The background features a light blue and green grid with a pattern of overlapping, colorful, irregular geometric shapes in shades of purple, yellow, and green. The shapes resemble stylized, interconnected paths or folds.

# **Oritatami:** **A computational model for** **cotranscriptional folding**

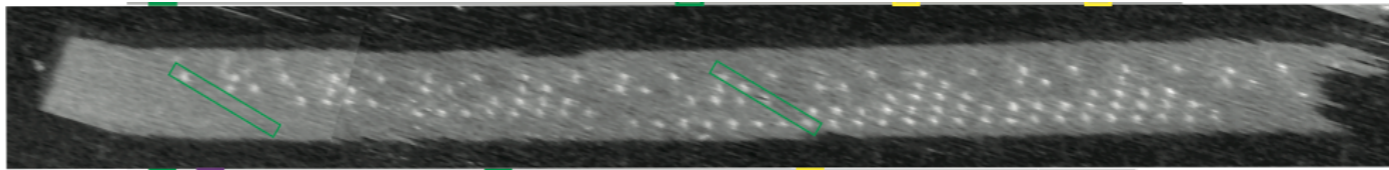
**Nicolas Schabanel**

**CNRS - LIP, ENS Lyon & IXXI - France**



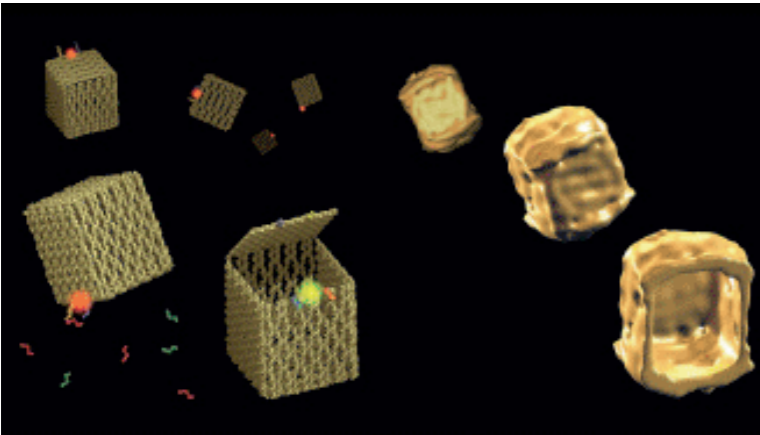
# Context: Biomolecular Computing & Engineering

— ~100 nm

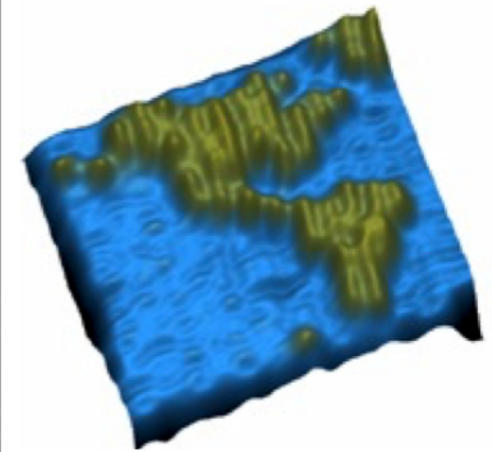
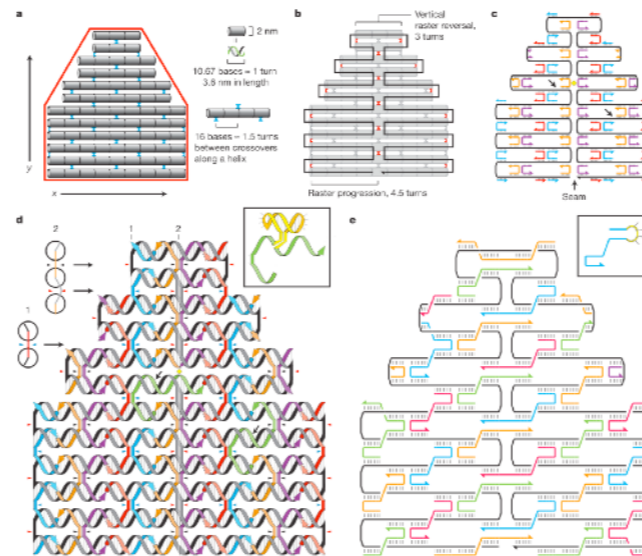


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0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1		

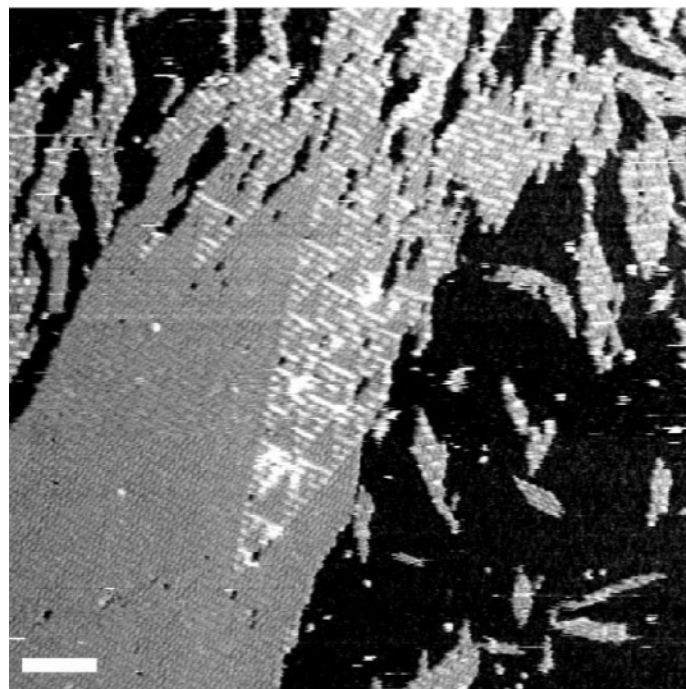
Constantine Evans, PhD Thesis, Caltech 2014



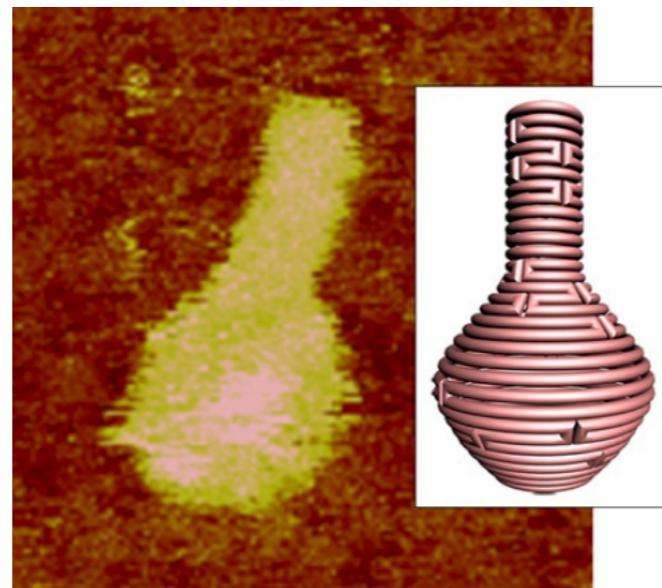
Andersen et al, 2009



Rothemund, Nature 2006



Fujibayashi et al, 2007



Han et al, Science 2011

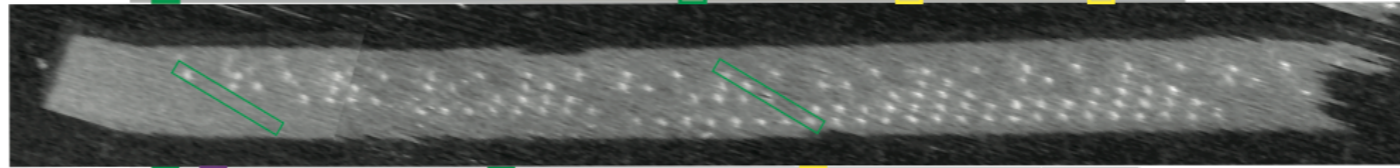


Wei, Dai, Yin, Nature 2013



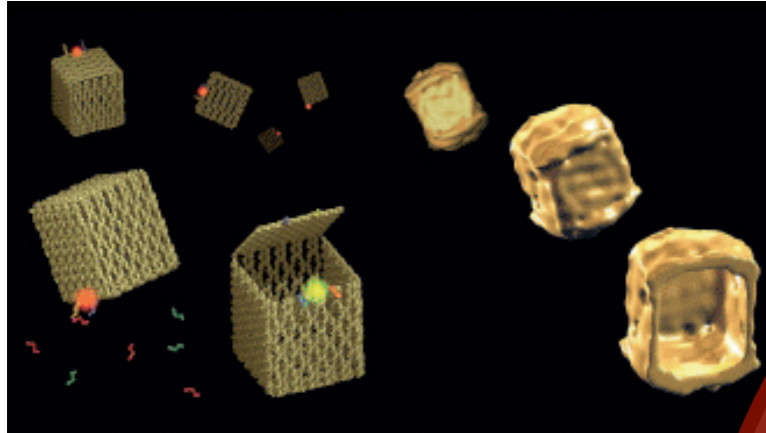
# Context: Biomolecular Computing & Engineering

~100 nm



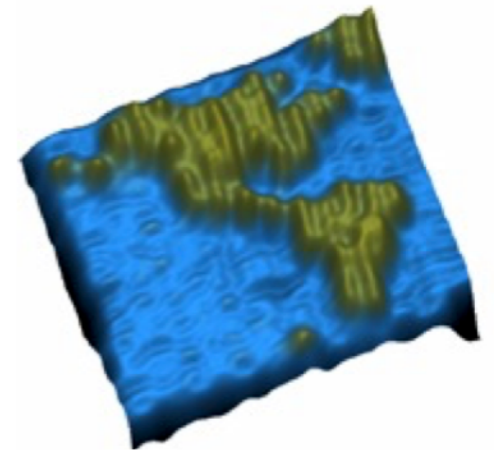
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0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	0	0	0	0	0	0	1	1

Constantine Evans, PhD Thesis, Caltech 2014

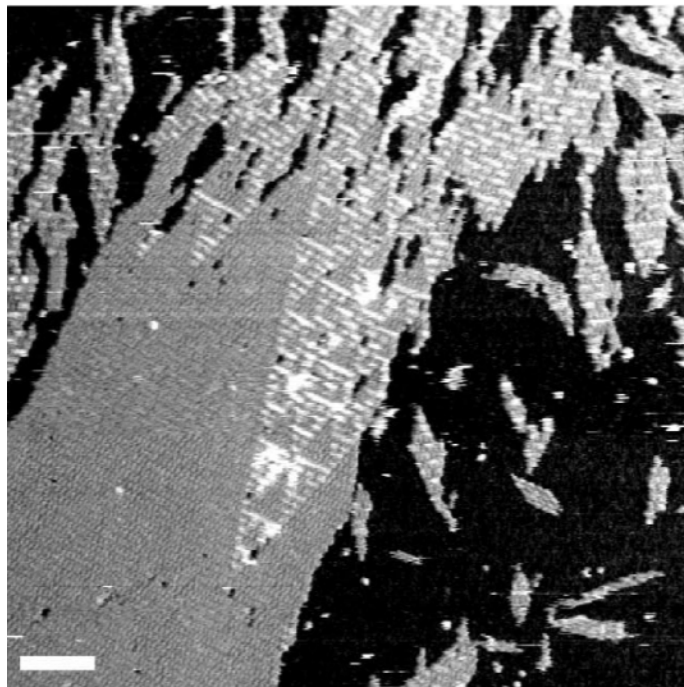


Andersen et al, 2008

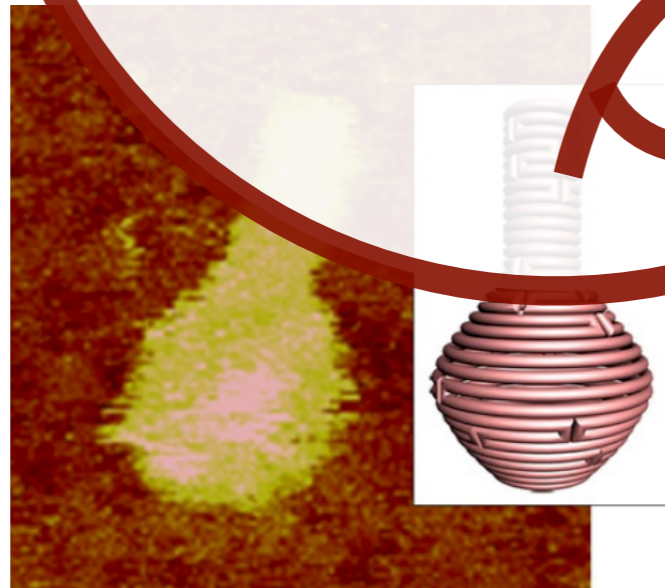
✘
✘  
**T<sup>o</sup> ≥ 70<sup>o</sup>C**  
o



Rothmund, Nature 2006



Fujibayashi et al, 2007



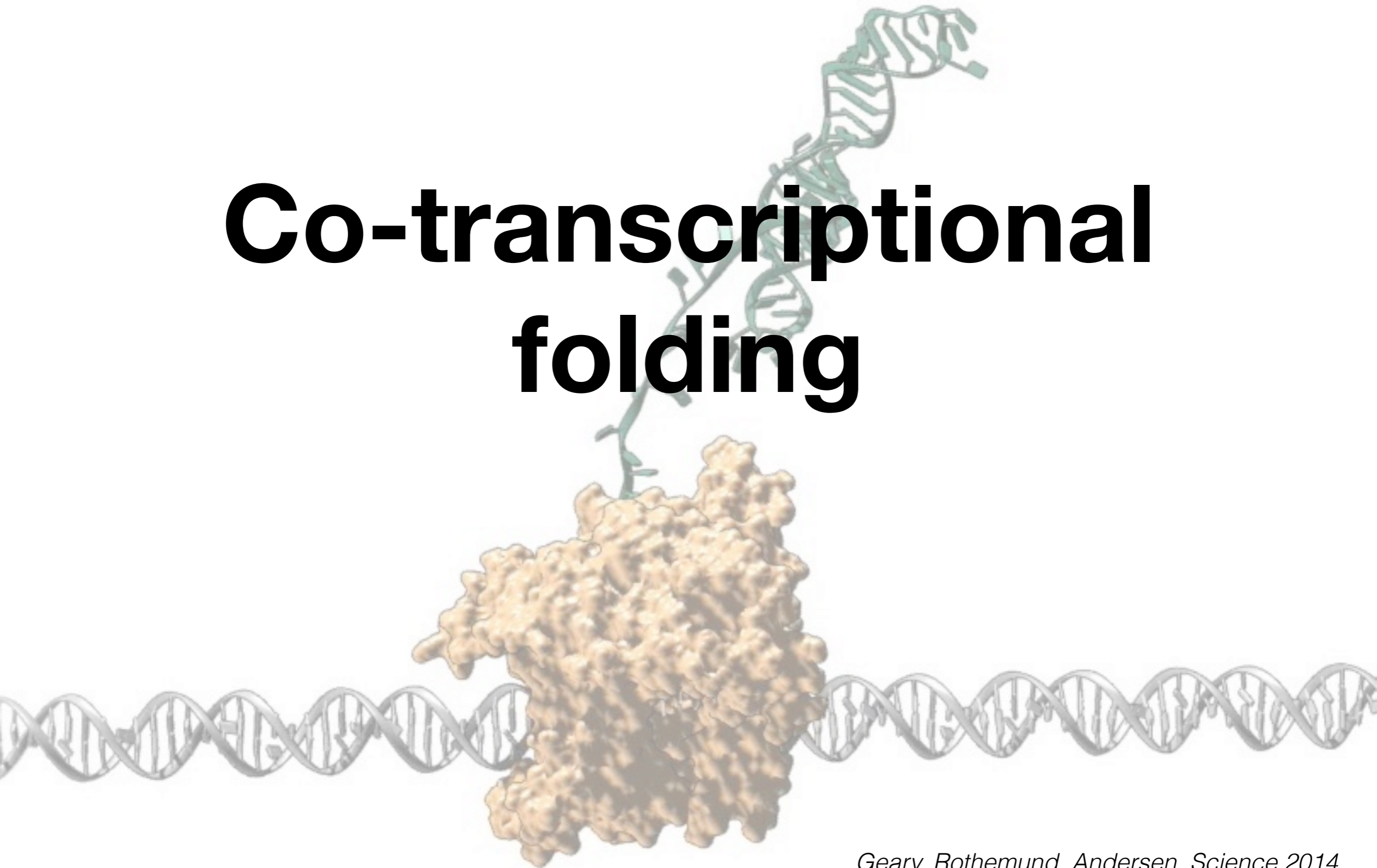
Han et al, Science 2011



Wei, Dai, Yin, Nature 2013



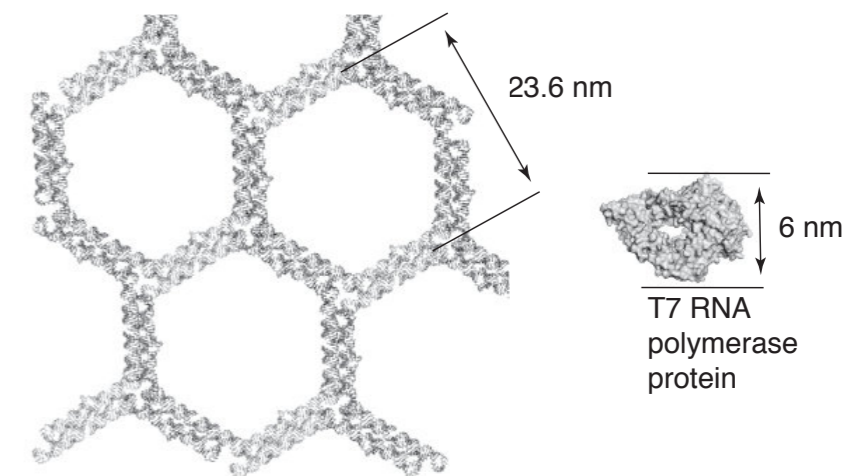
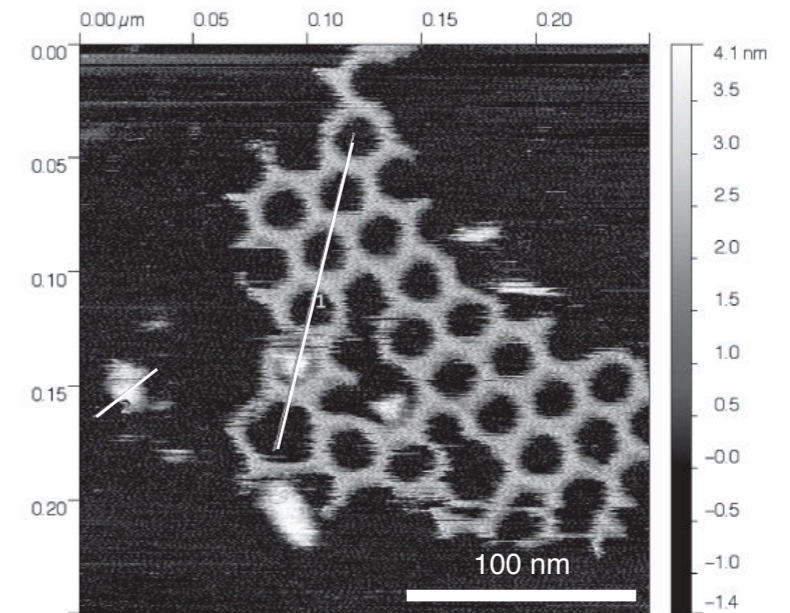
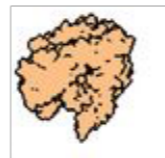
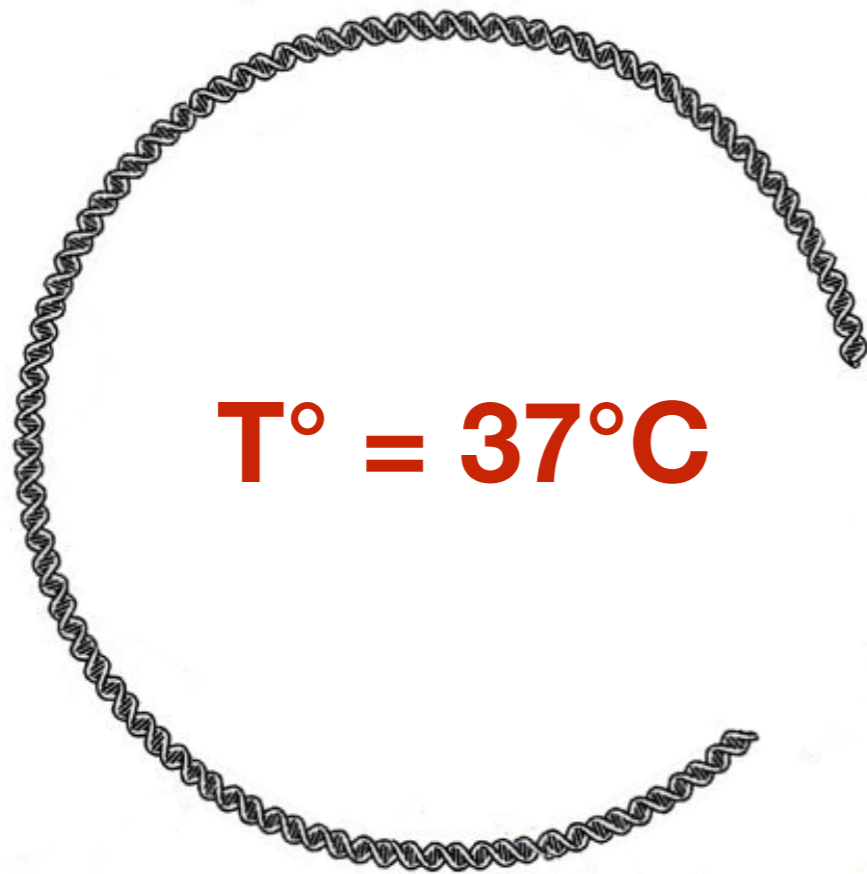
# Co-transcriptional folding



*Geary, Rothmund, Andersen, Science 2014*

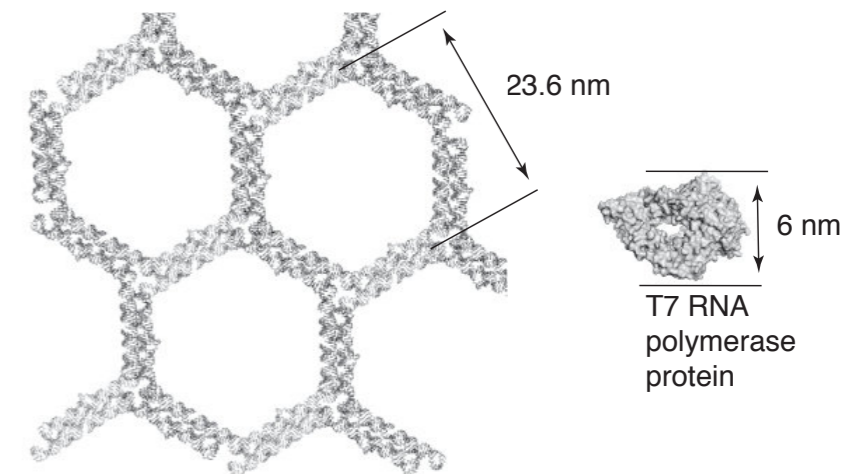
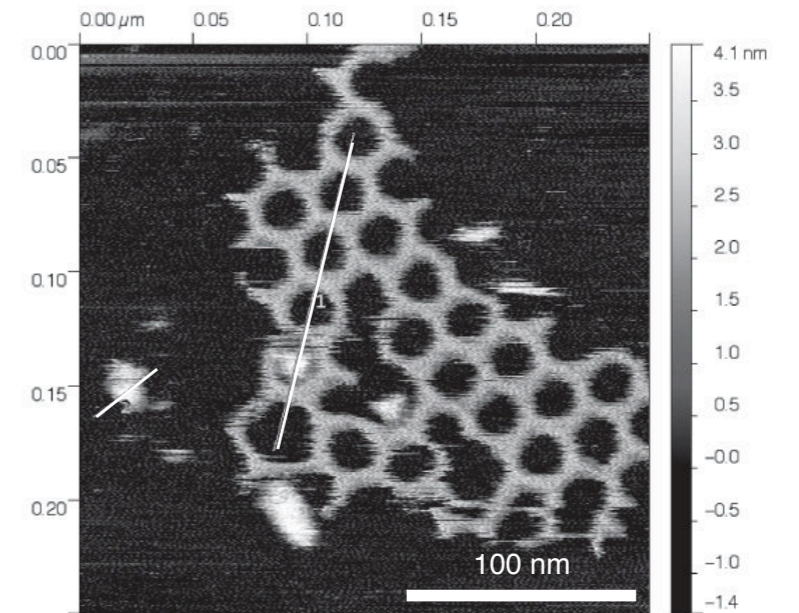
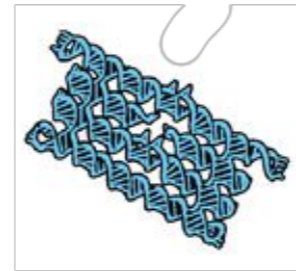
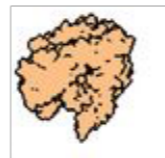
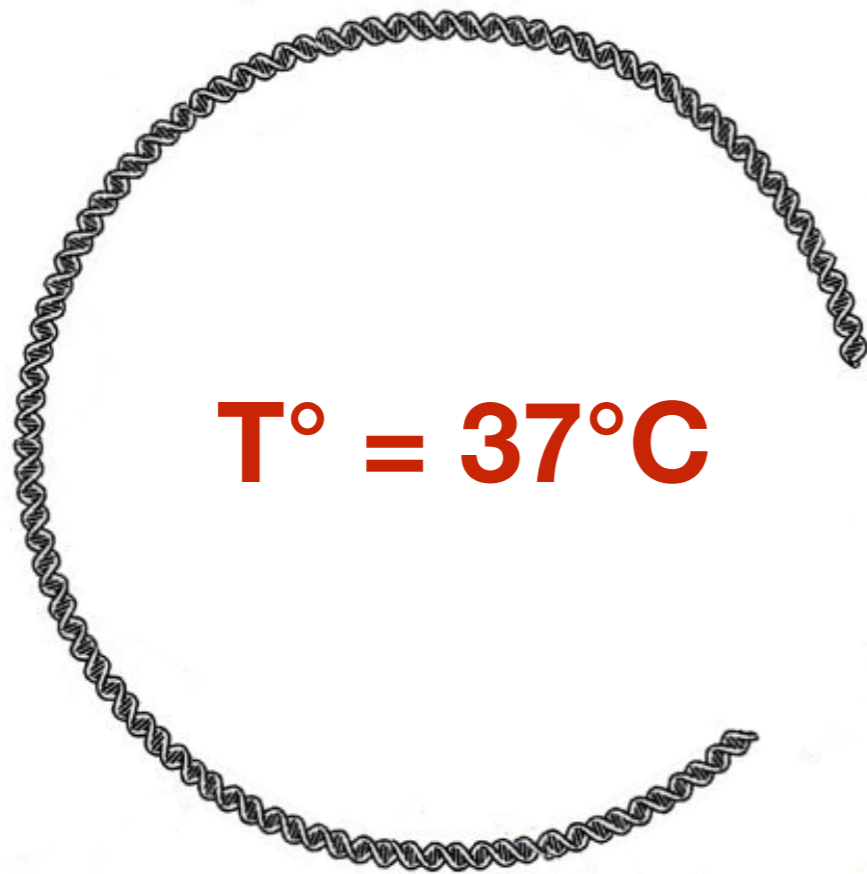


