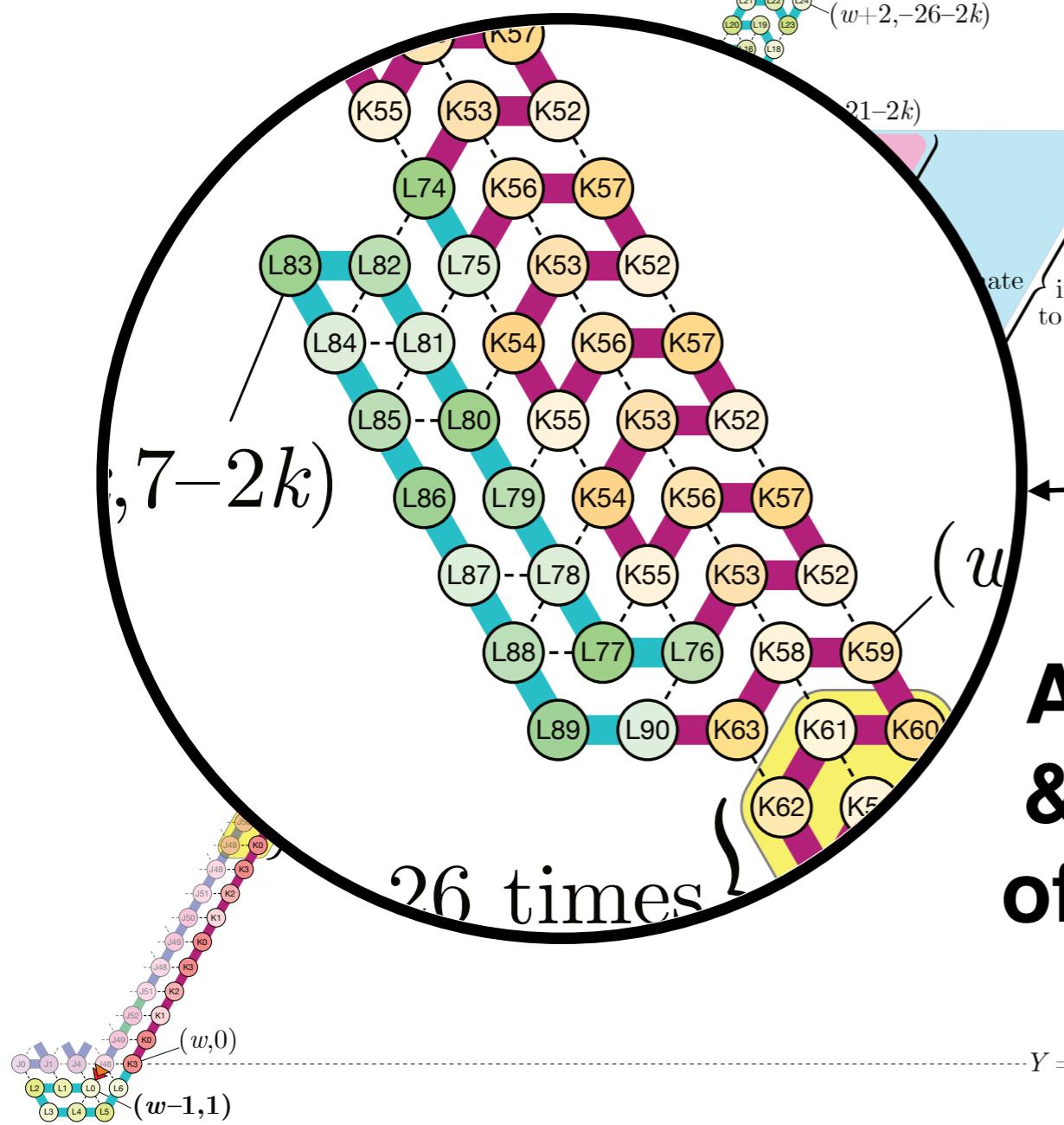
(c) Confinement

(a) Let fold parts in their natural forms, simplify the design