# RNA co-transcriptional folding



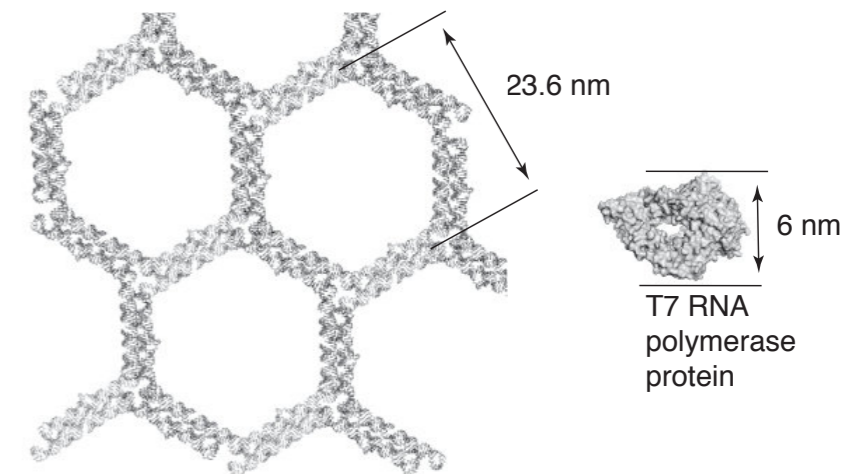
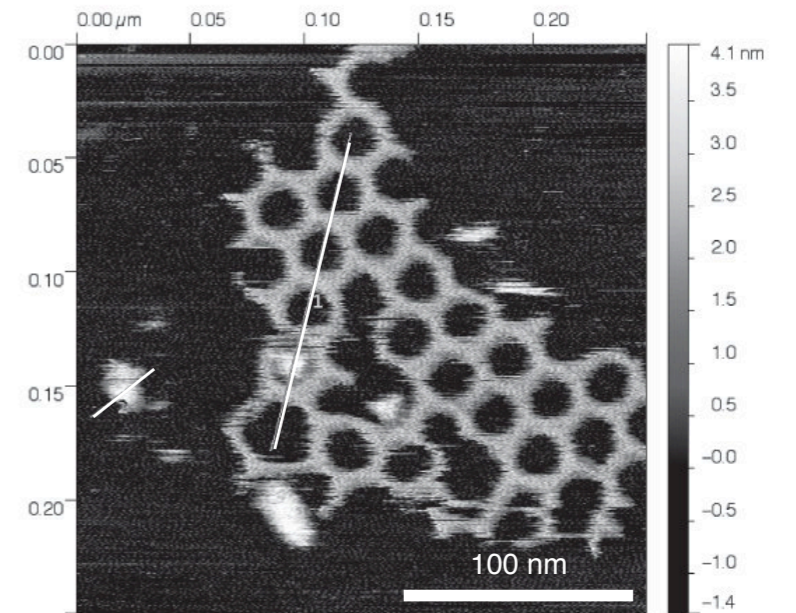
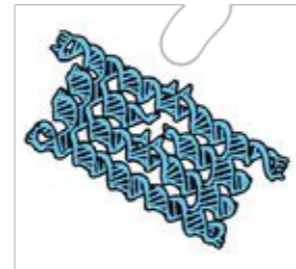
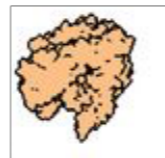
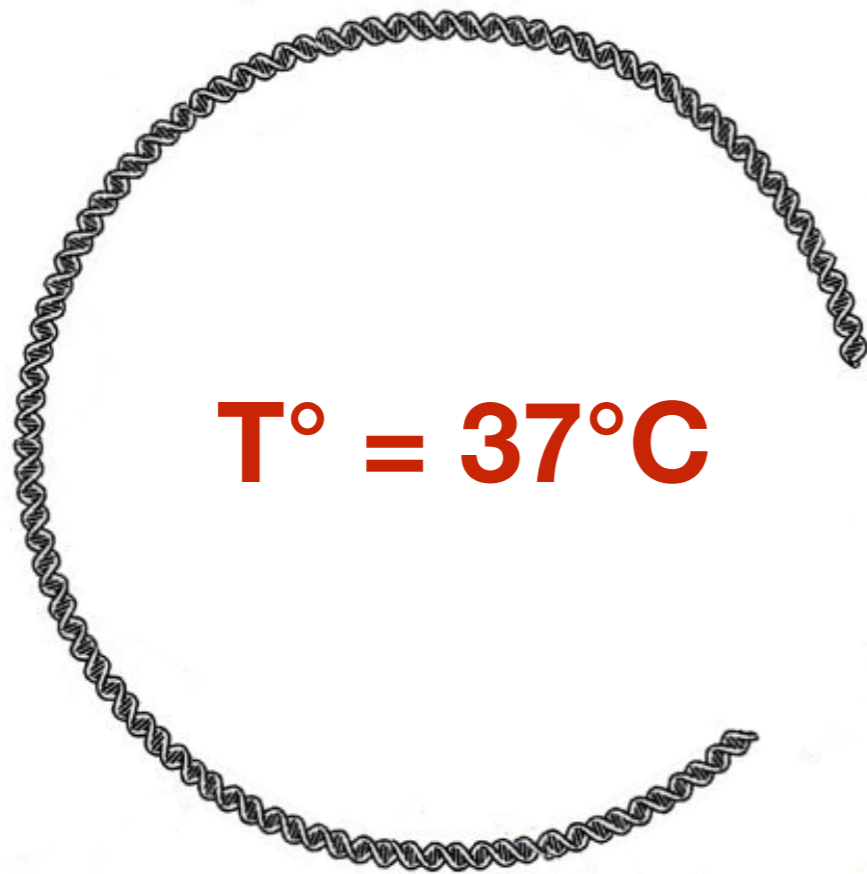


# RNA co-transcriptional folding



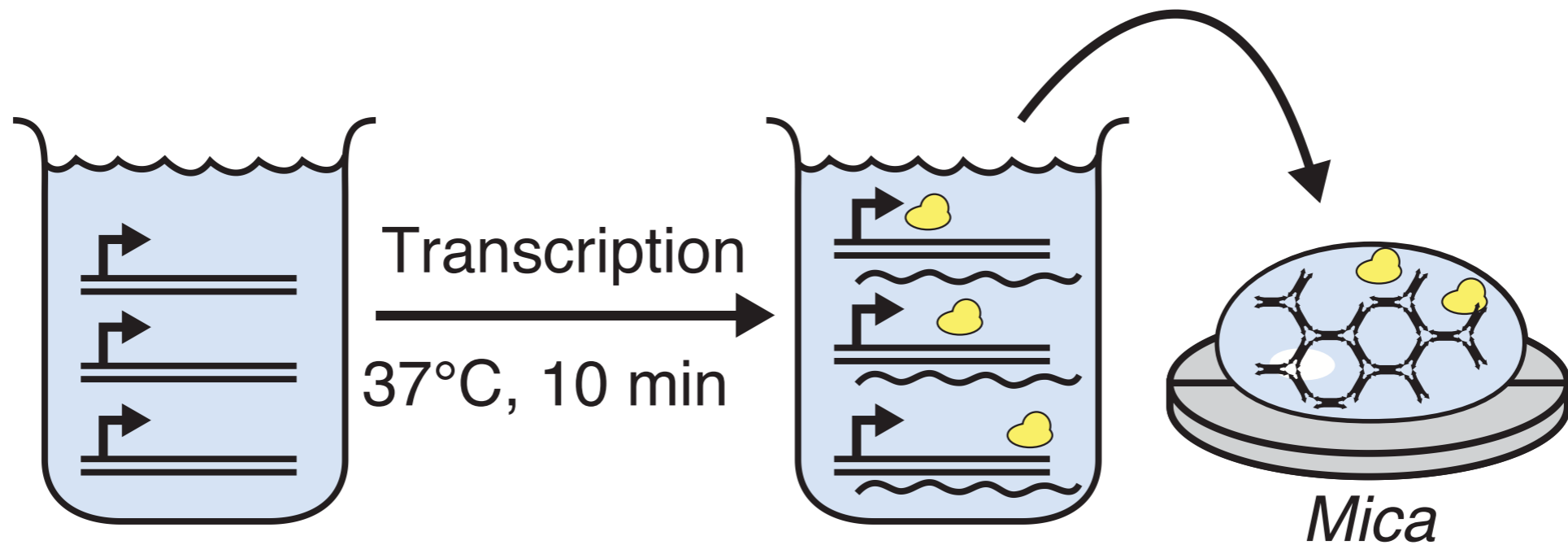


# RNA co-transcriptional folding



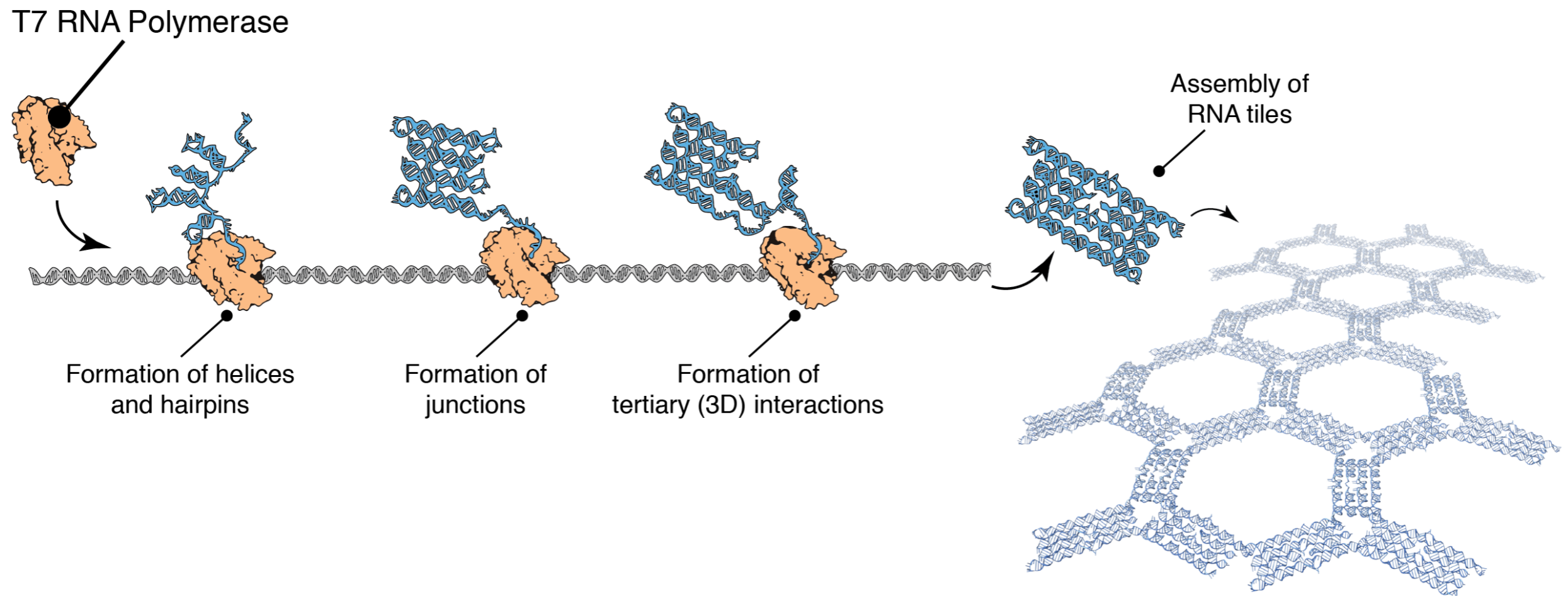


# Protocol





# RNA Origami in Real Time

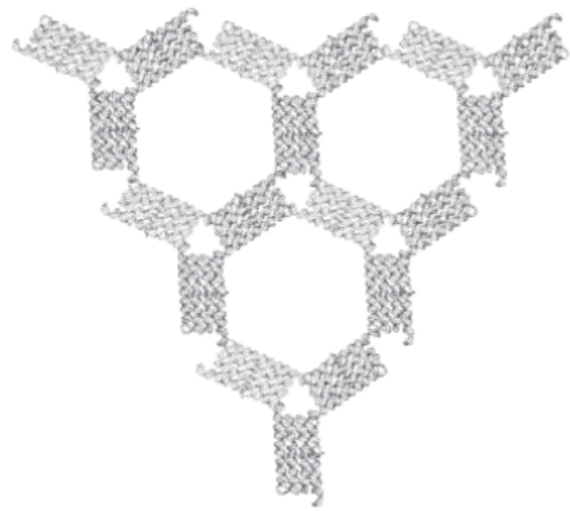


T7 RNA polymerase produces RNA directionally from 5' to 3', **at a rate much slower than the RNA folds up (few microseconds).**

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

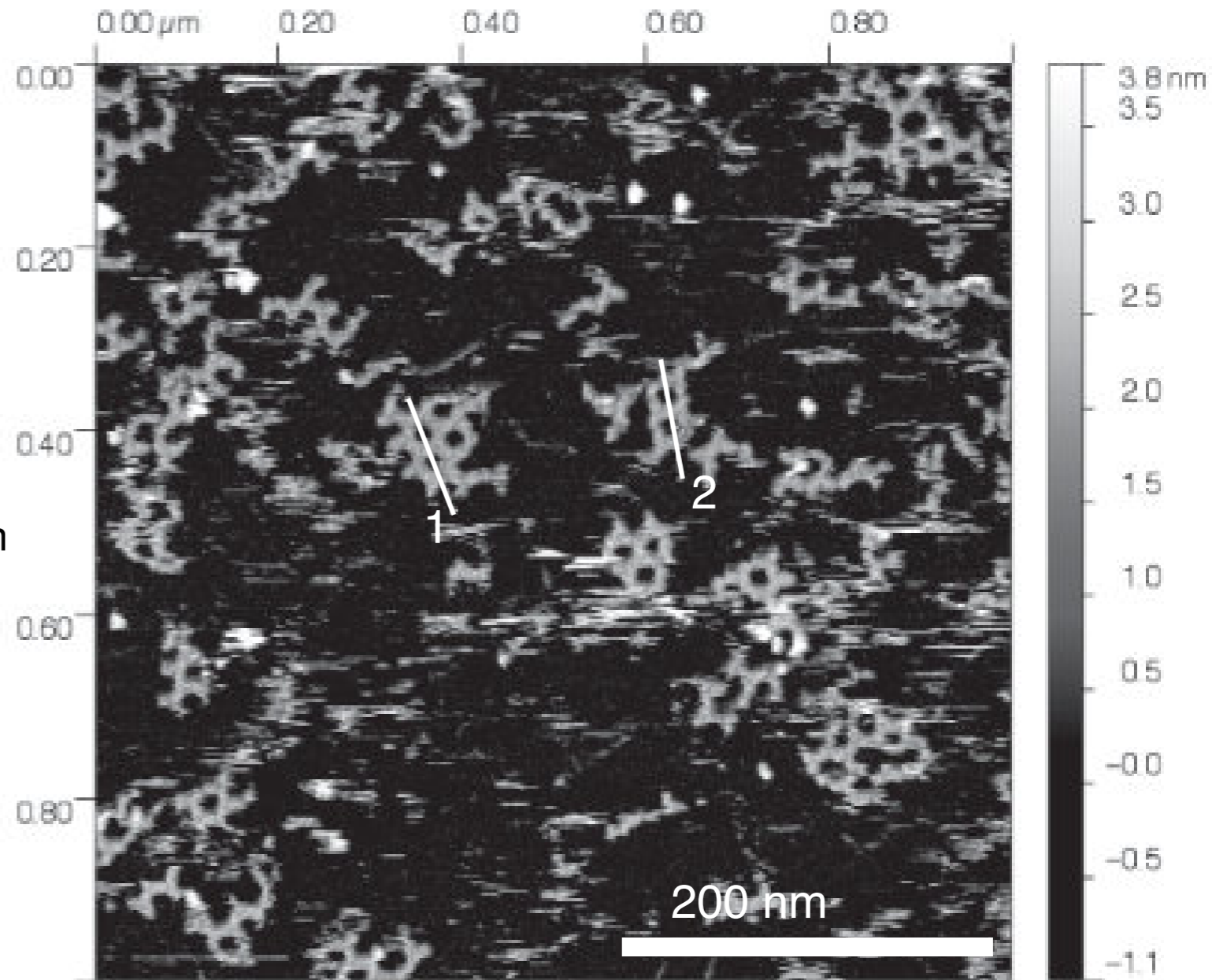
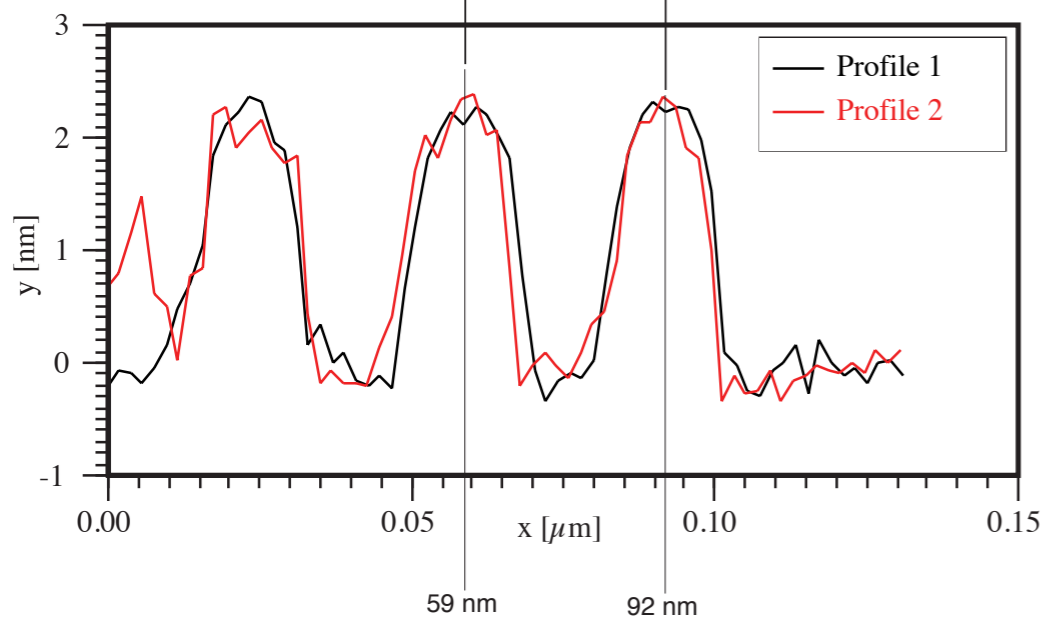


# AFM imaging of 4H-AE co-transcriptional assembly



period = 33.0 nm

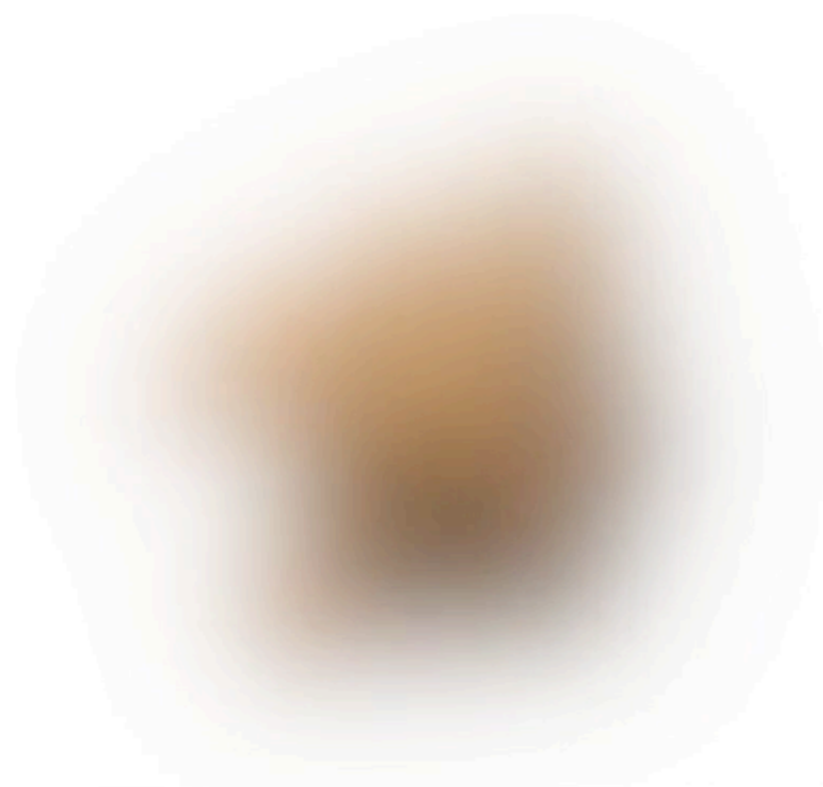
Note that the modeled spacing was 33.5nm





# RNA Folding

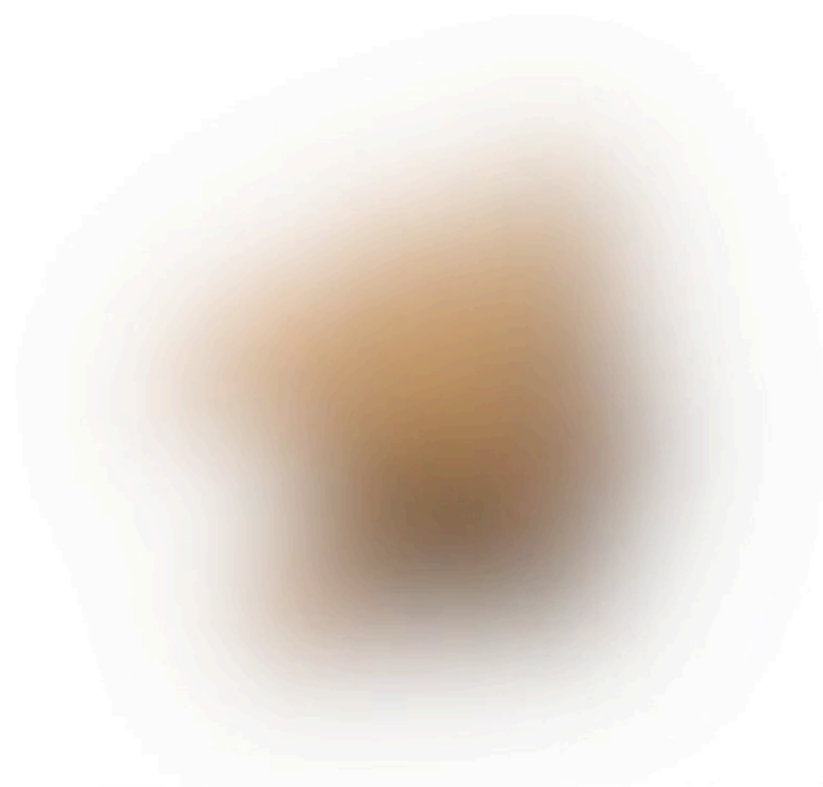
(Real time: ~1 second)



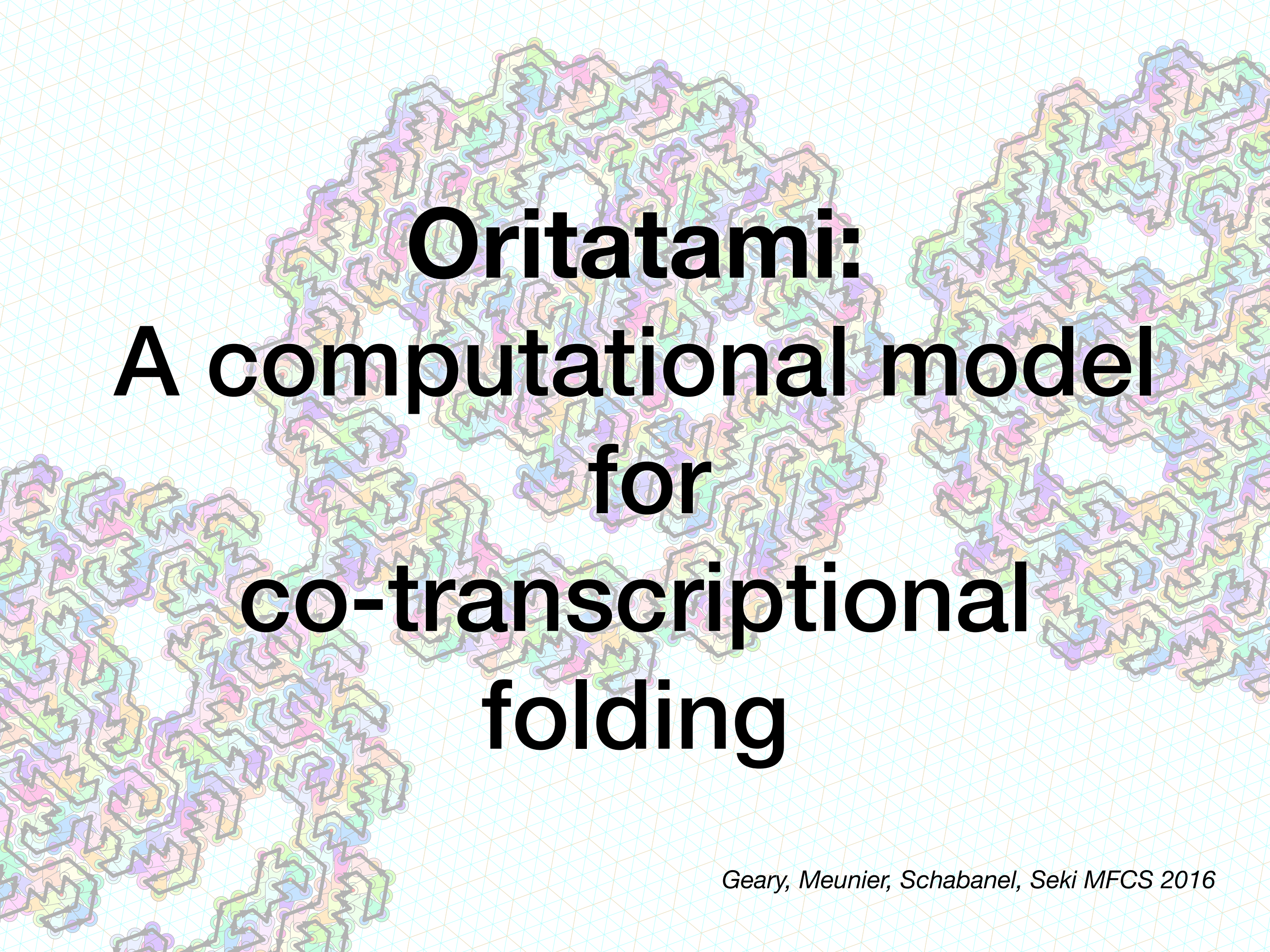
*Video: Geary*

# RNA Folding

(Real time: ~1 second)





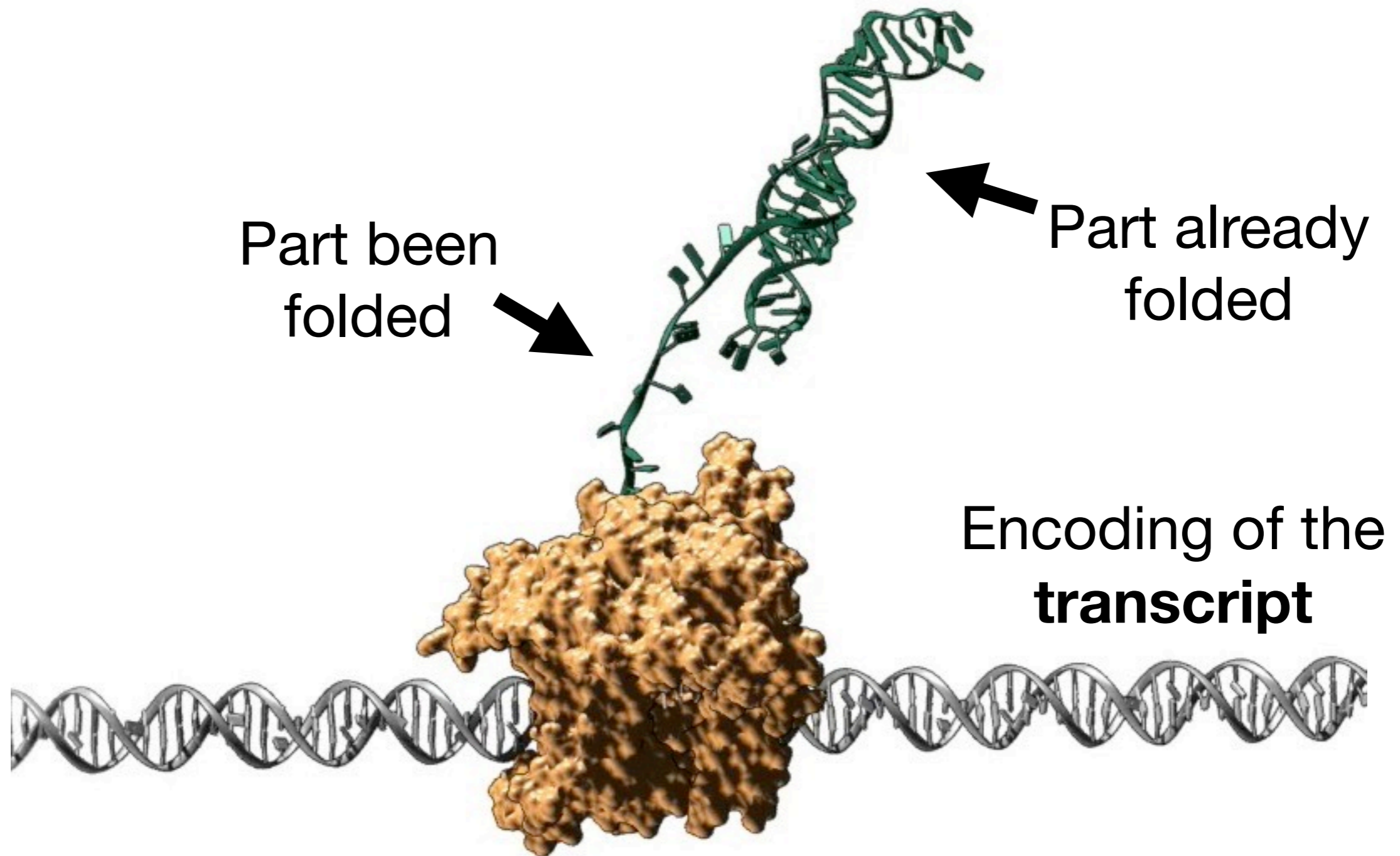


**Oritatami:  
A computational model  
for  
co-transcriptional  
folding**



# RNA Folding

(Real time: ~1 second)





# Oritatami:

## A model for co-transcriptional folding

### The program:

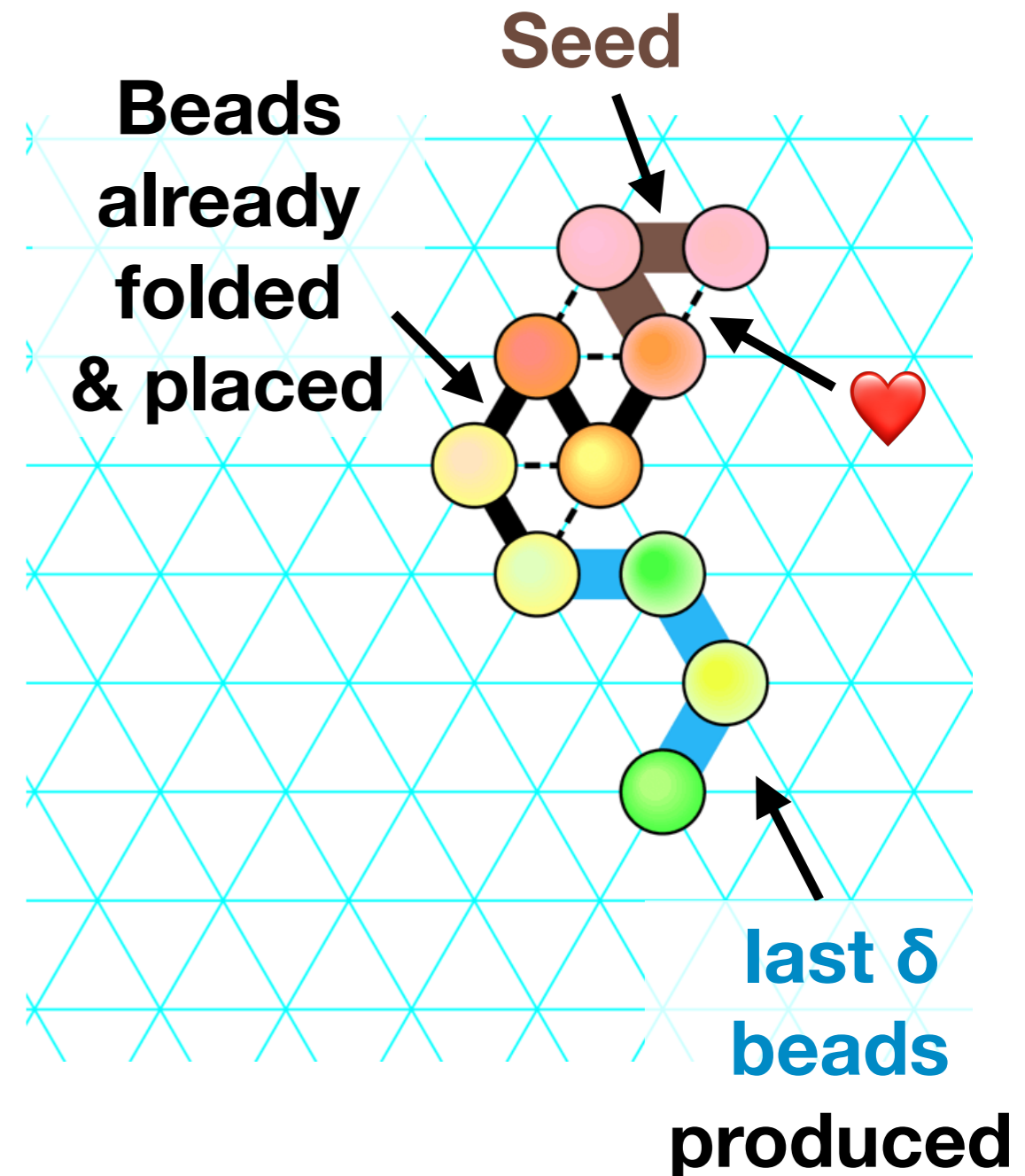
- a sequence of **bead types** (the **transcript**)

### The instructions:

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

### The input configuration:

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

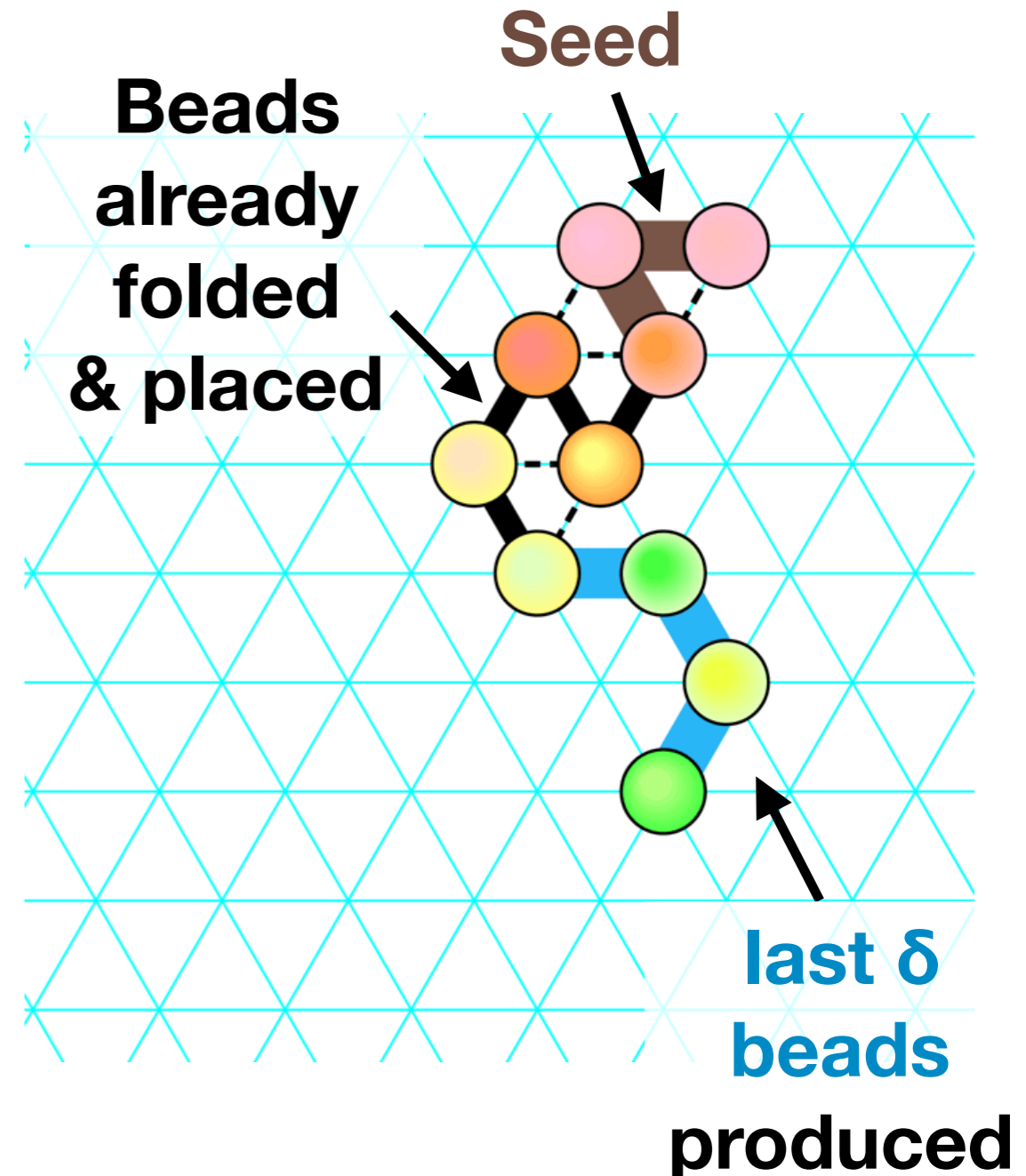


# Oritatami: A model for co-transcriptional folding

## The dynamics

- Starting from the seed, the sequence is *produced one bead at a time*
- **Only the  $\delta$  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  $\delta = 3$



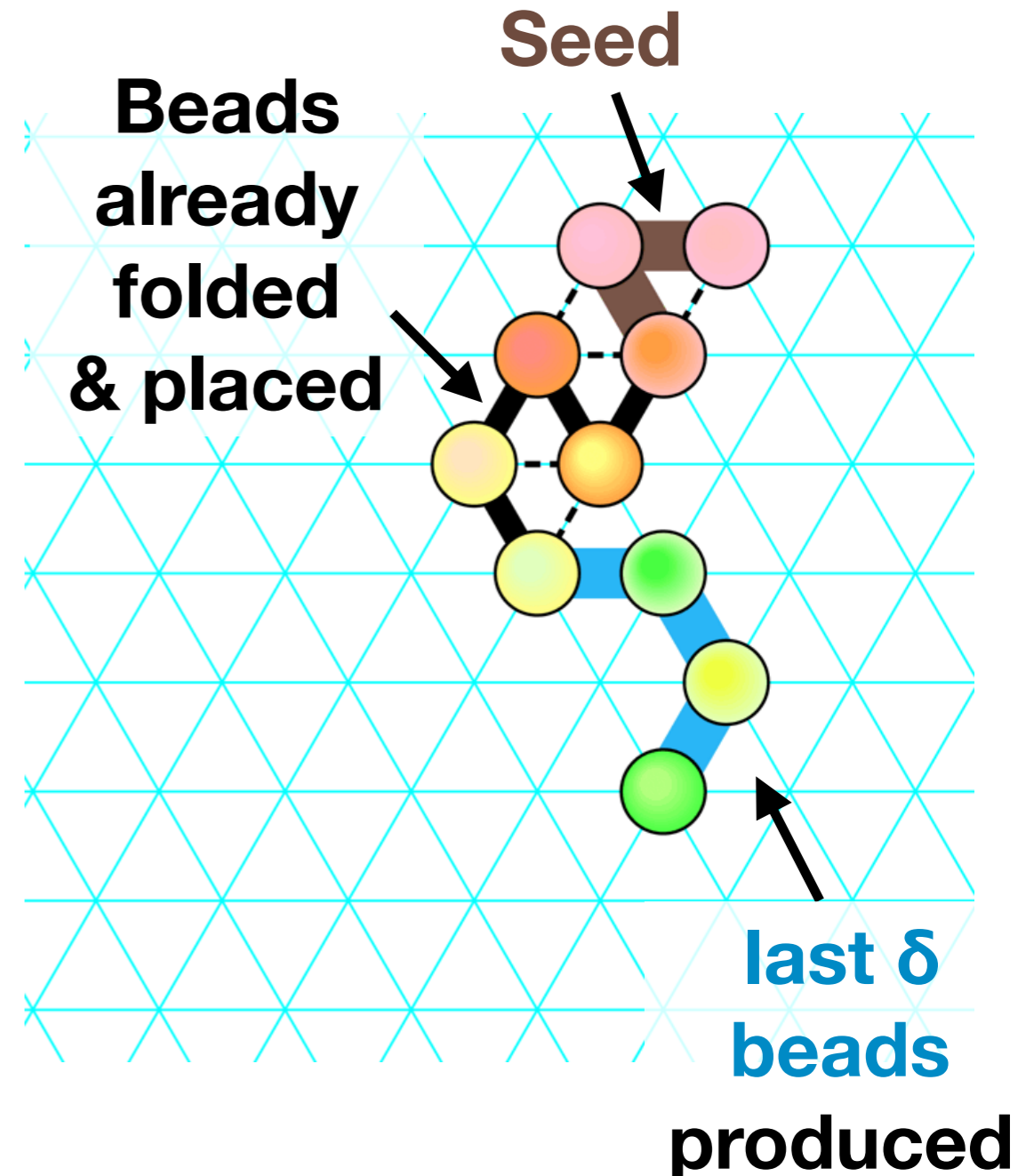


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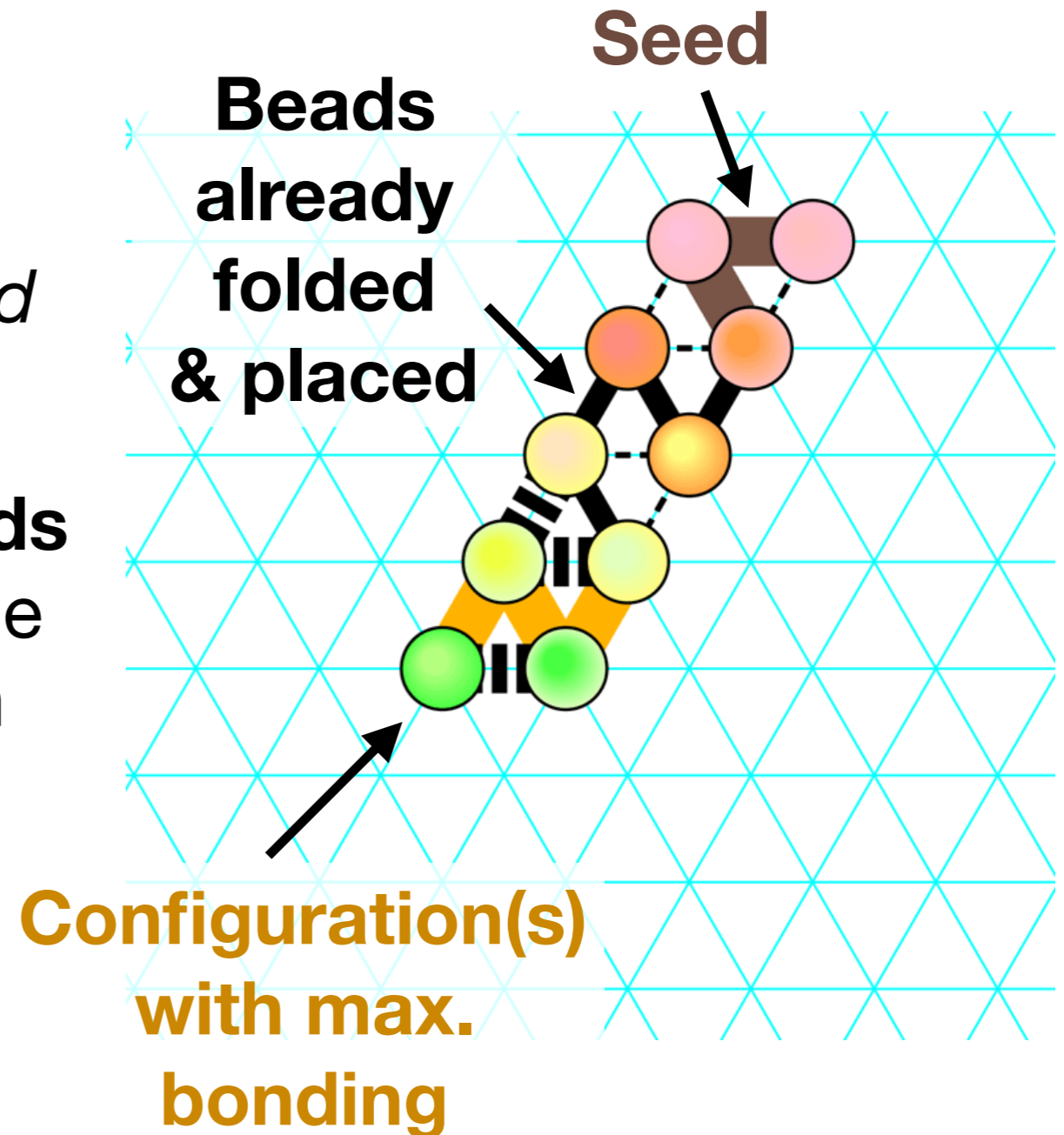
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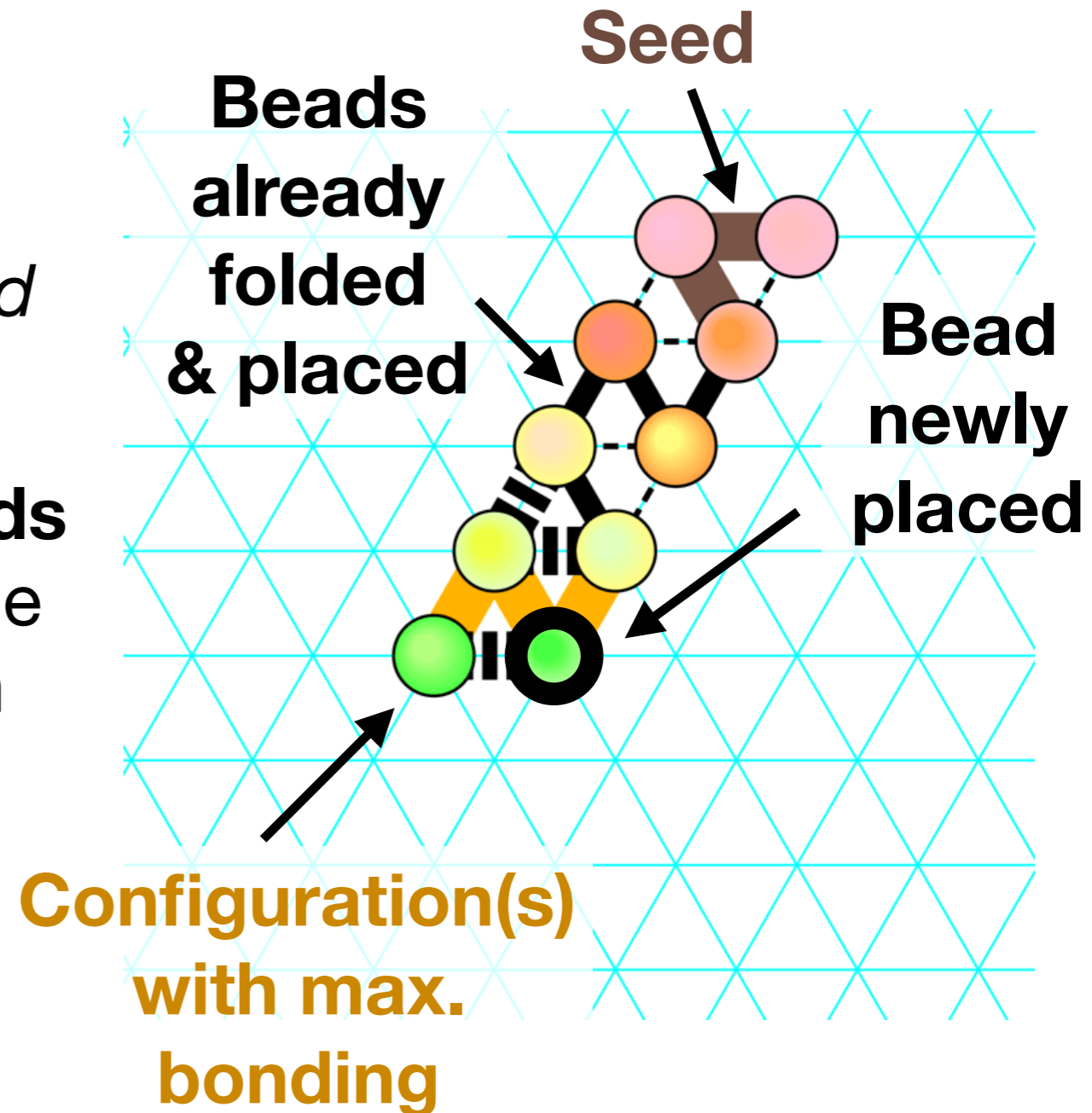


# Oritatami:

## A model for co-transcriptional folding

### The dynamics.

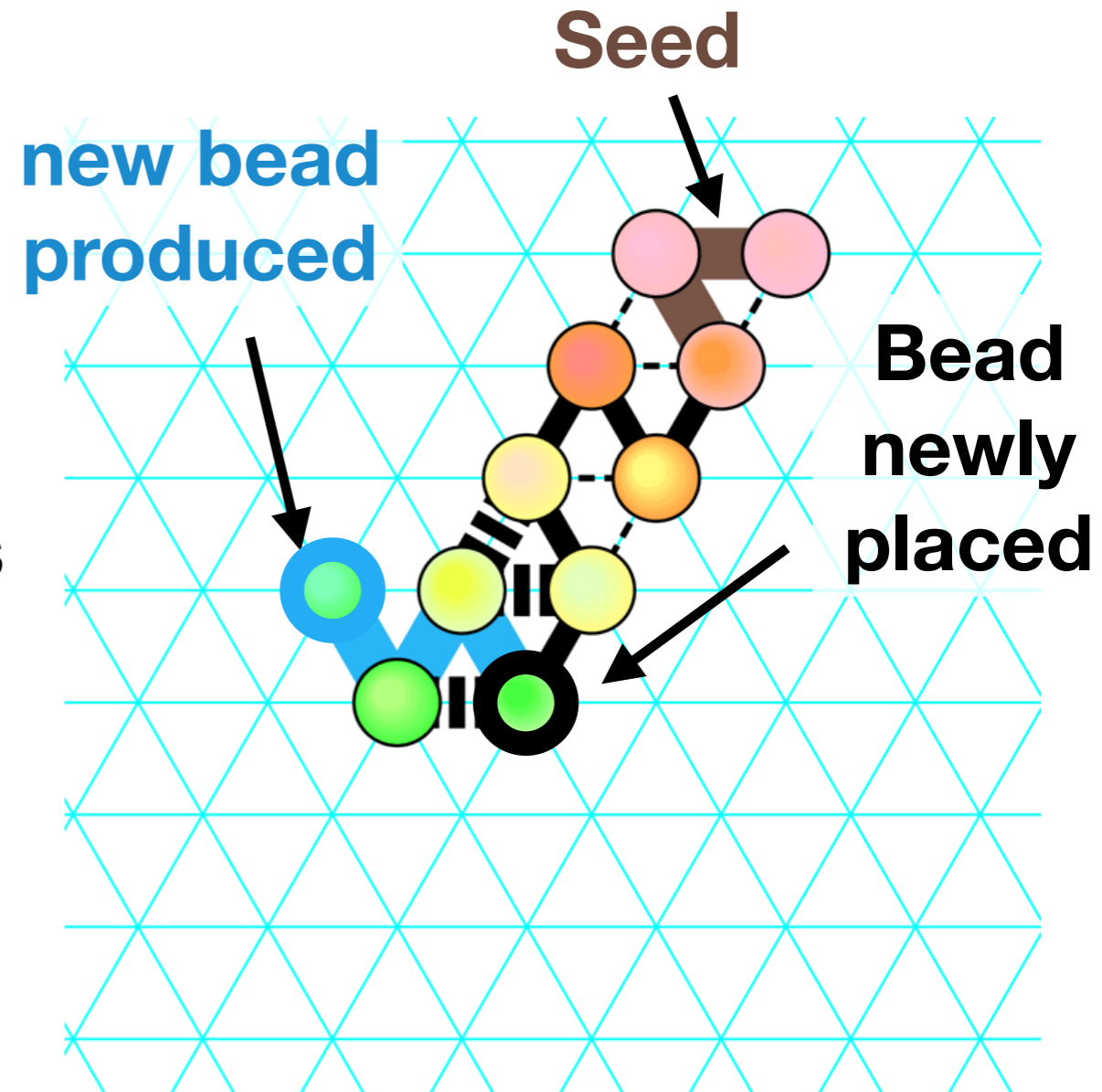
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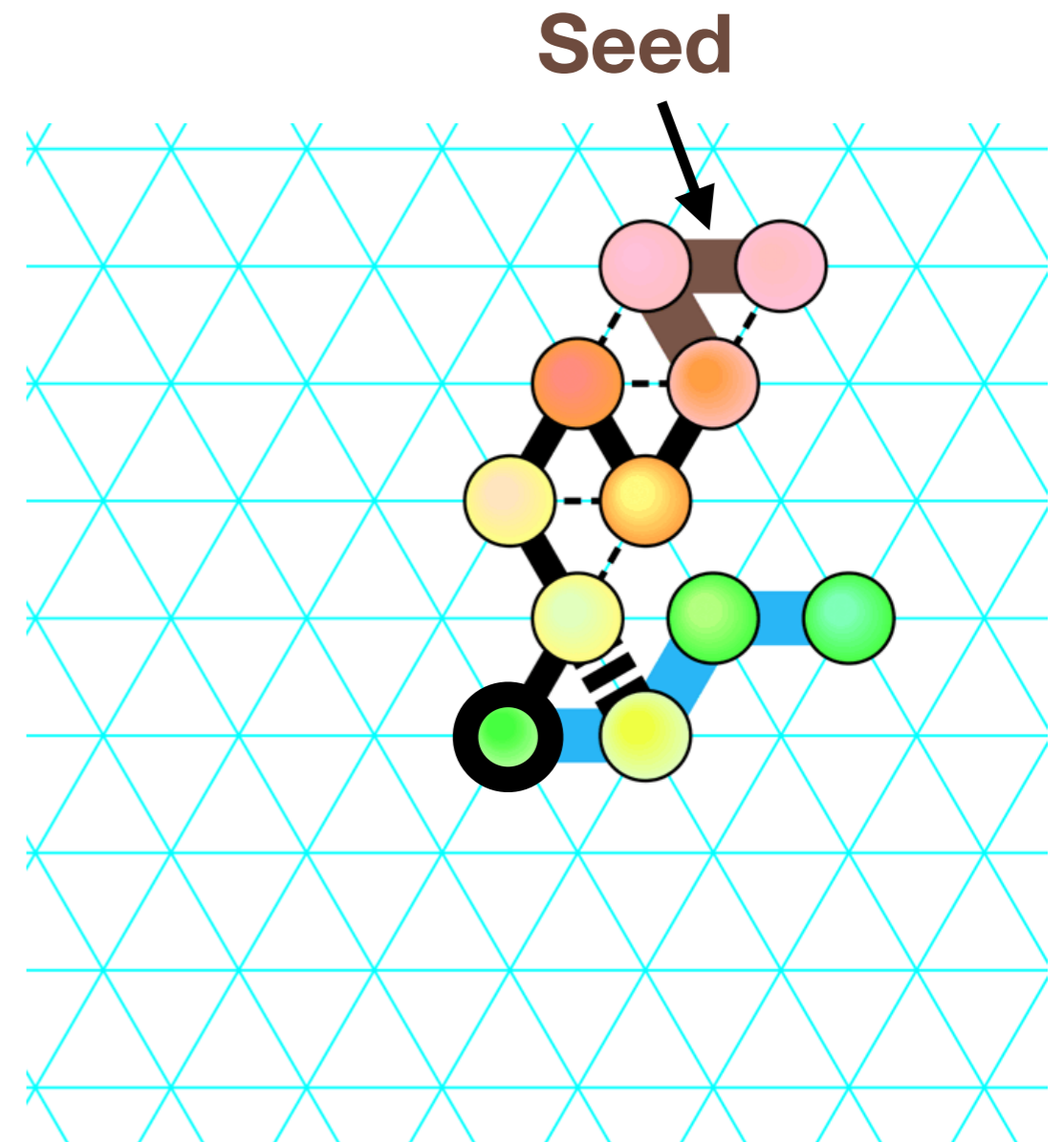