(b) Delaying and shifting to space out various functions

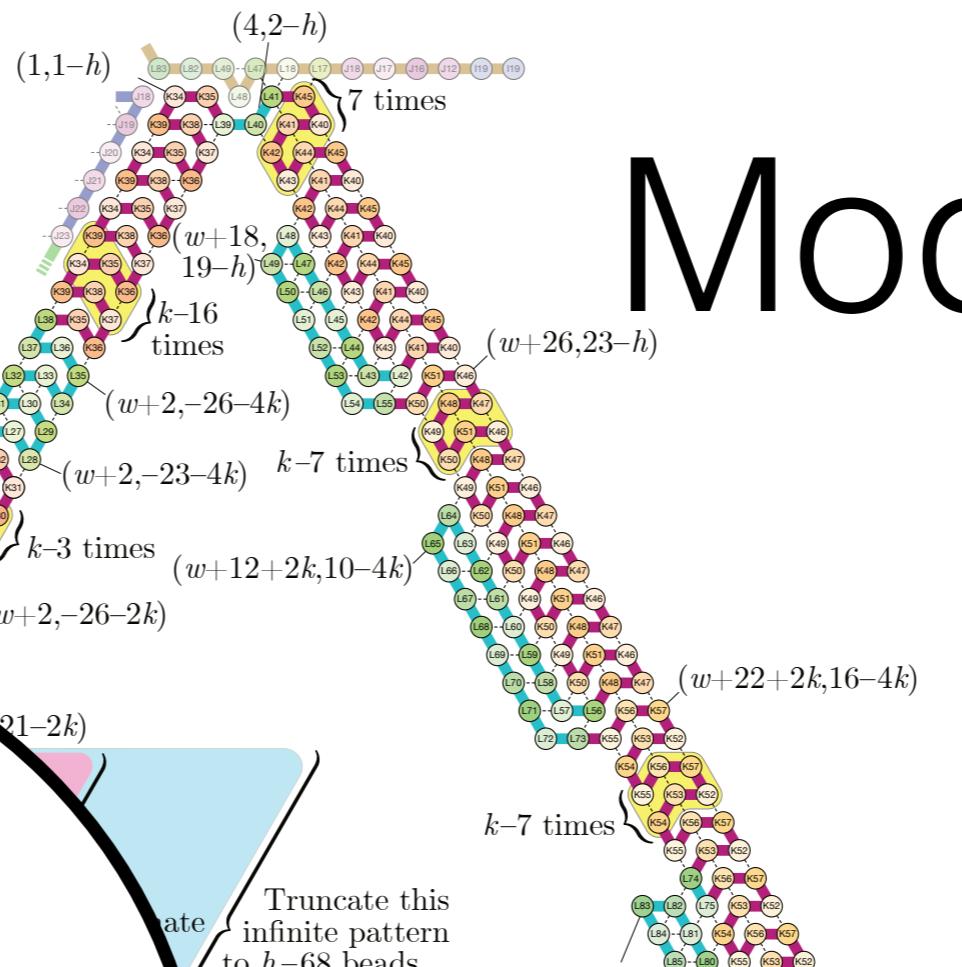
(c) Confinement to prevent unwanted interactions