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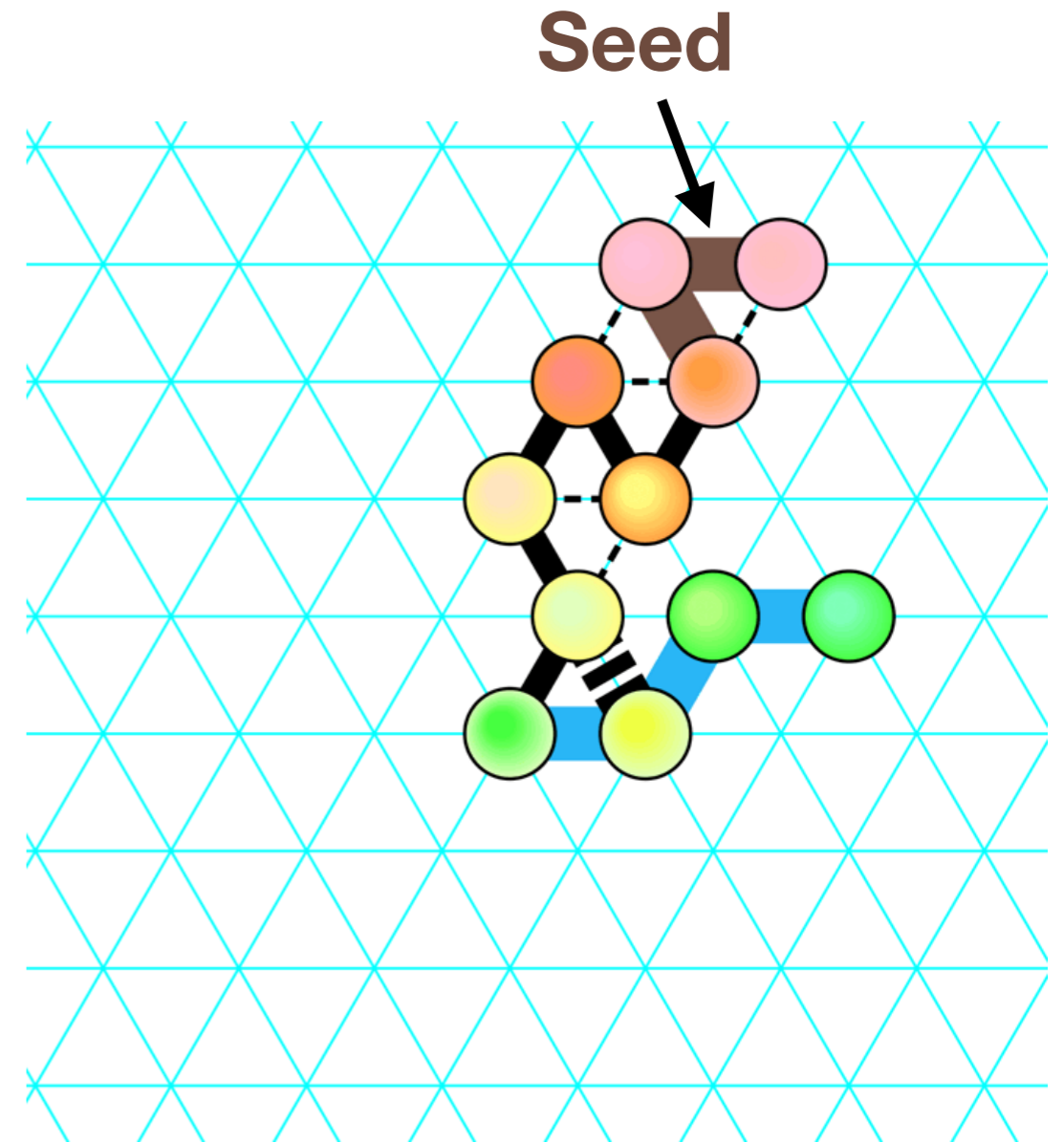
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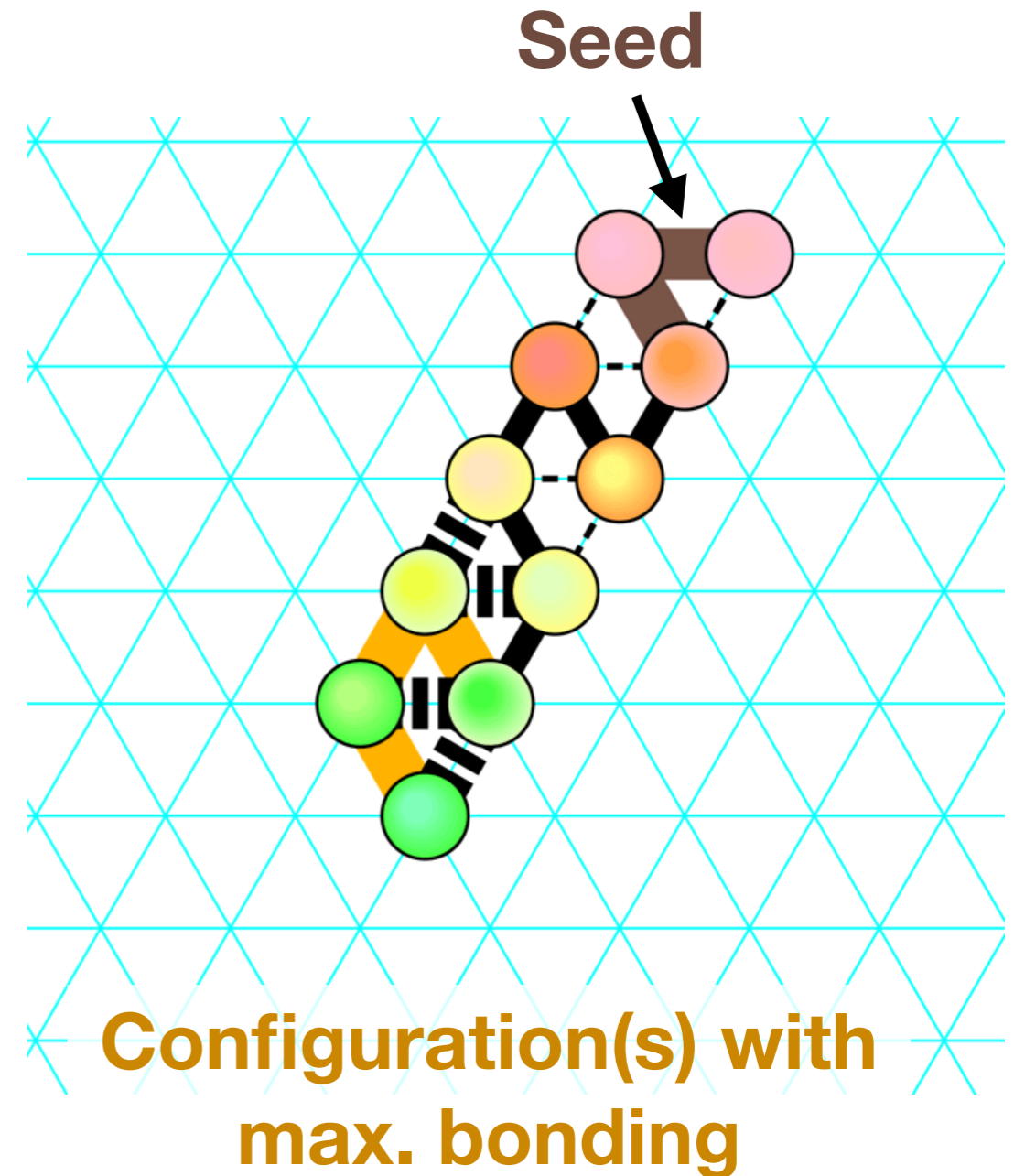
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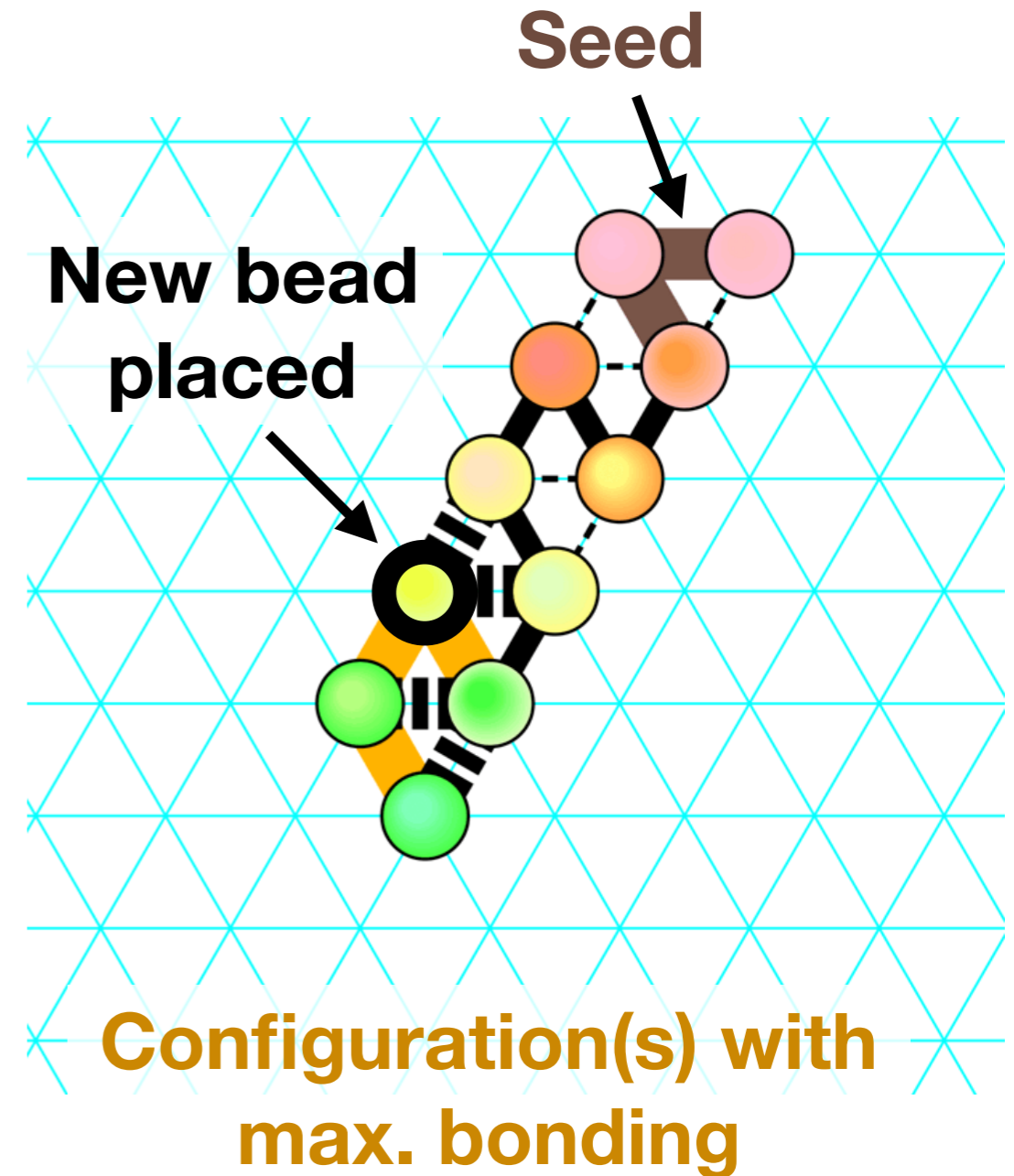




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**There might be several configurations with max. bonding**

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The bead has same position in all maximal extension  $\Rightarrow$  *deterministic*



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# Oritatami:

## A model for co-transcriptional folding

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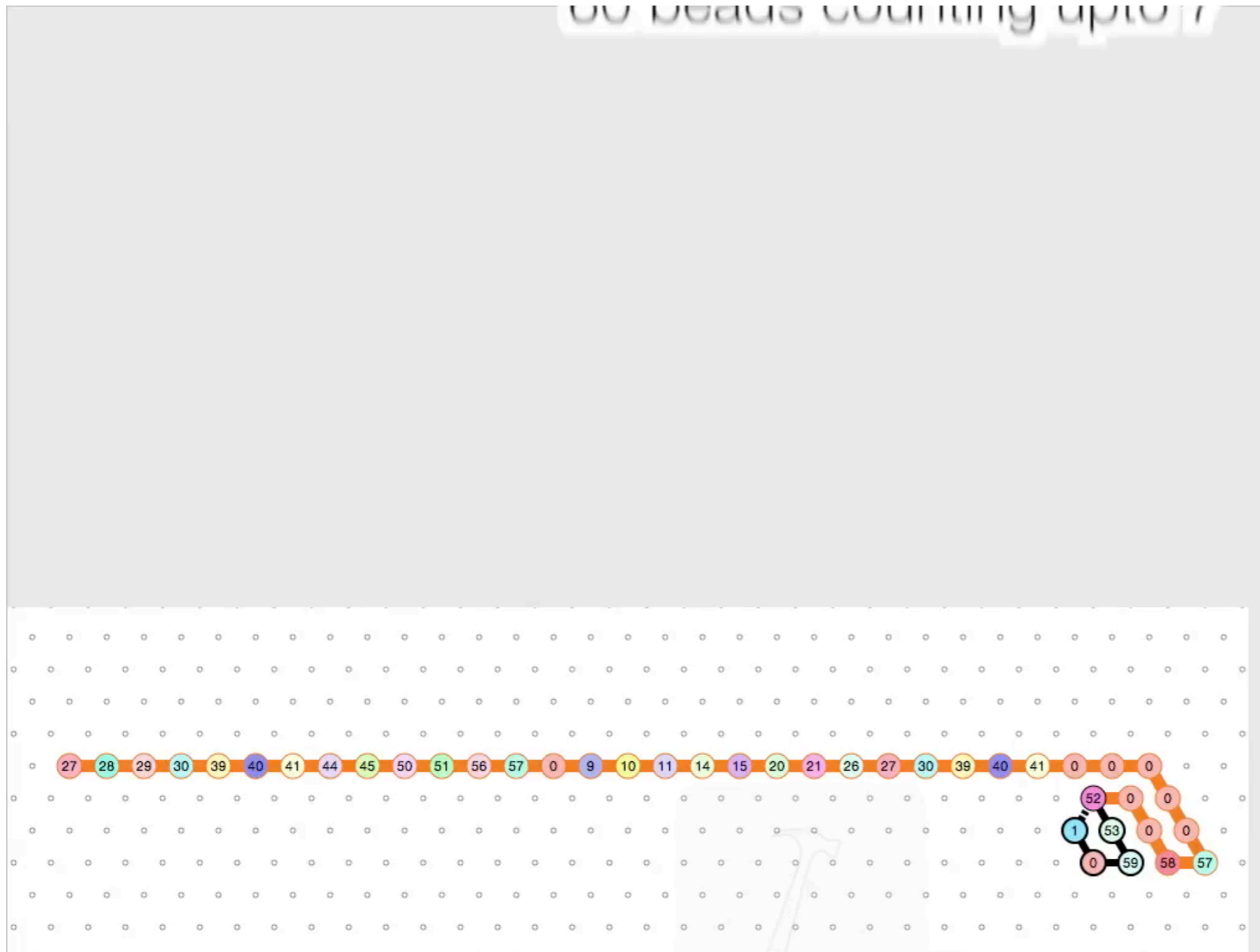


**There might be several configurations with max. bonding**

# Oritatami

## A first example

60 beads counting upto 7



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

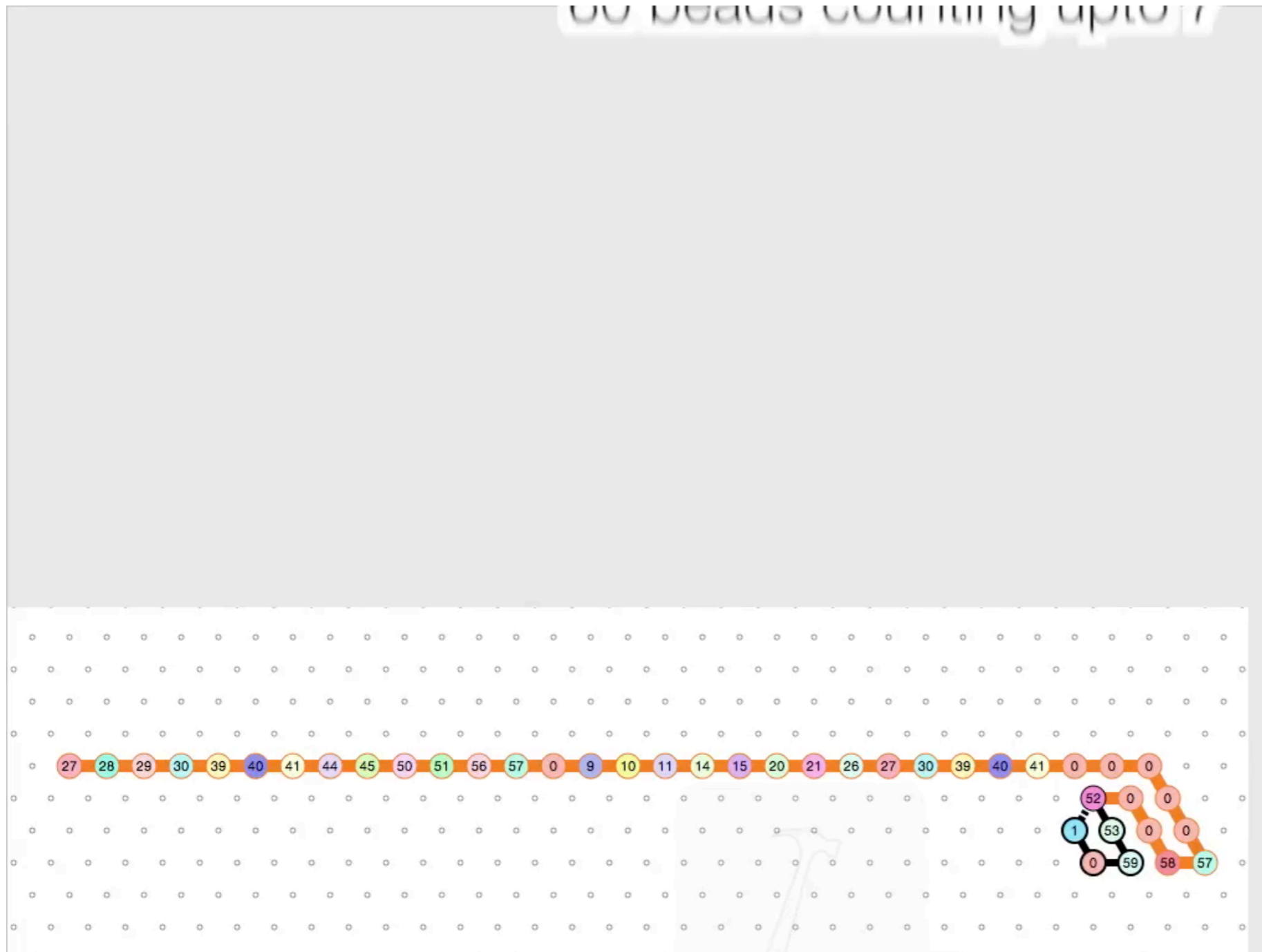
*Geary Meunier Seki  
Schabanel 2015*



# Oritatami

## A first example

60 beads counting upto 7



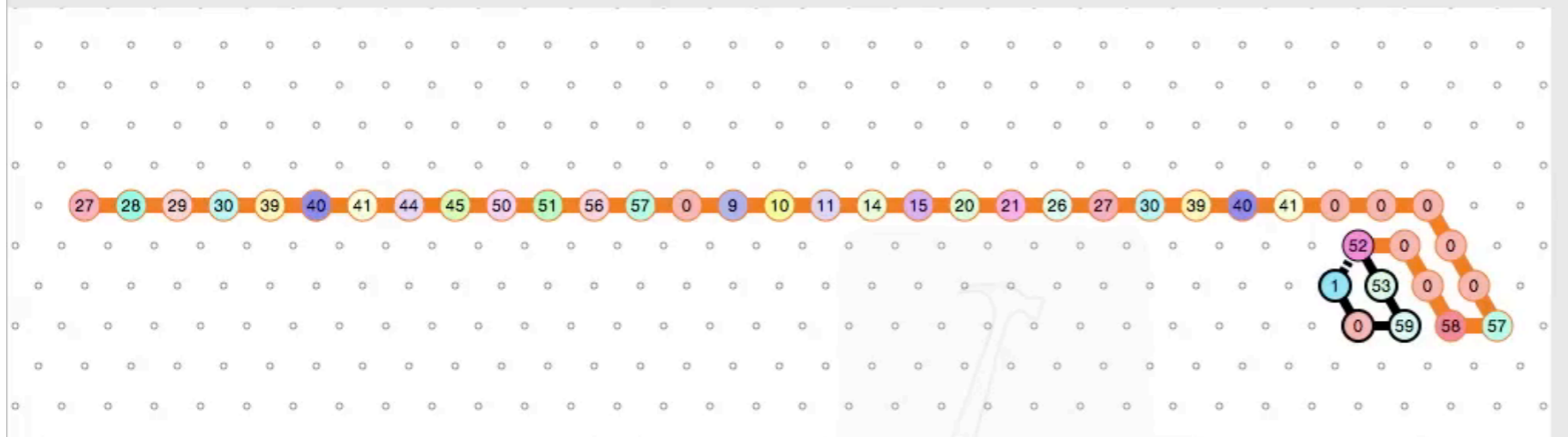
A binary counter made of a **single** 60-beads periodic molecule folding upon itself

# Oritatami

## A first example

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

of a **single** 00  
beads  
periodic  
molecule  
folding upon  
itself



# Oritatami

## A first example

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

An attraction rule

of a **single** 60  
beads  
periodic  
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folding upon  
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# Oritatami

## A first example

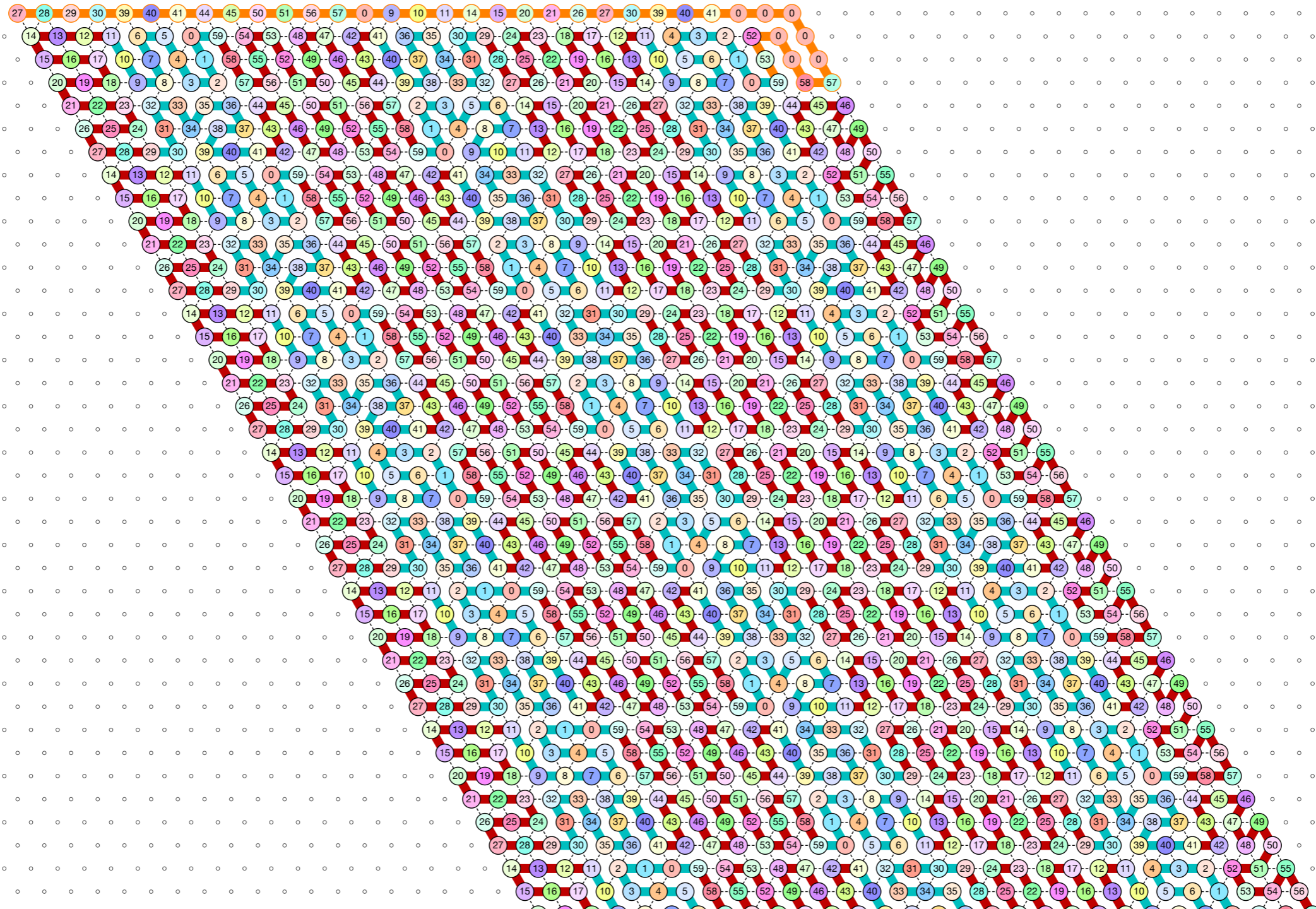
The molecule:  $0, \dots, 59, 0, \dots, 59, 0, \dots$

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# Oritatami. A binary counter

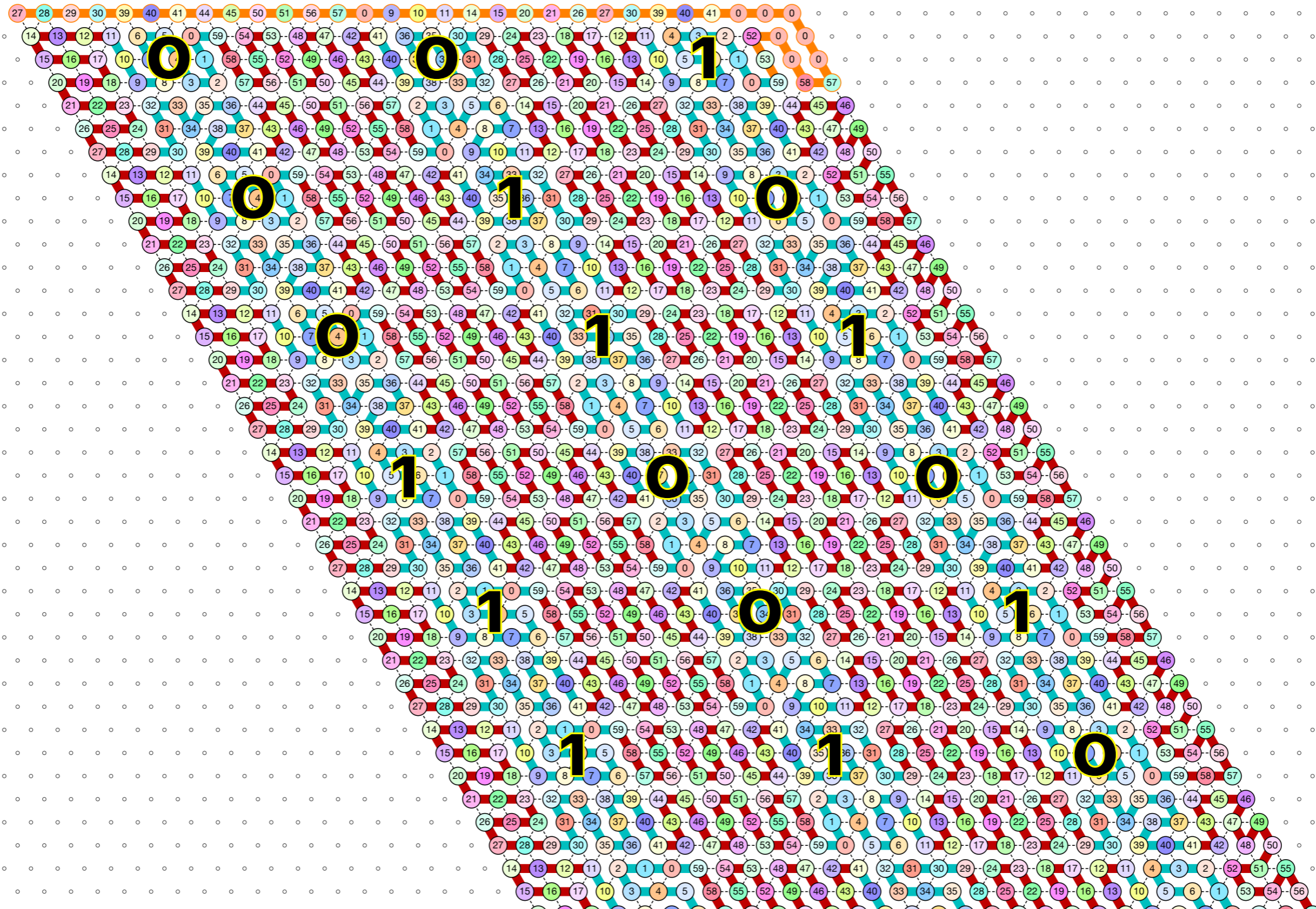
Information is encoded in the geometry





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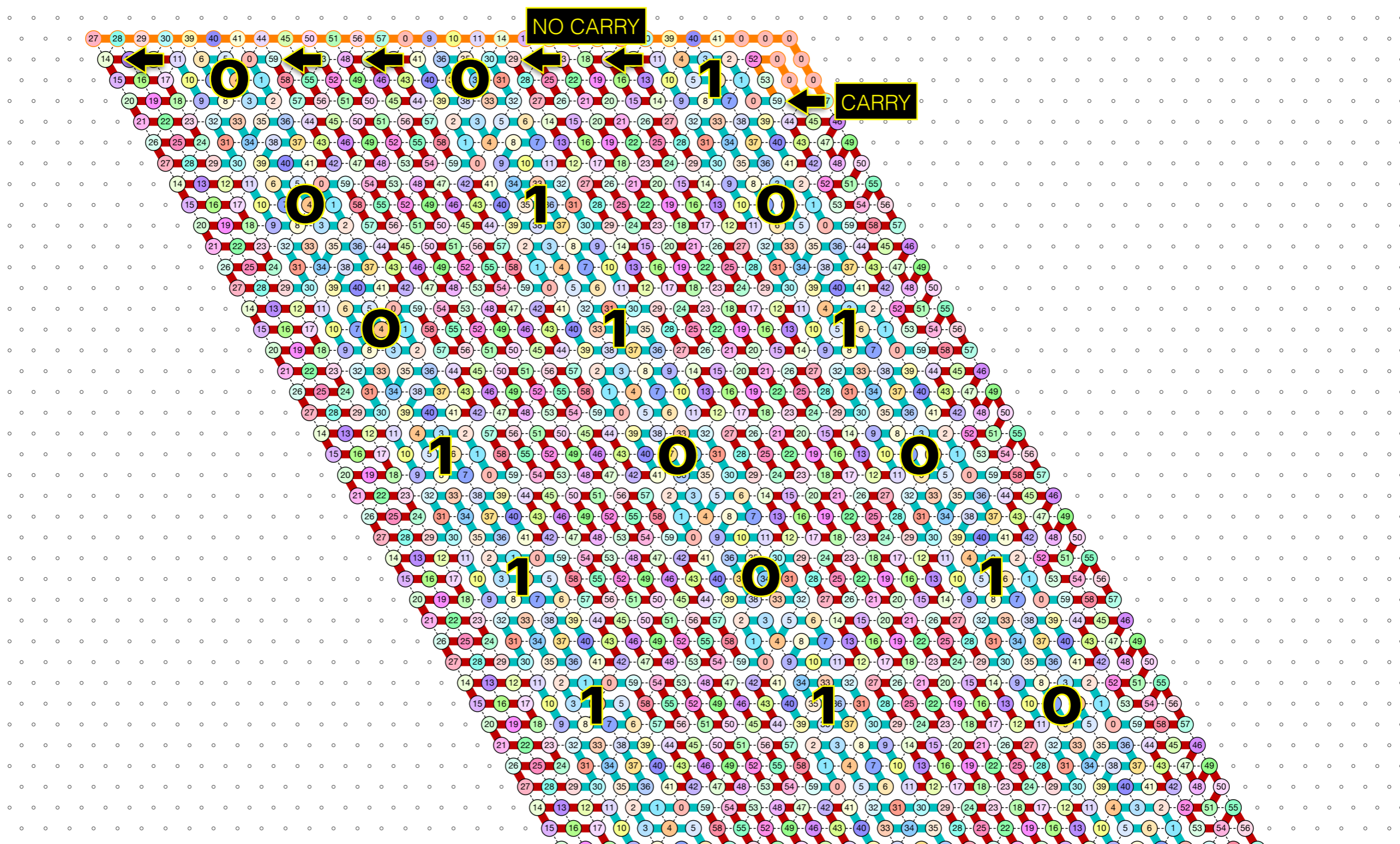
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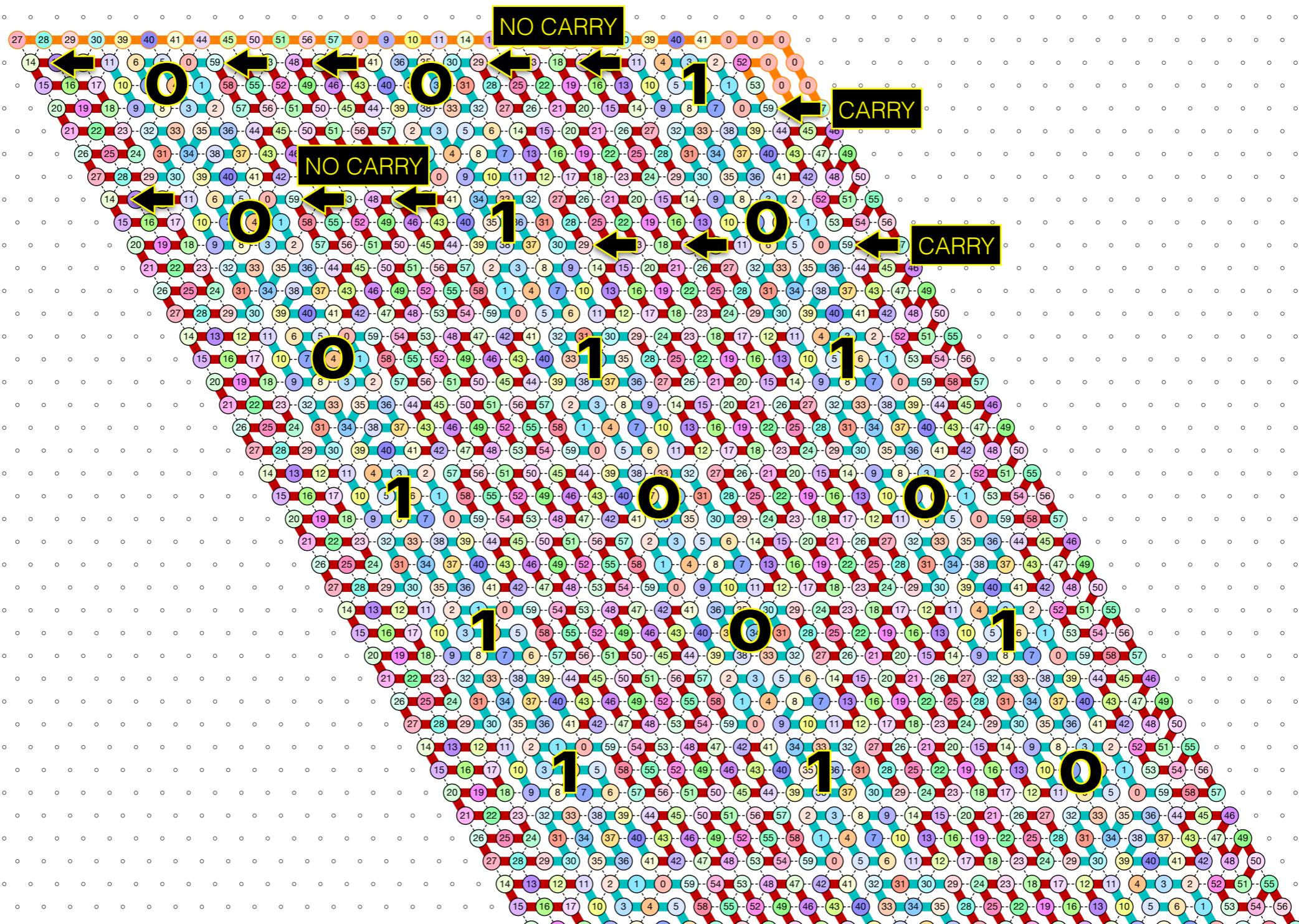
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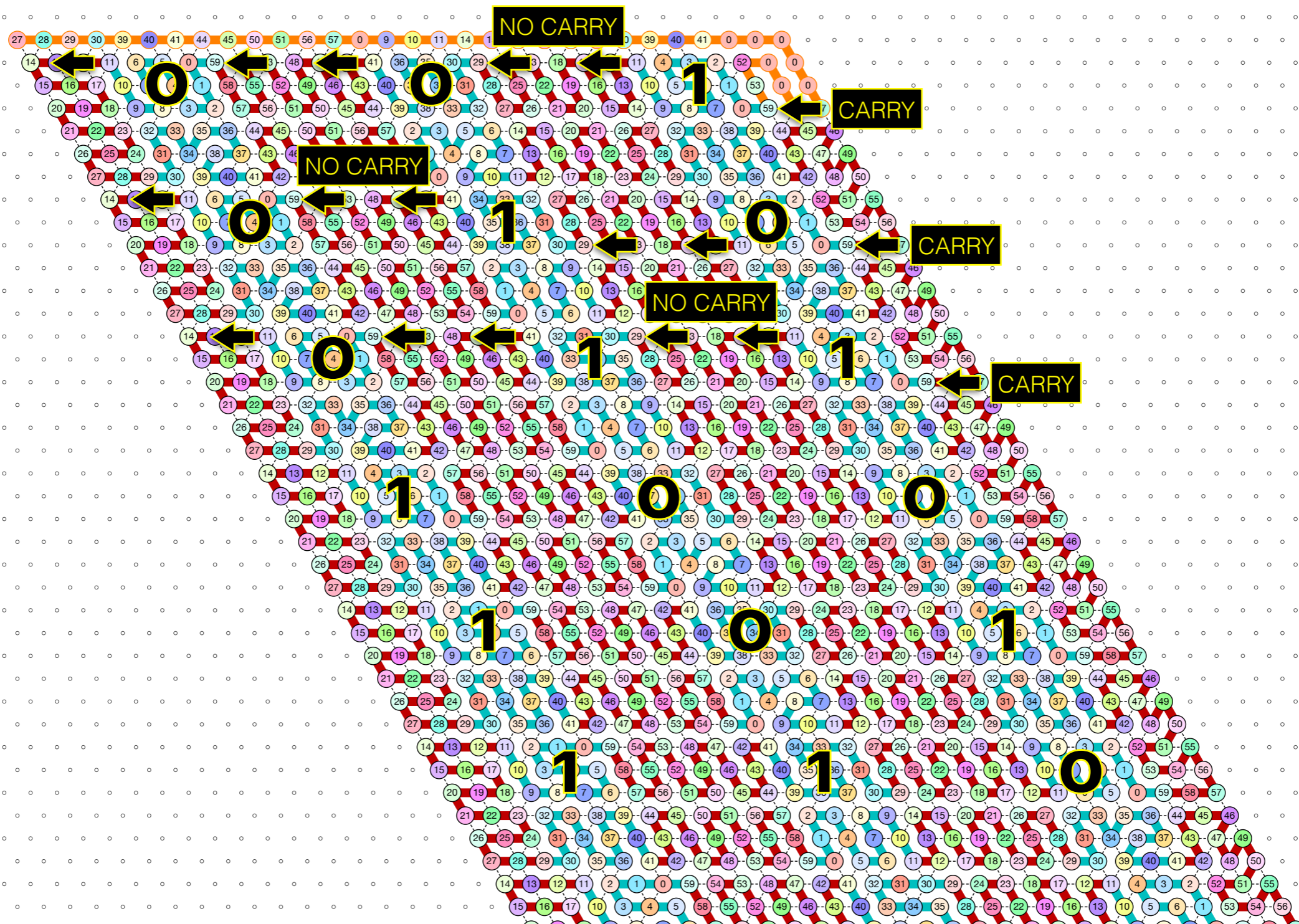
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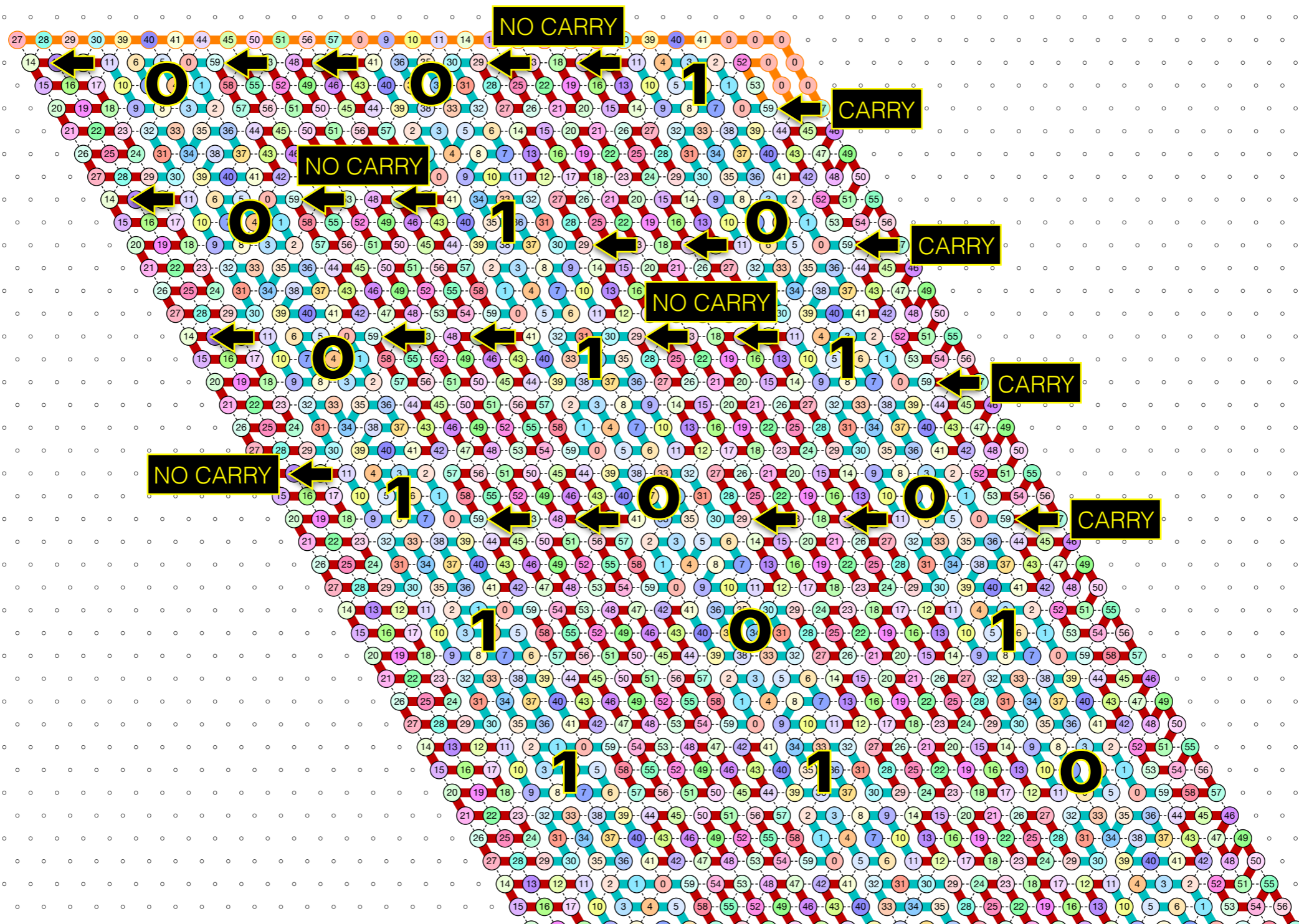
Information is encoded in the geometry





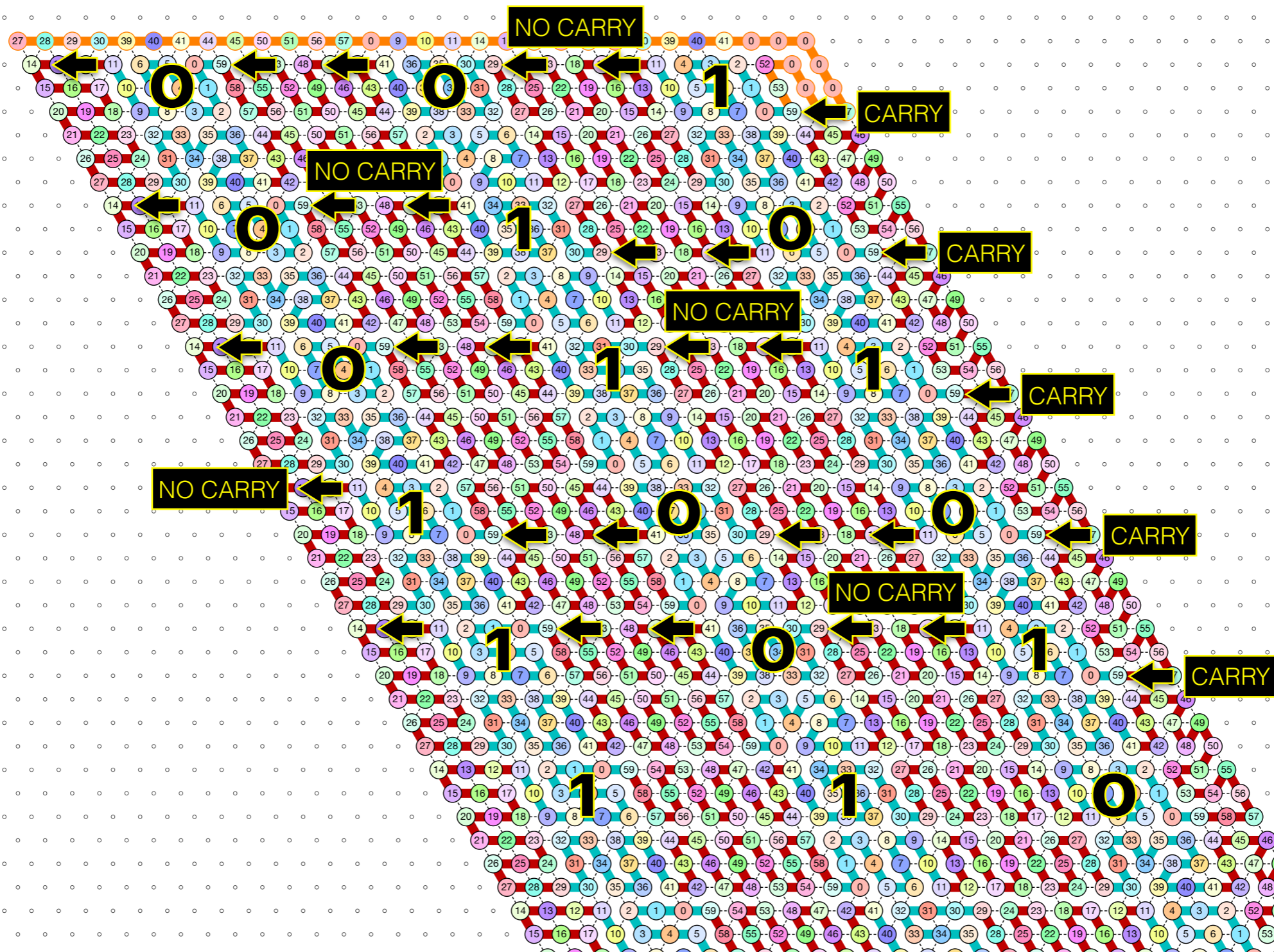
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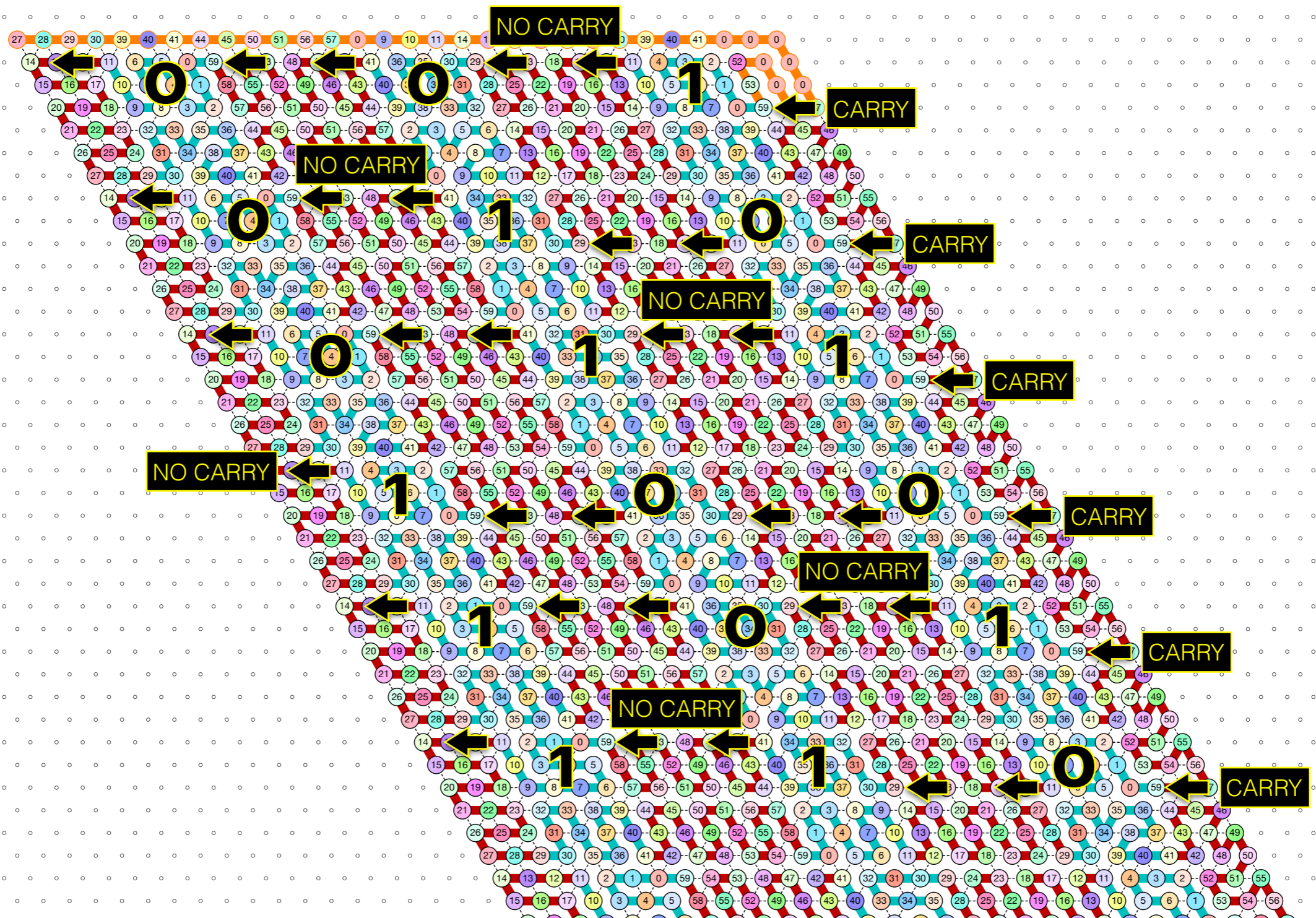
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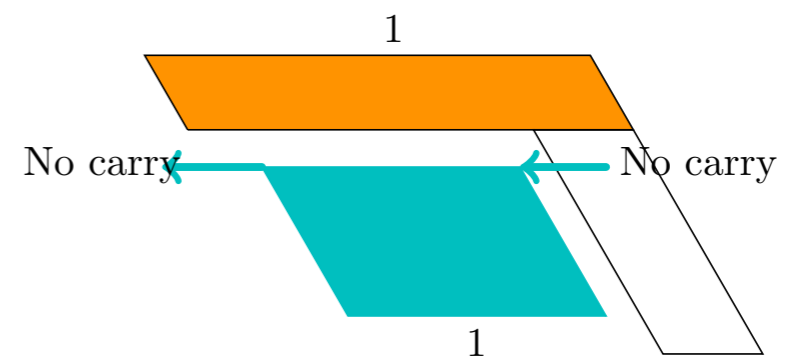
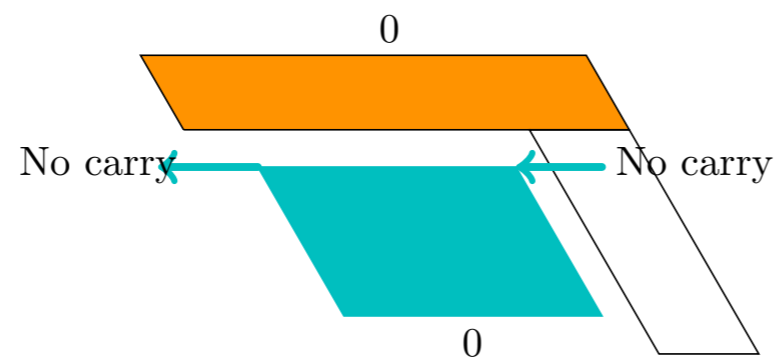
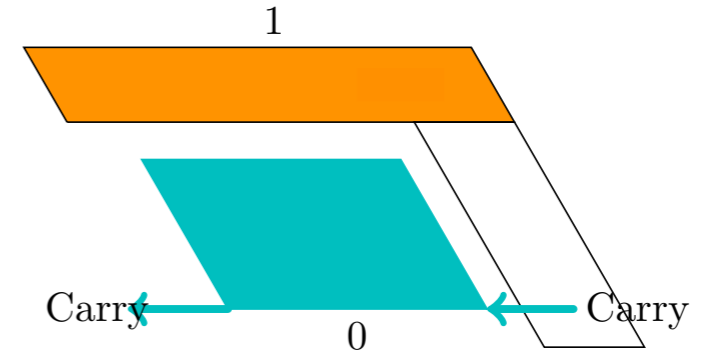
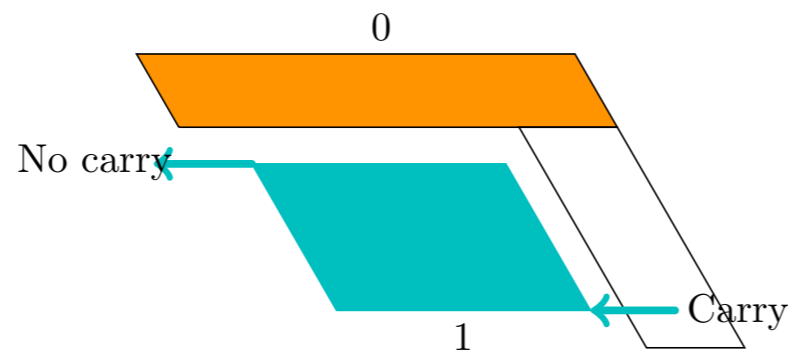