Module G



**Absorbing
& Creating
offsets with
Socks**

$Y = 0$

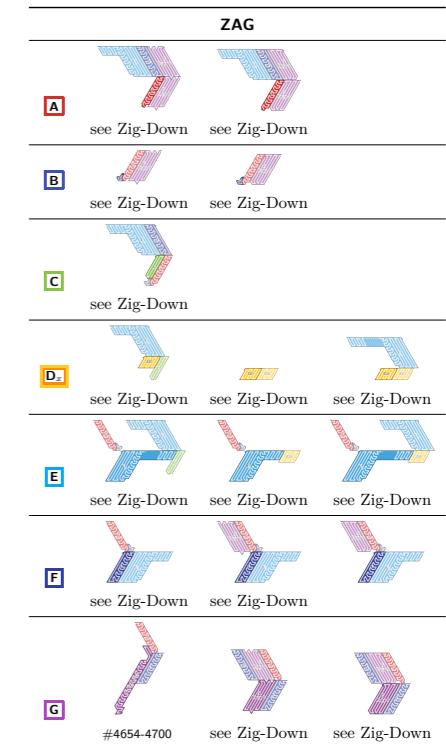
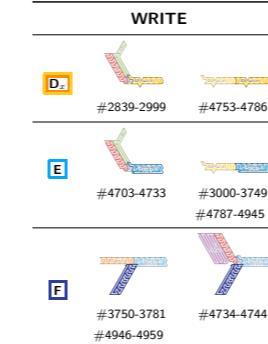
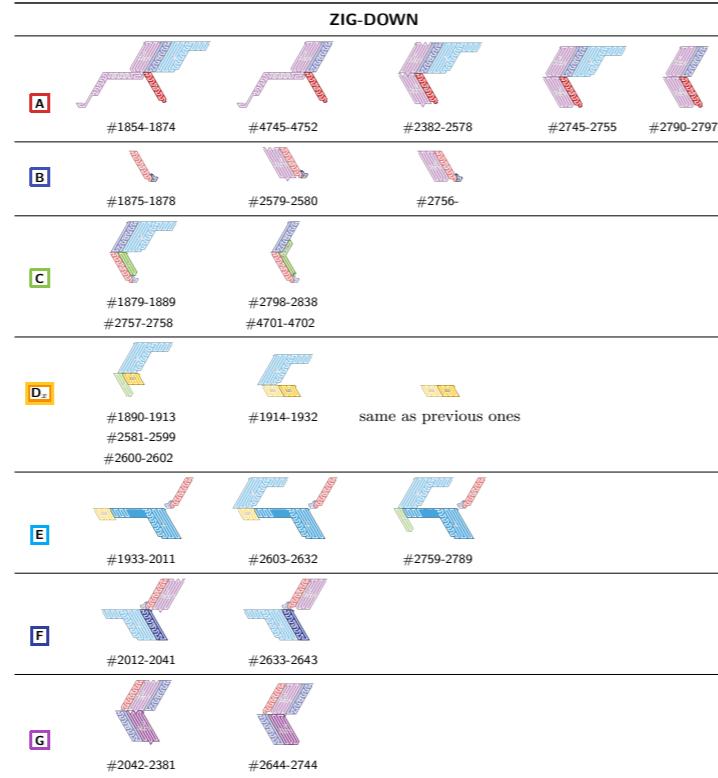
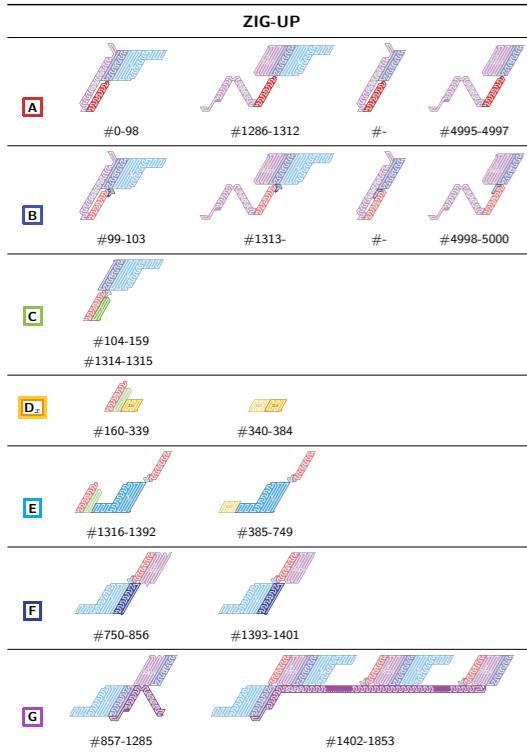