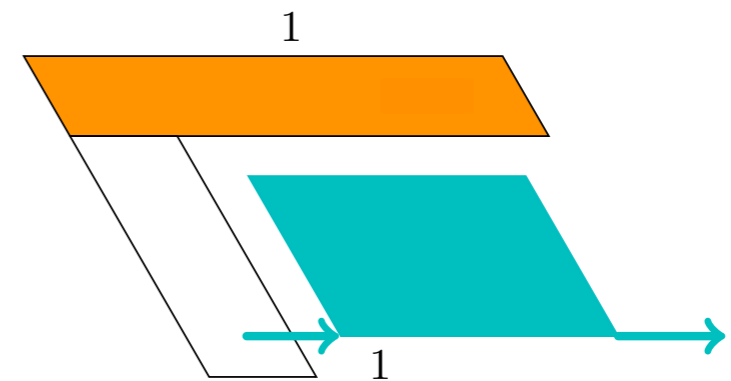
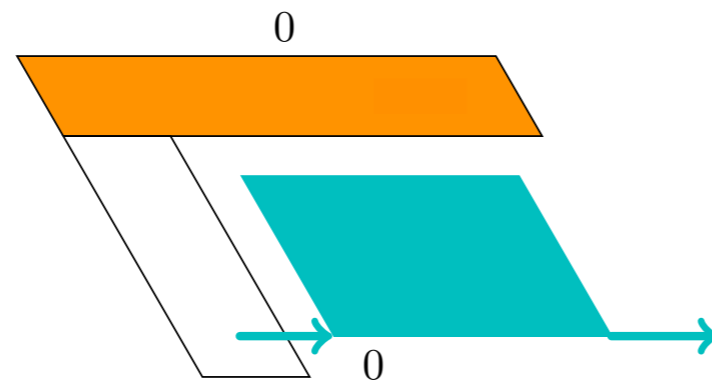
# Oritatami. A binary counter

Information is encoded in the geometry

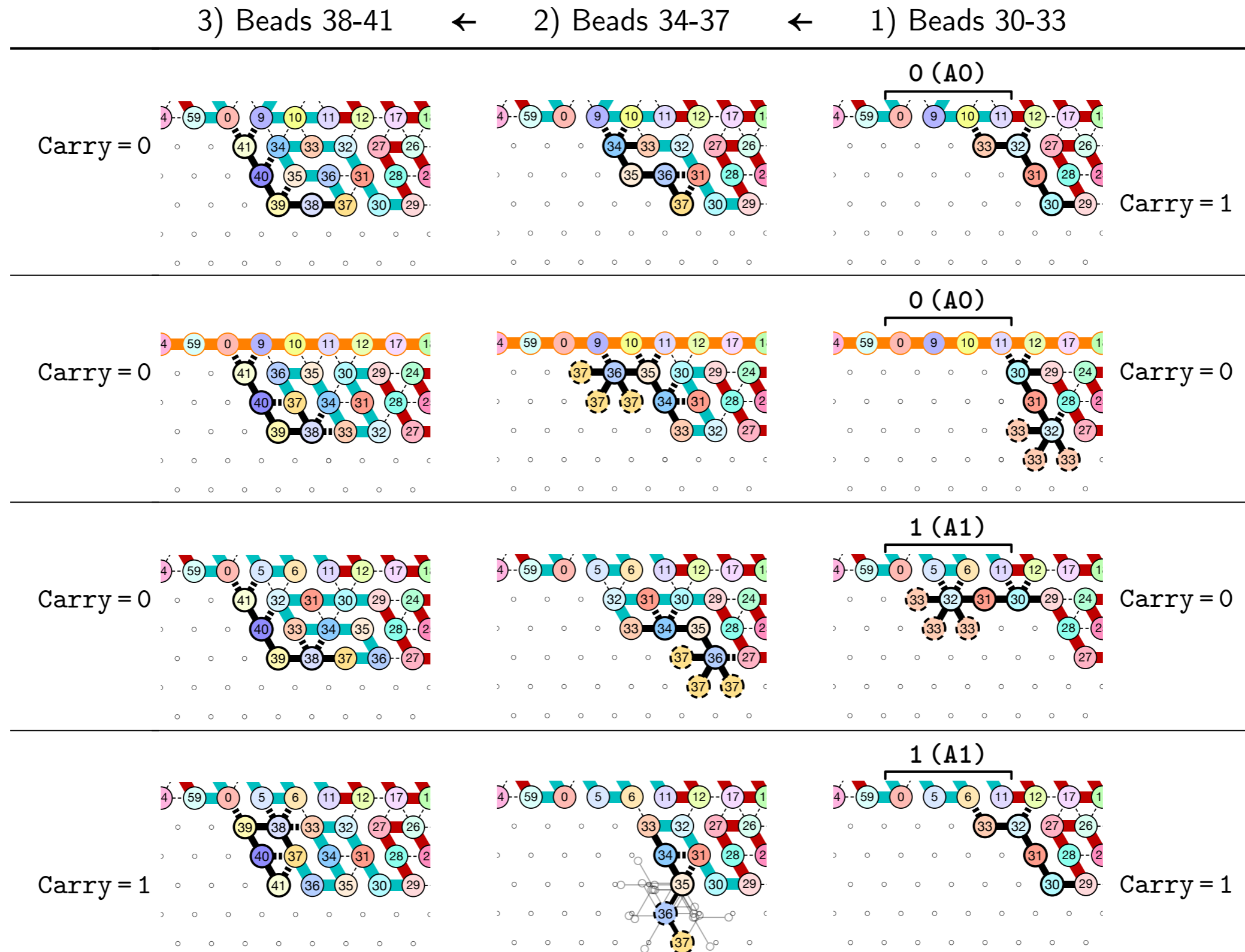
Carry propagation



Line feed

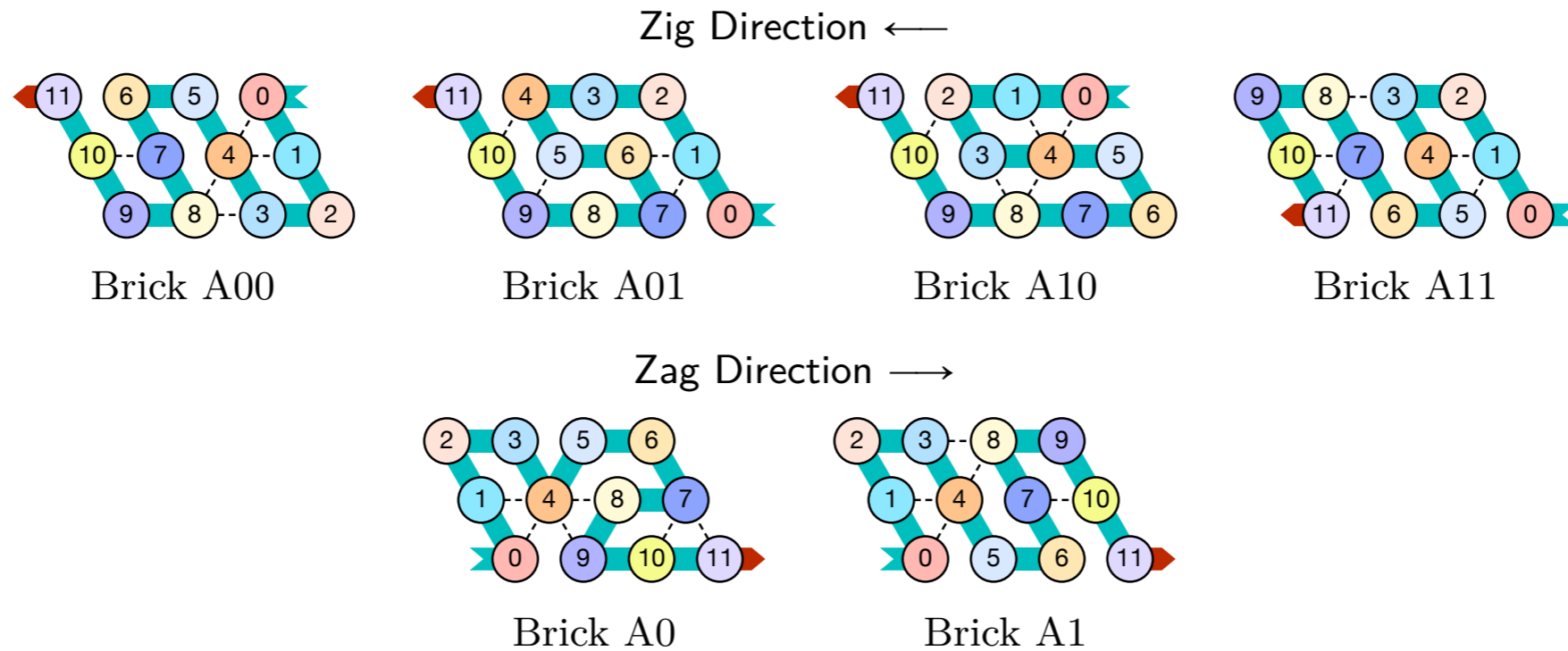


# How does computation work?

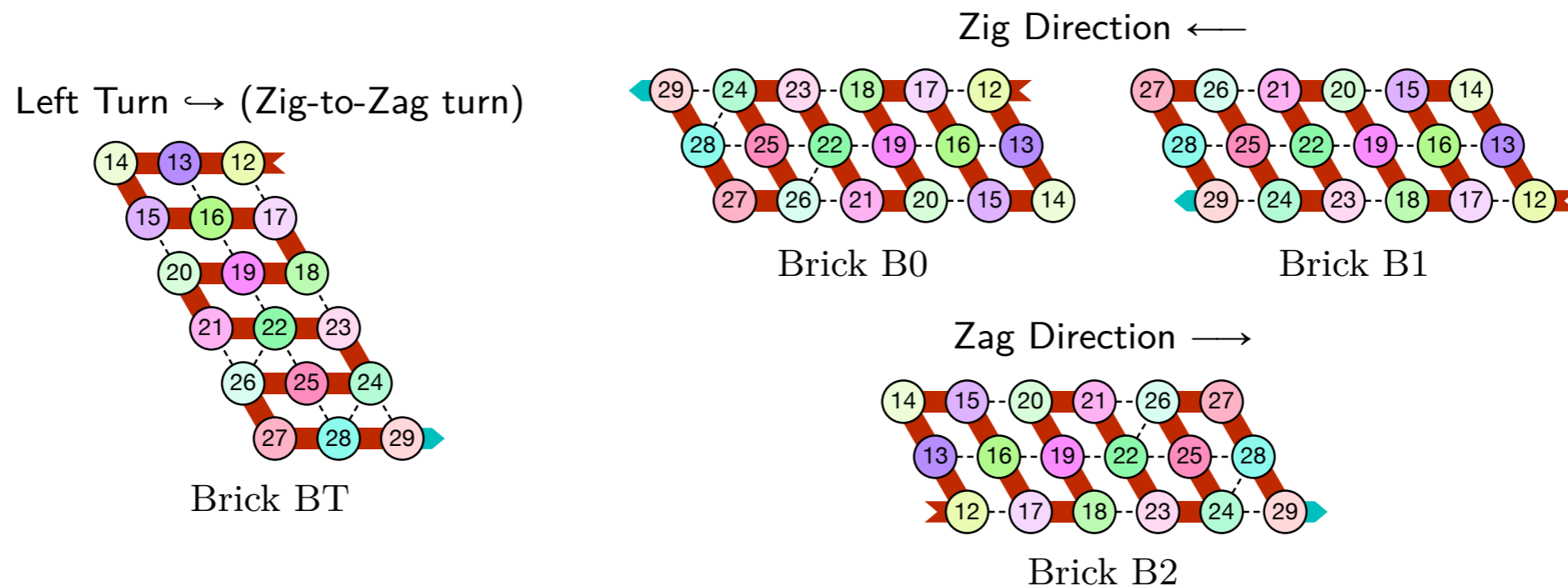


# Proving the binary counter: First, define the *bricks*

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



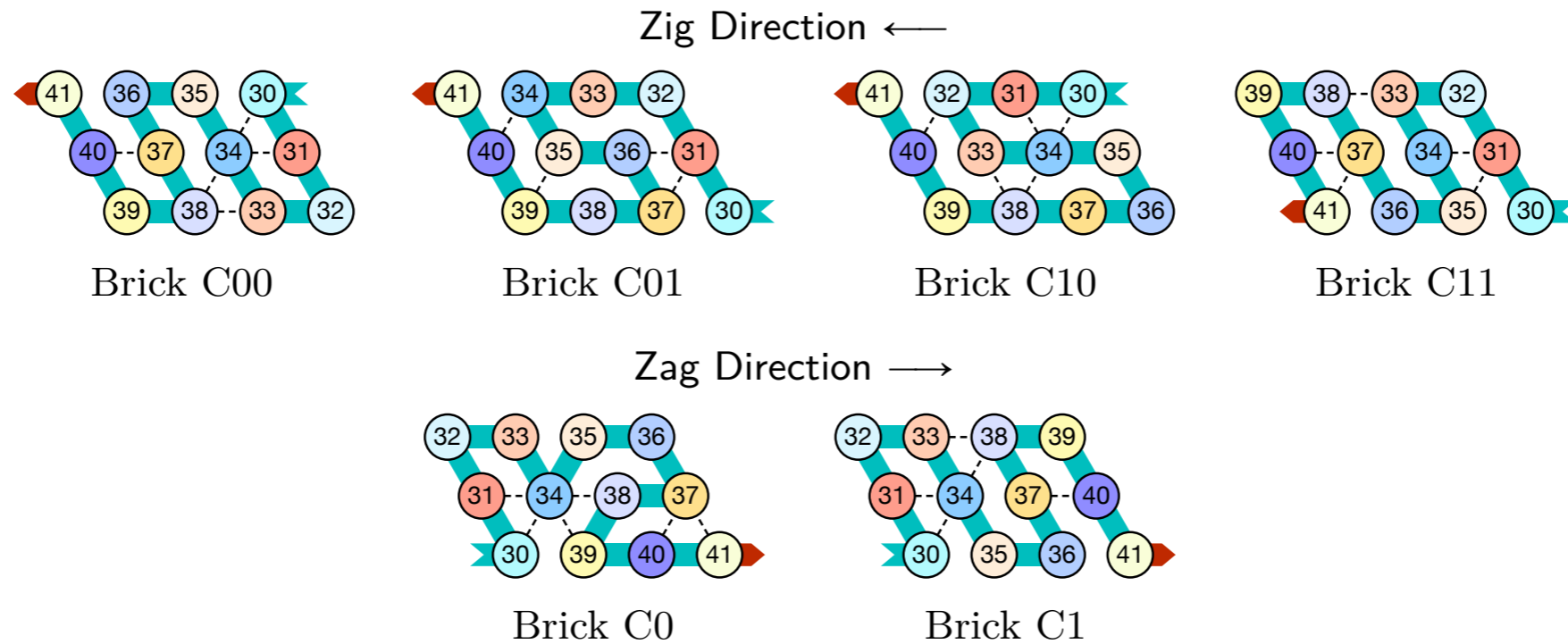
- Module *B*, Left-Turn module (beads 12–29)



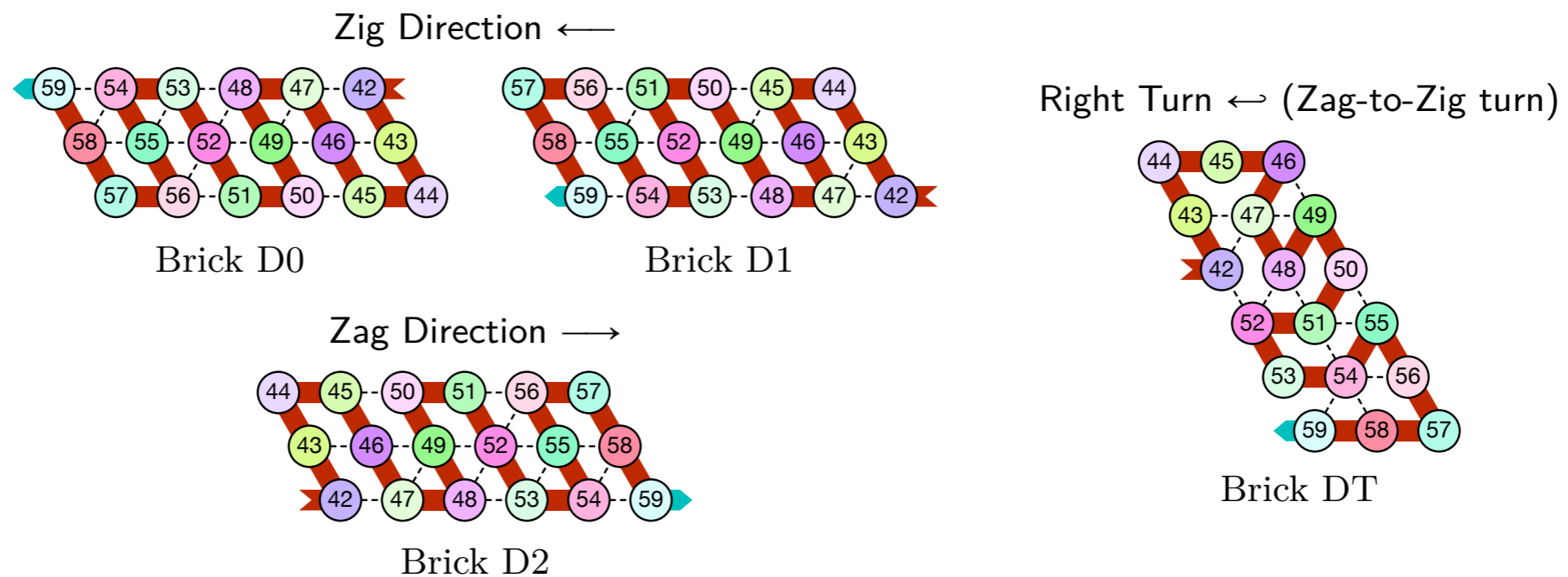


# Proving the binary counter: First, define the *bricks*

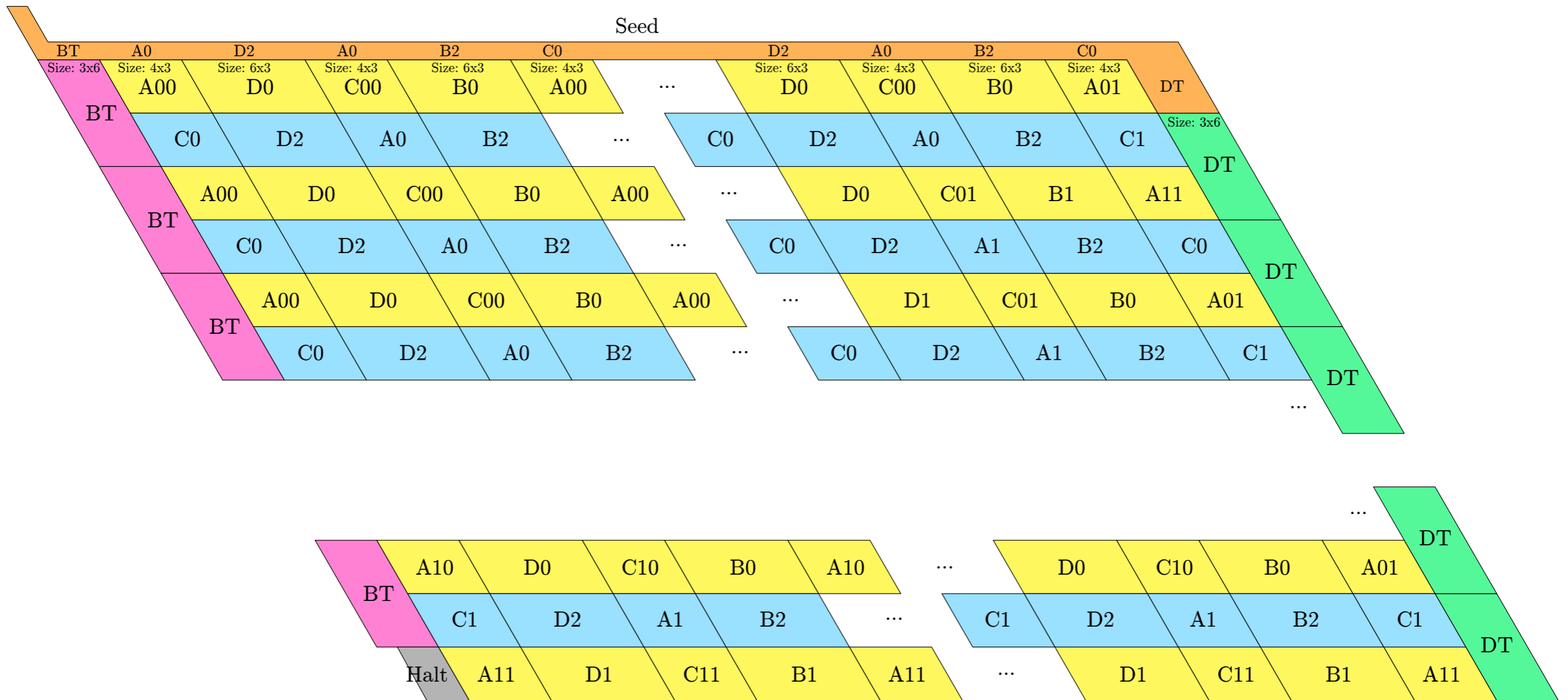
- Module *C*, Second Half-Adder (beads 30–41)



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

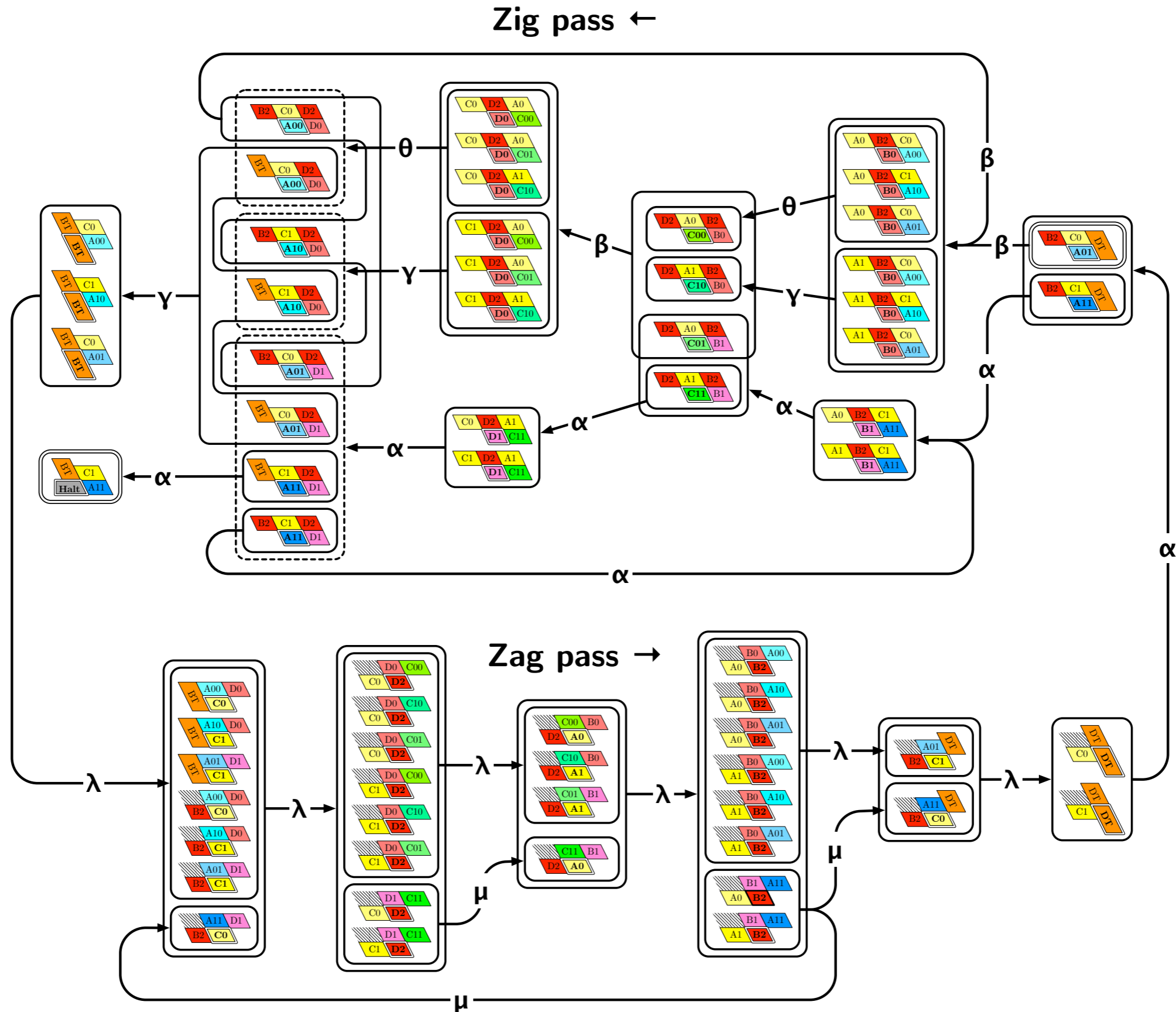


# 2nd, describe the final folding



We prove that the molecule folds like this by induction

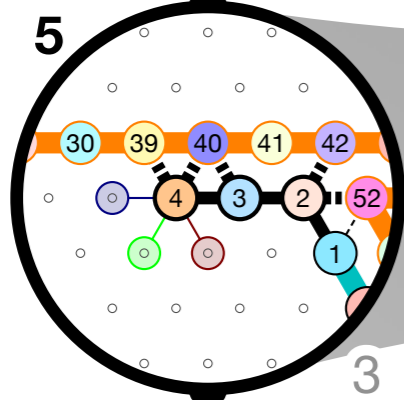
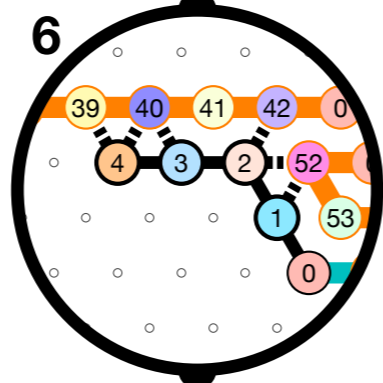
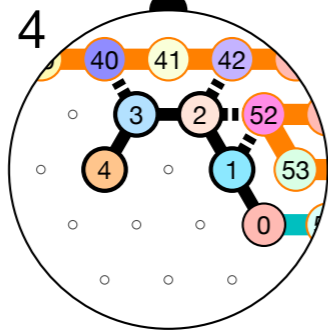
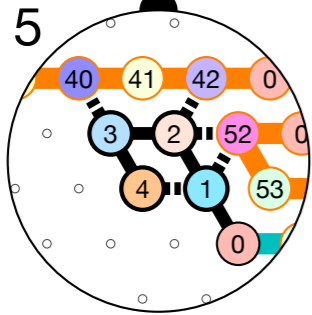
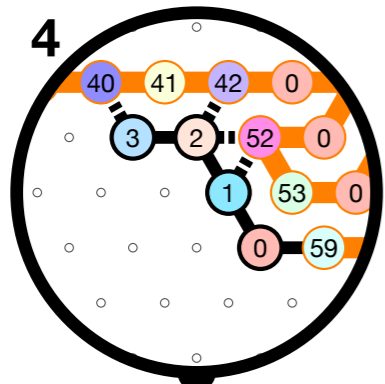
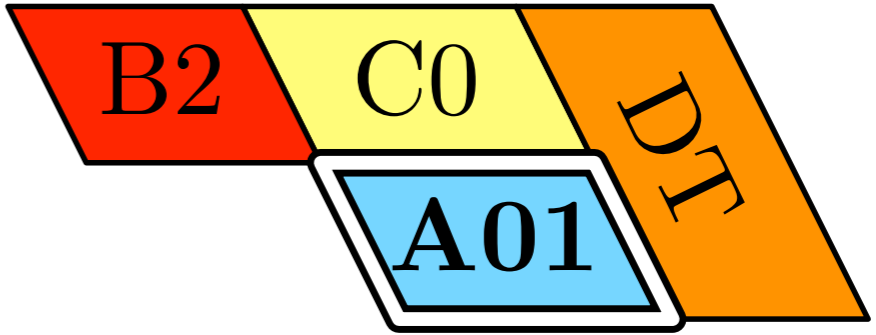
# 3rd, enumerate all the environments for each brick



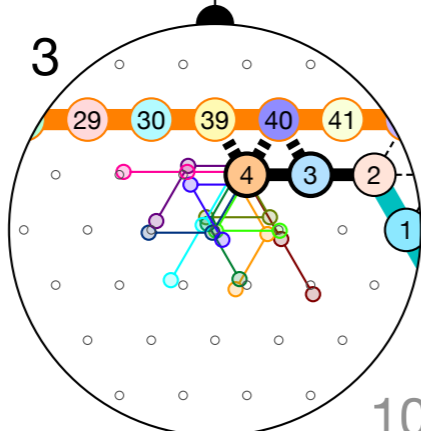
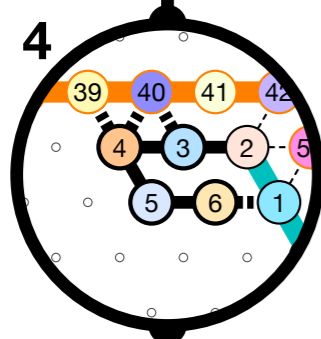




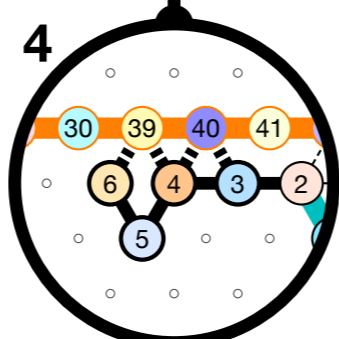
4th, prove the folding  
for each brick



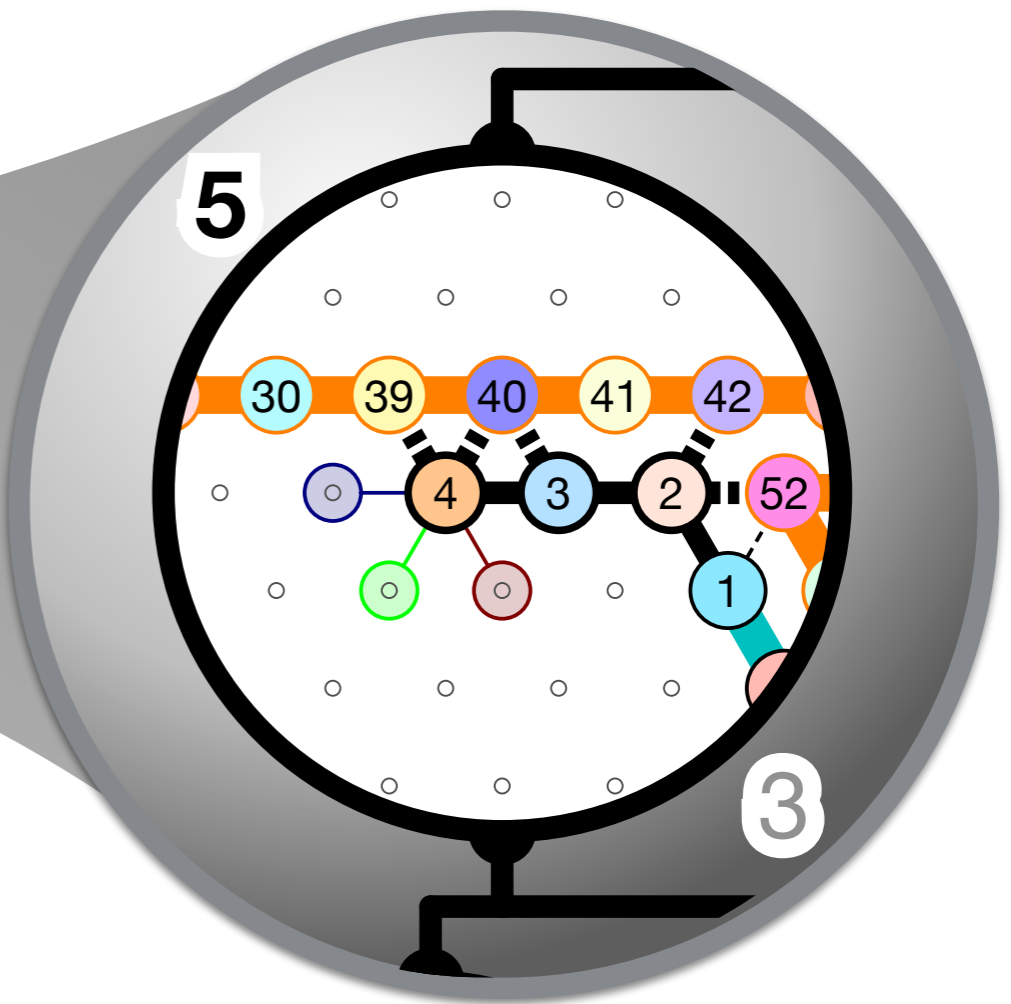
3



10



5



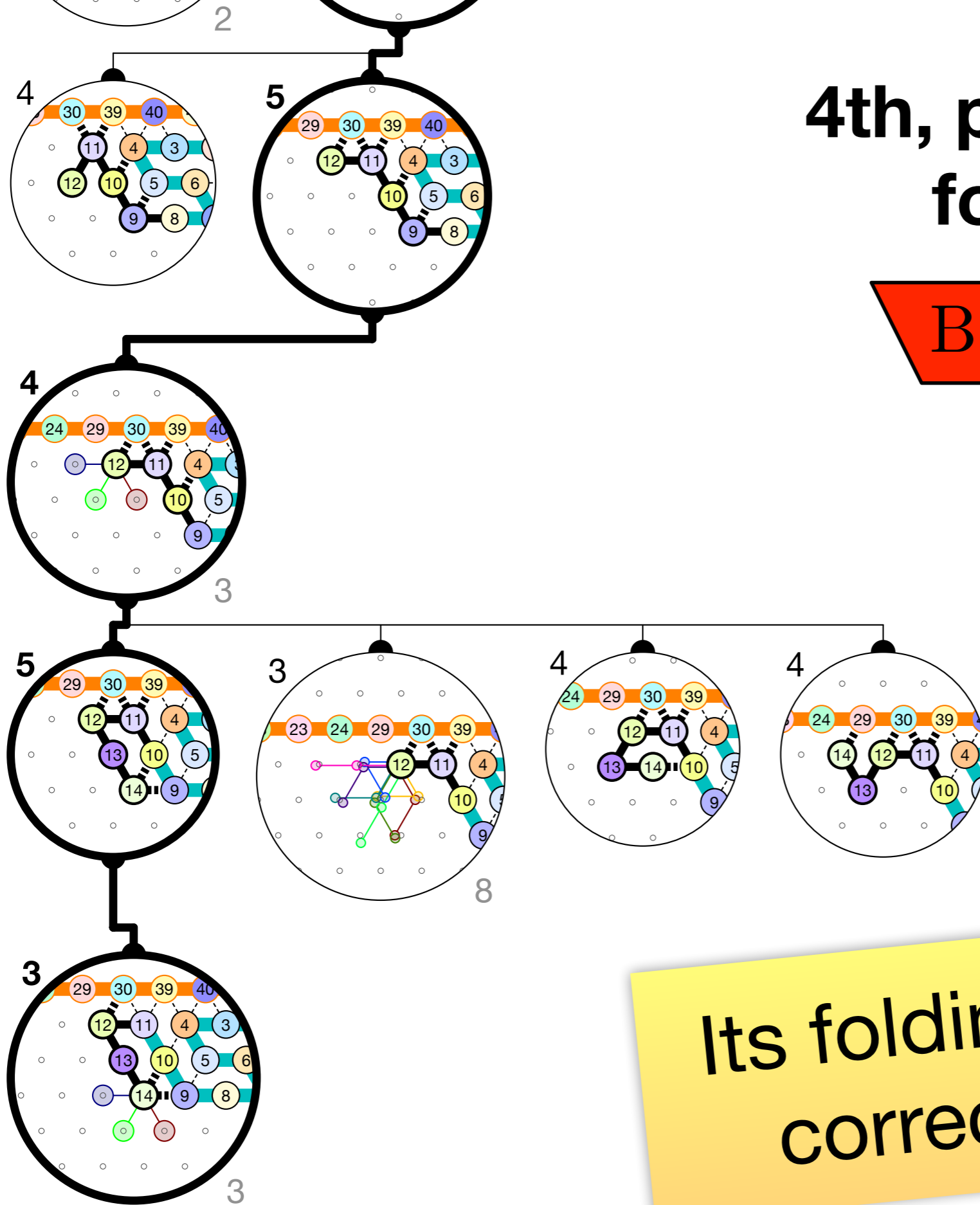
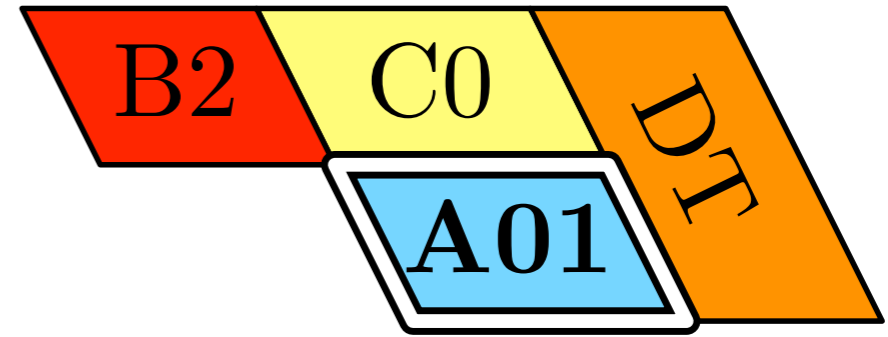
3

4

3

3

# 4th, prove the folding for each brick



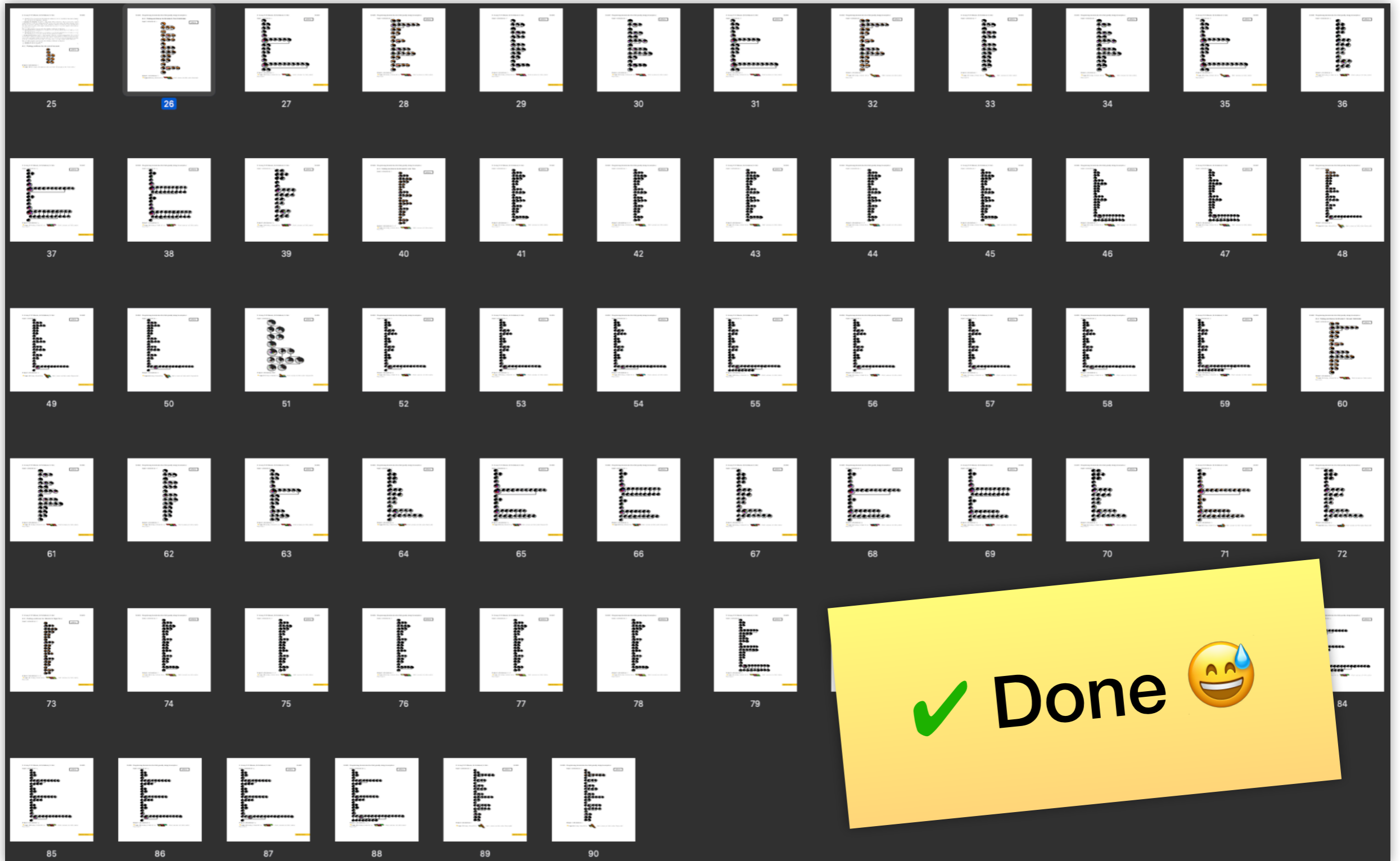
Its folding is correct !



**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.

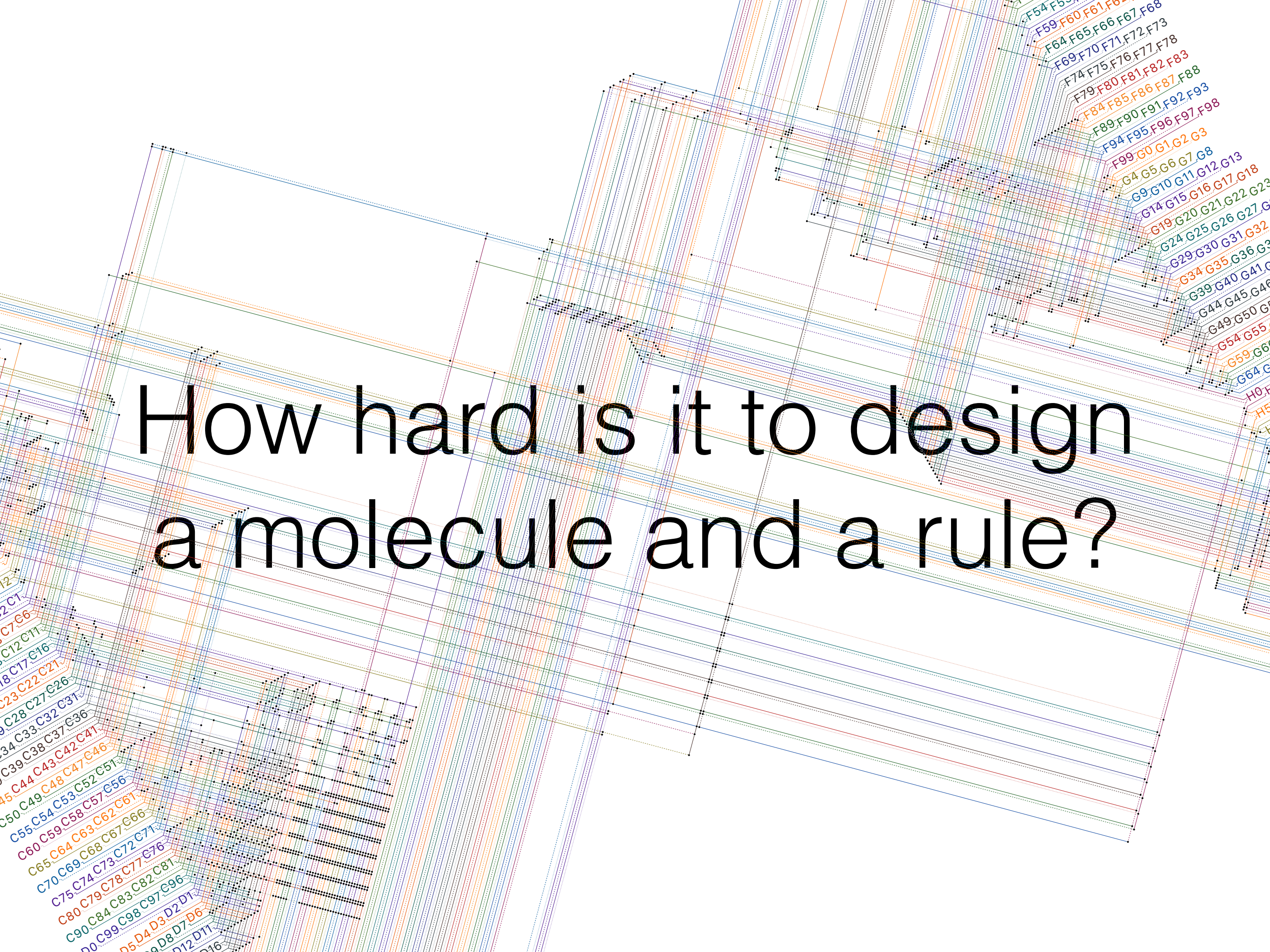
# Back to general oritatami

- How hard is it to design a rule?
- What can it compute?

# 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!



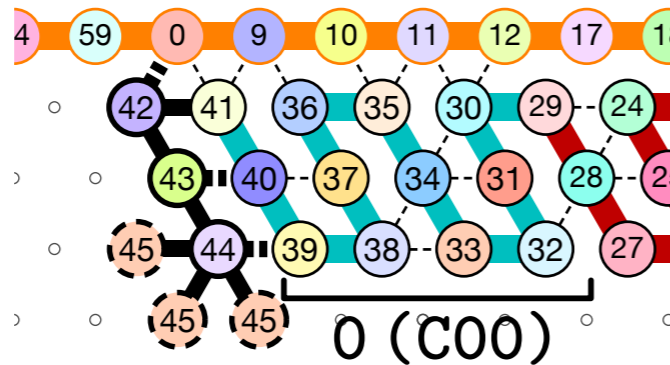
The background of the image is a dense, multi-layered network diagram. It consists of numerous nodes, represented by small black dots, connected by a complex web of edges. The edges are color-coded in various colors, including blue, orange, green, purple, and red. The network is organized into several distinct clusters or layers, with labels such as 'F54-F59', 'G4-G9', 'C1-C12', and 'D5-D12' visible at the periphery. The overall appearance is that of a highly interconnected and complex system, possibly representing a molecular structure or a computational network. Overlaid on this network is a large, black, sans-serif text question.

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

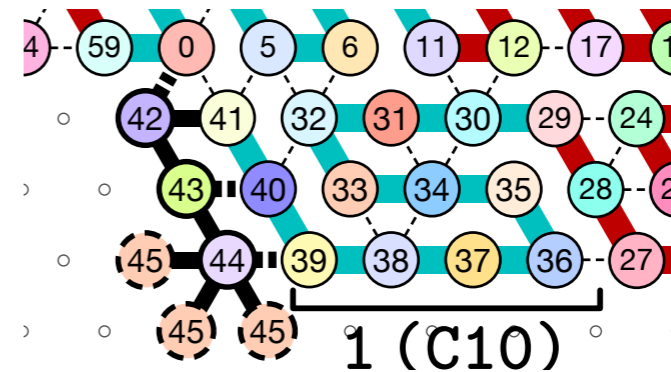


# The first challenge: Designing the desired shapes

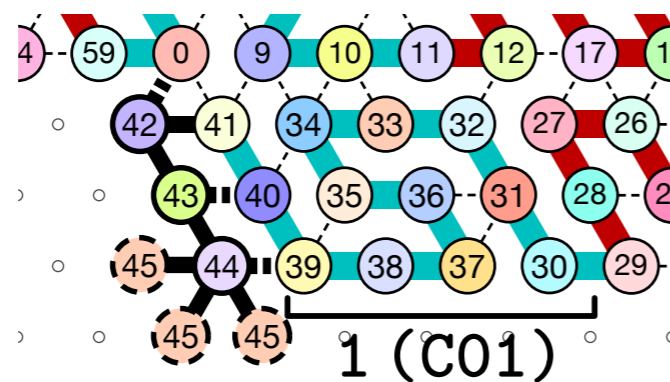
- Design shapes for which a **common** rule ♥ exists