Truncate this infinite pattern to $h=68$ beads

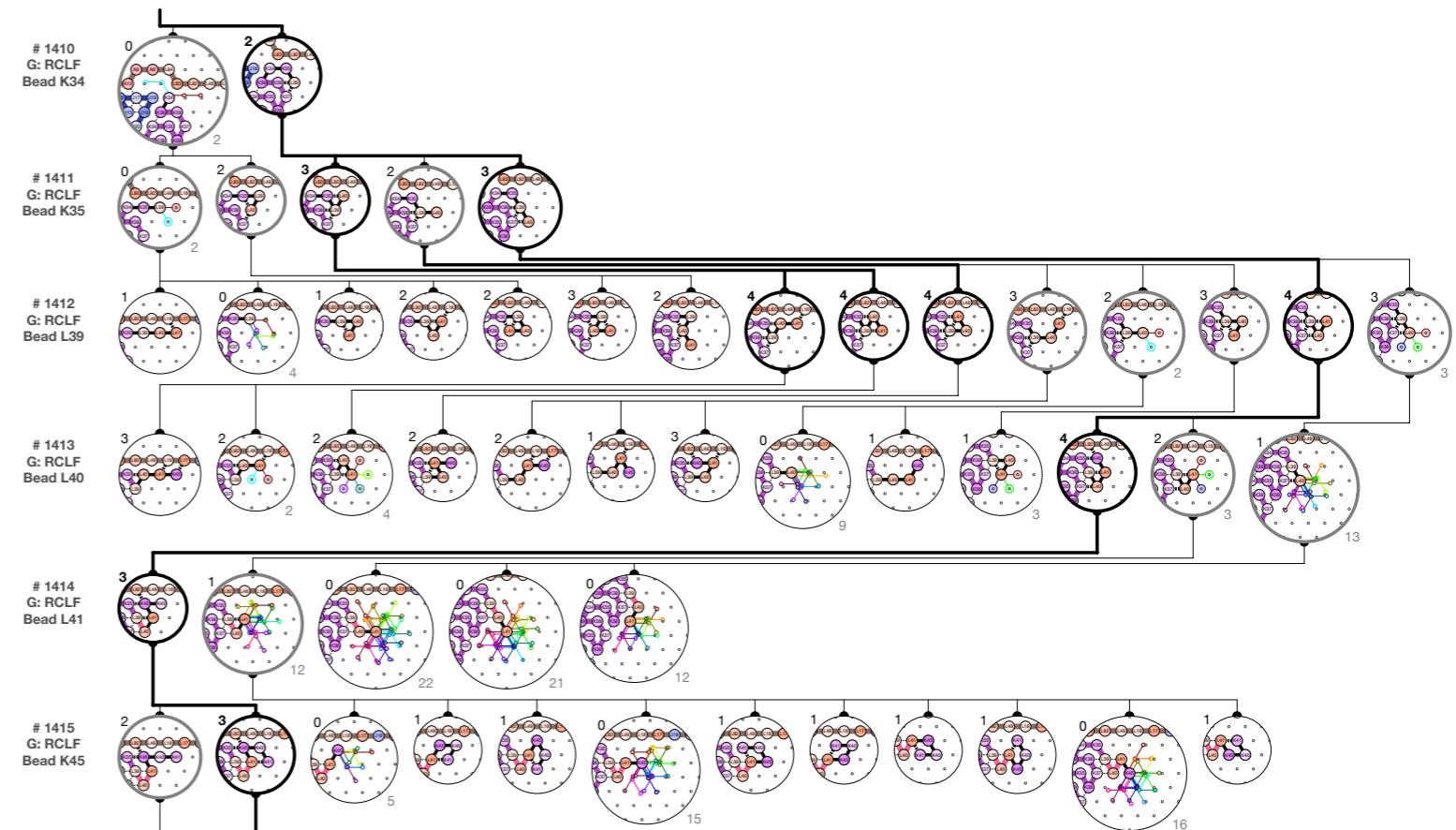
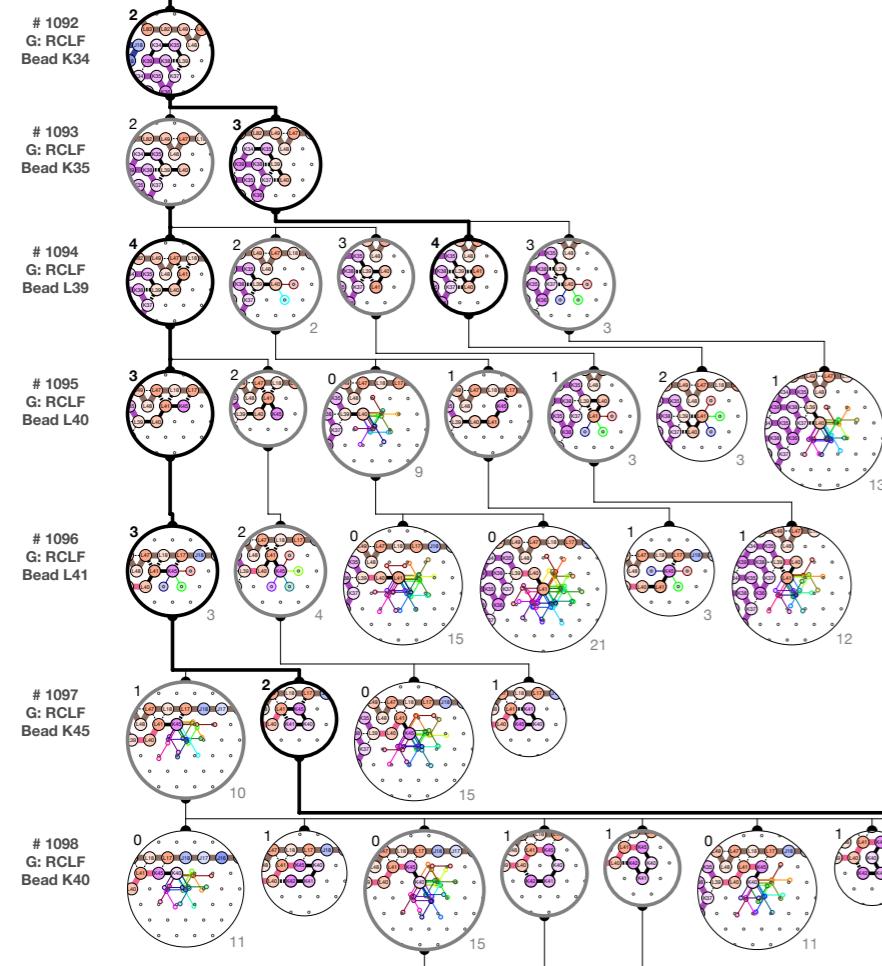
Proof of correctness

- Enumerate all possible environments for each brick
- Compute proof trees for each brick in all of its fixed environments
- Deal separately with the only three bricks having variable environments

Listing all environments



Example: Reading 0/1



The rule

543 bead types