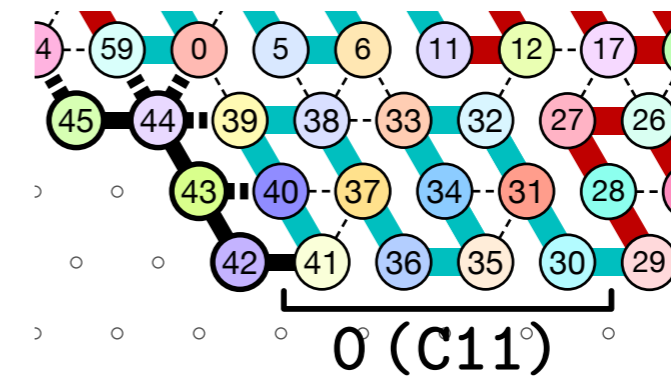
$$0+0 = 0 + \text{no } C$$



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



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



$$1+1 = 0 + C$$

# The first challenge: Designing the desired paths

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

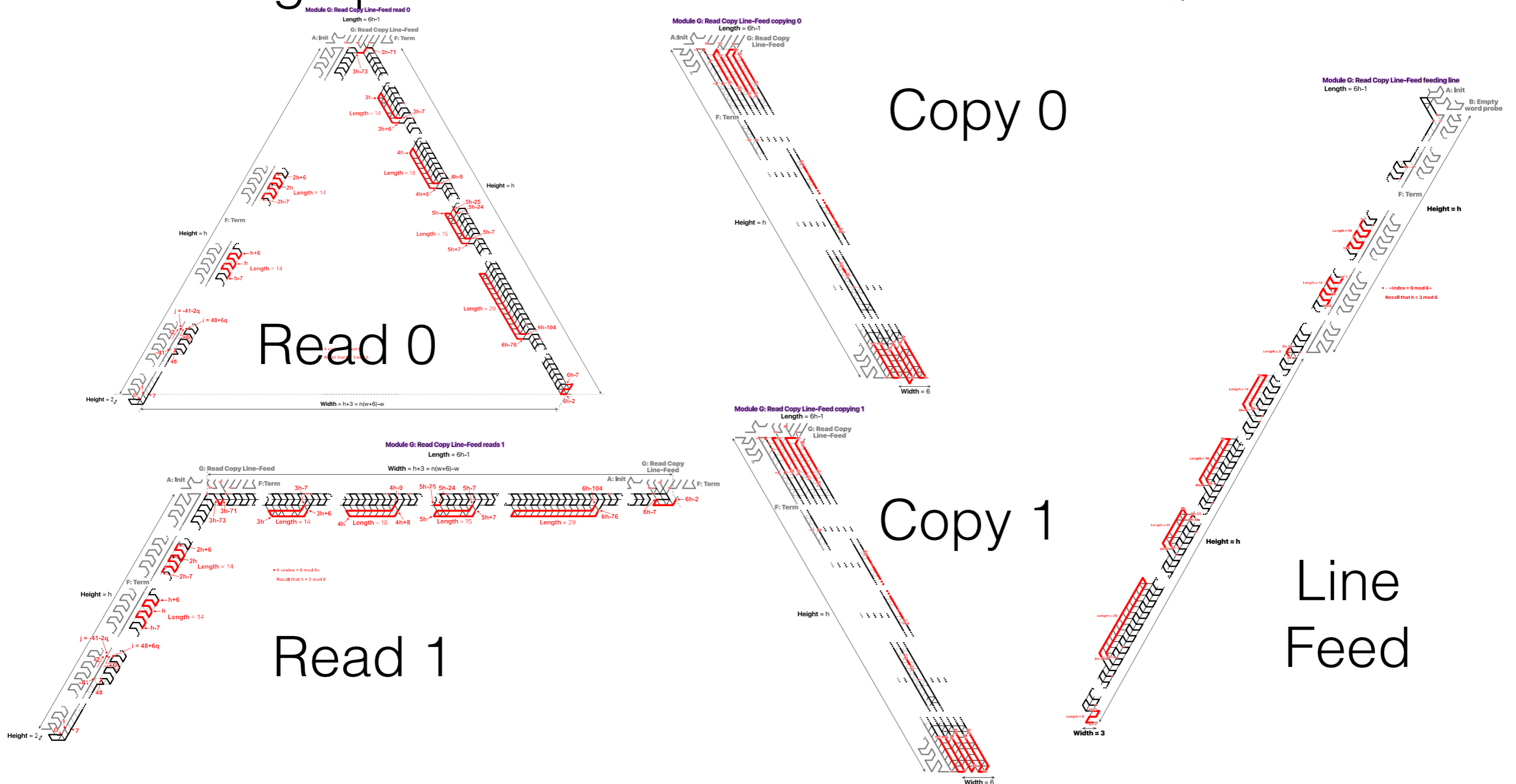
Copy 0

Read 0

Copy 1

Read 1

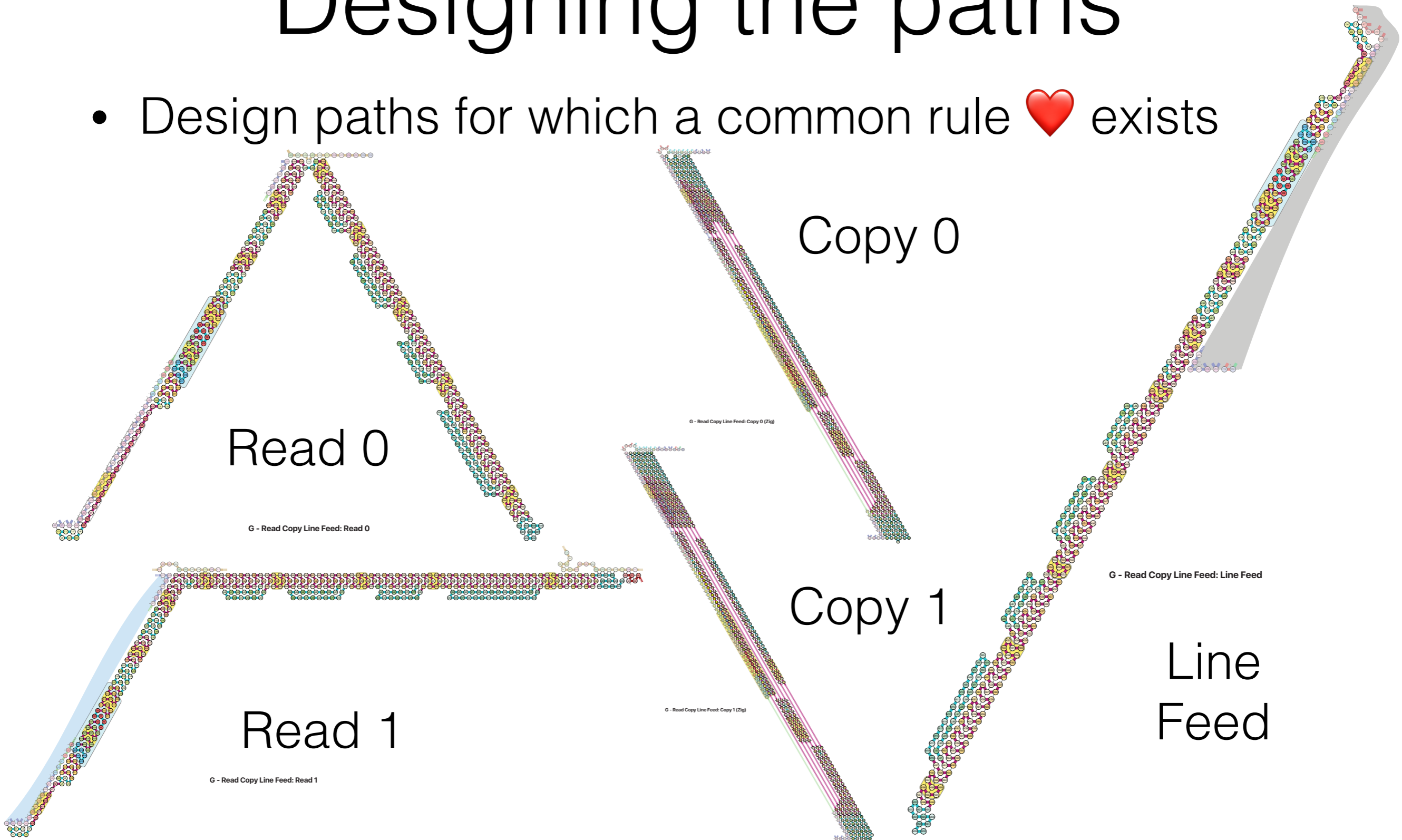
Line  
Feed





# The first challenge: Designing the paths

- Design paths for which a common rule  exists

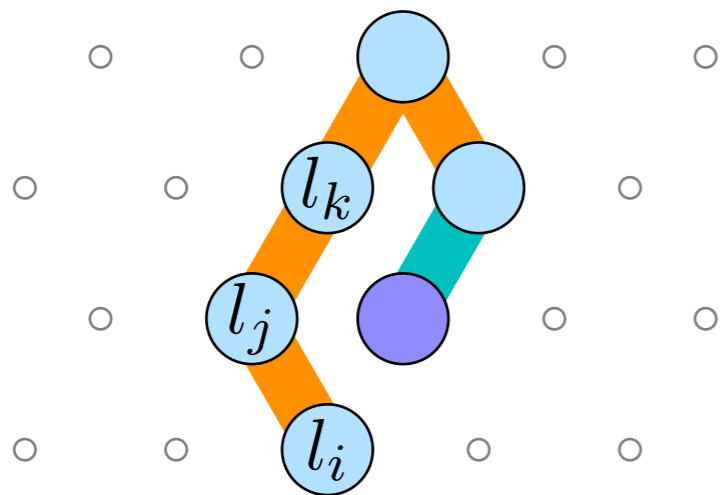


# Oritatami design is NP-hard

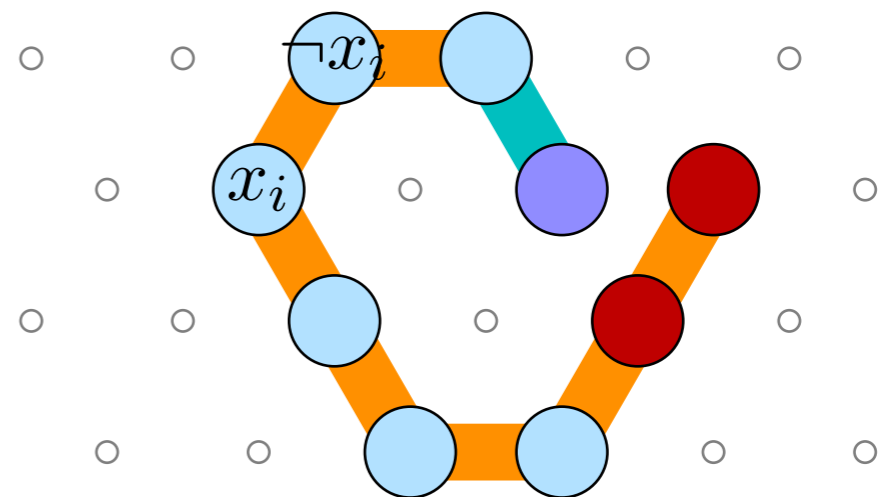
INPUT:	a delay time $\delta$ , a list of $n > 0$ seeds $\sigma_1, \sigma_2, \dots, \sigma_n$ , and a list of $n$ conformations $c_1, c_2, \dots, c_n$ of the same length $l$
OUTPUT:	an attraction rule $\heartsuit$ such that for all $i \in \{1, 2, \dots, n\}$ , Oritatami system $\mathcal{O}_i = (s, \sigma_i,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

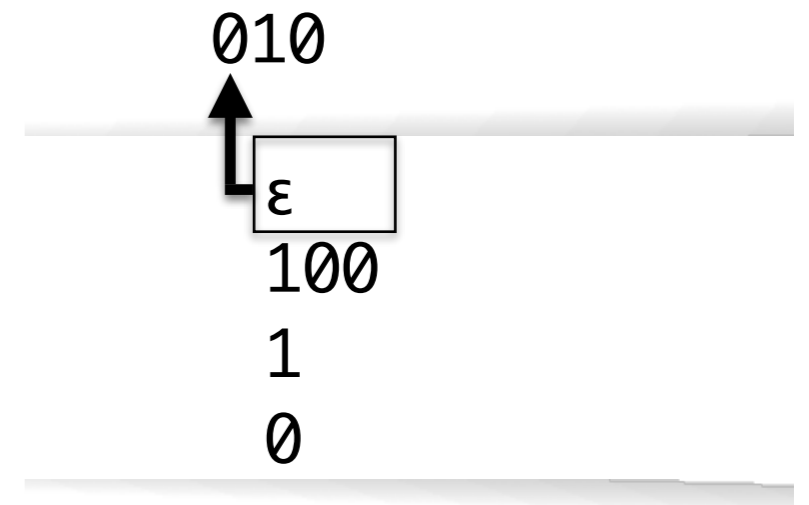


**Oritatami is  
Turing complete**

# Skipping Cyclic Tag Systems

- A finite **cyclic sequence** of finite binary **code words** with a pointer  $p$  to one of them
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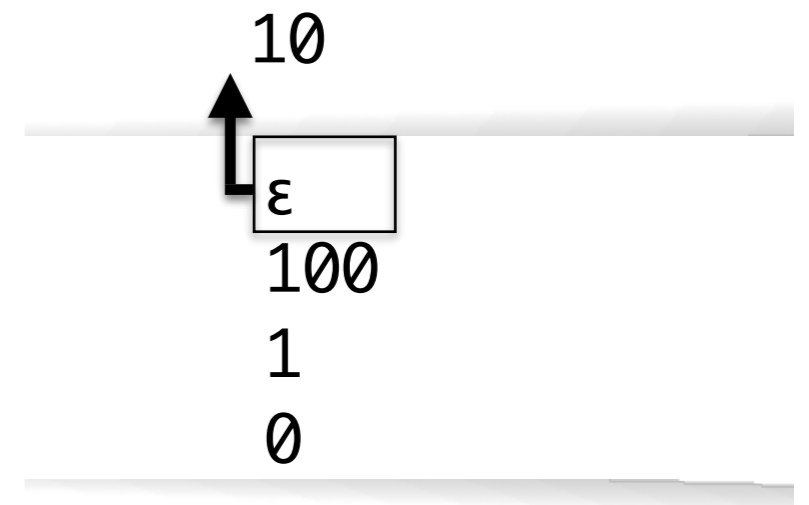
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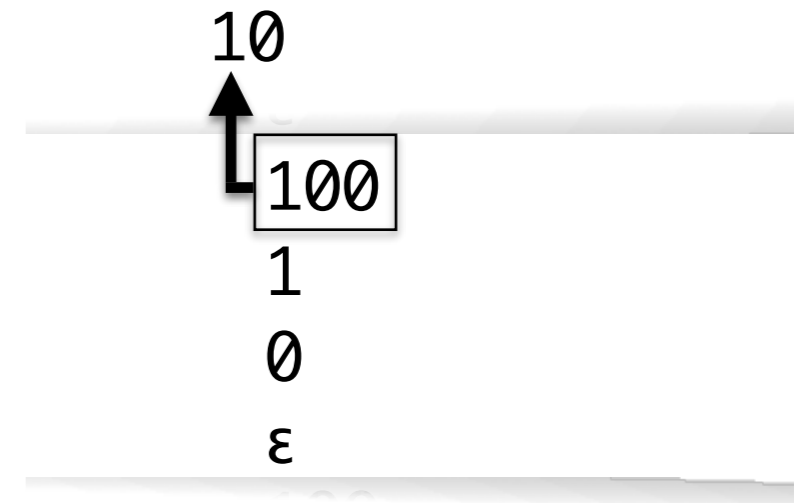




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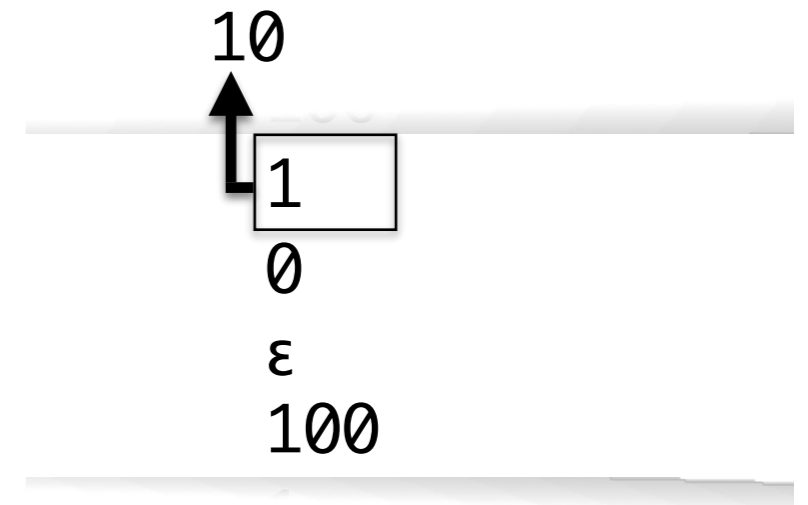
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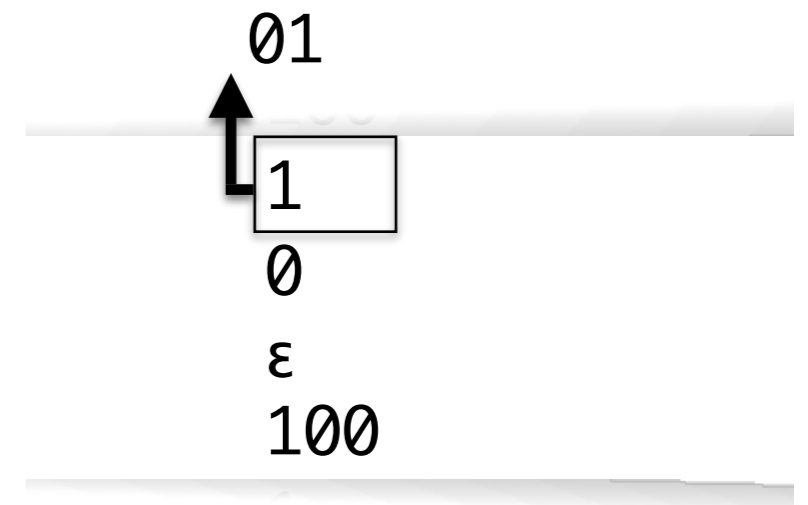
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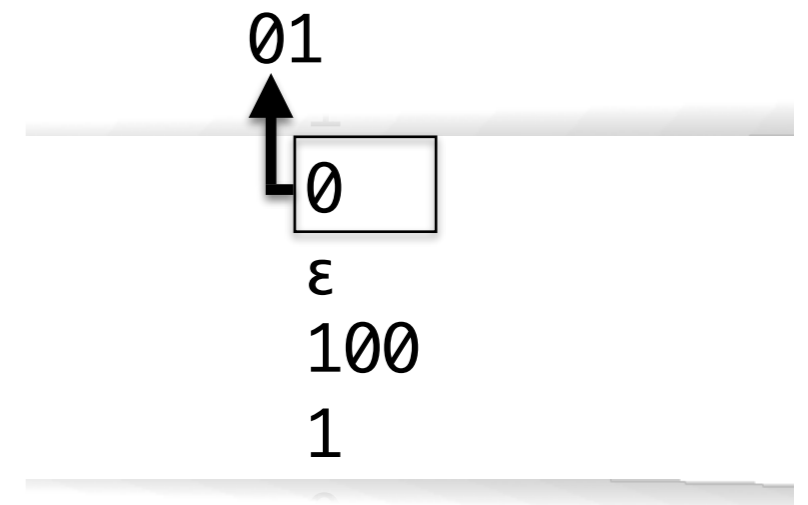
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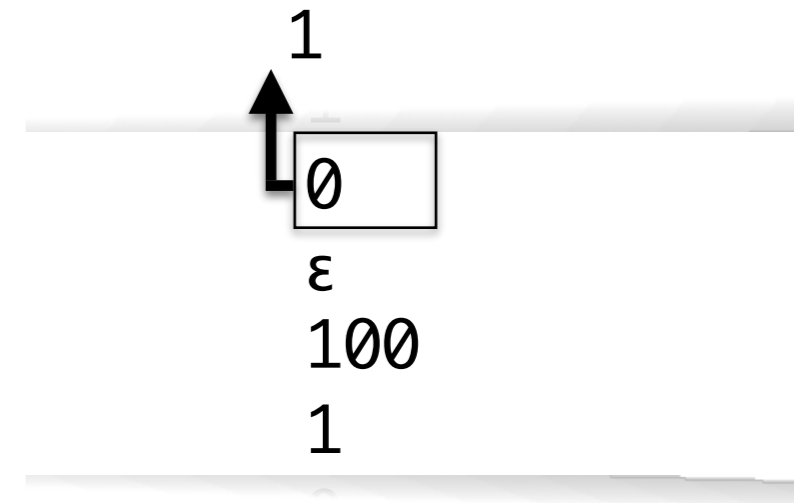




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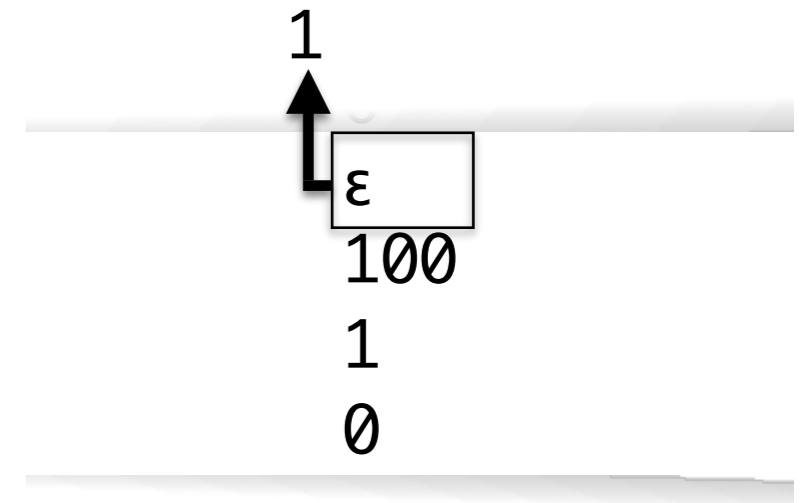
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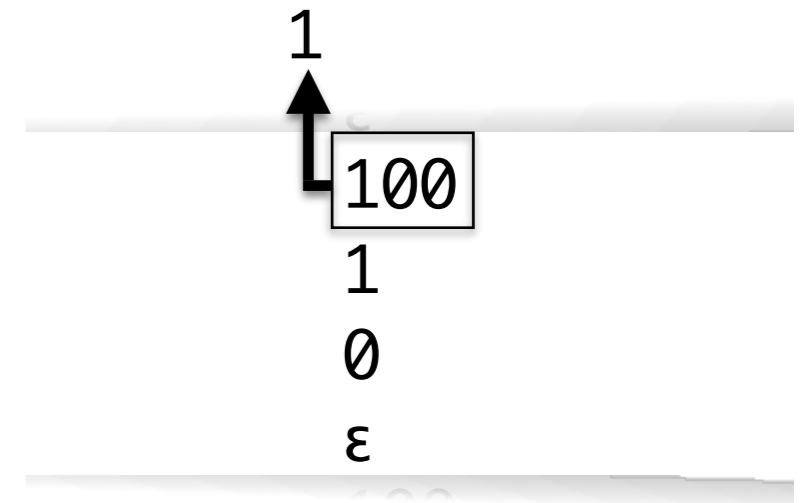
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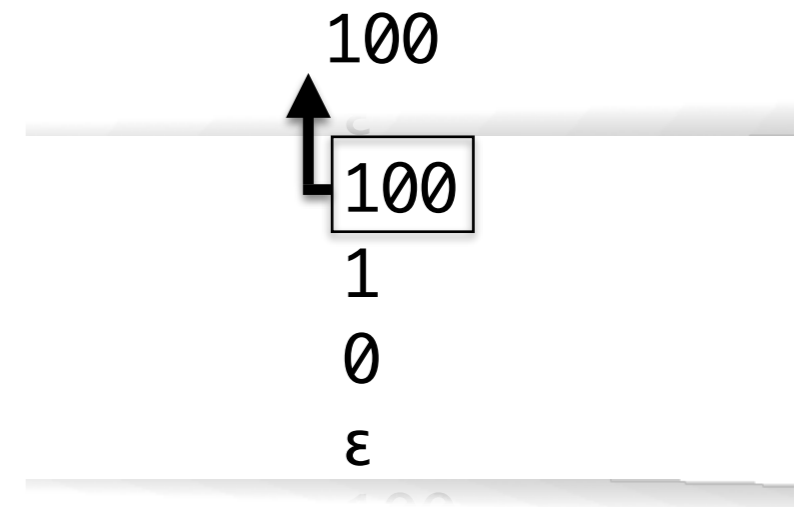
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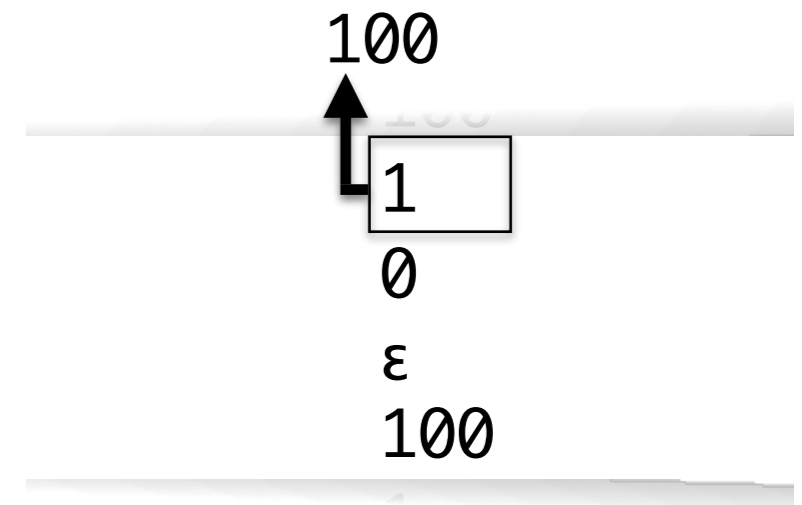




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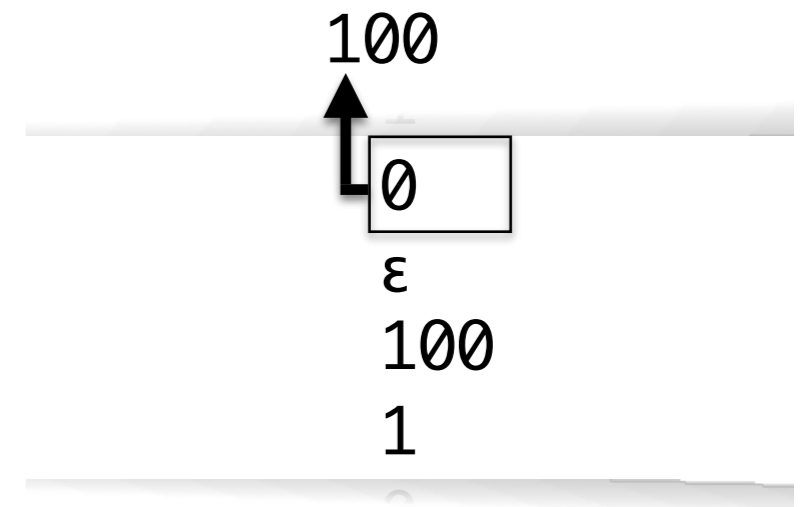
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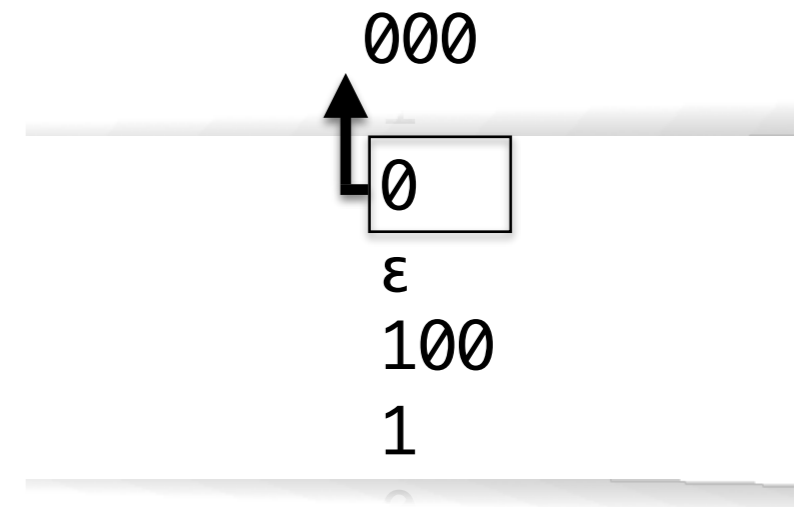
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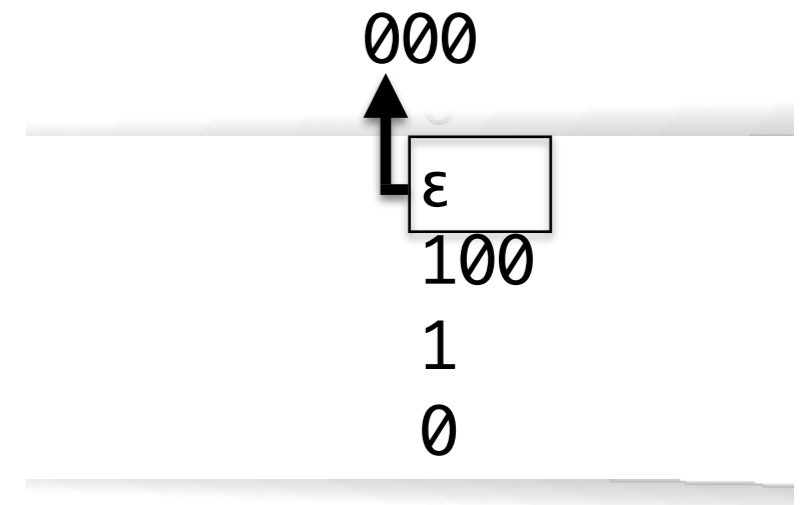
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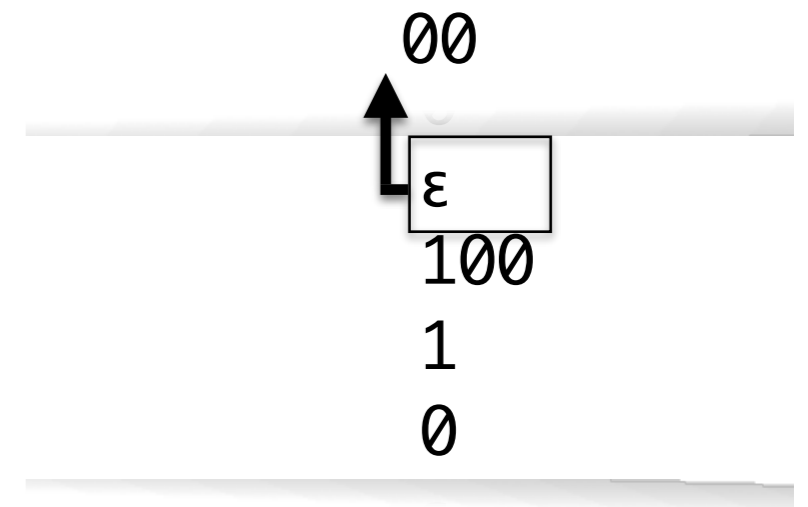




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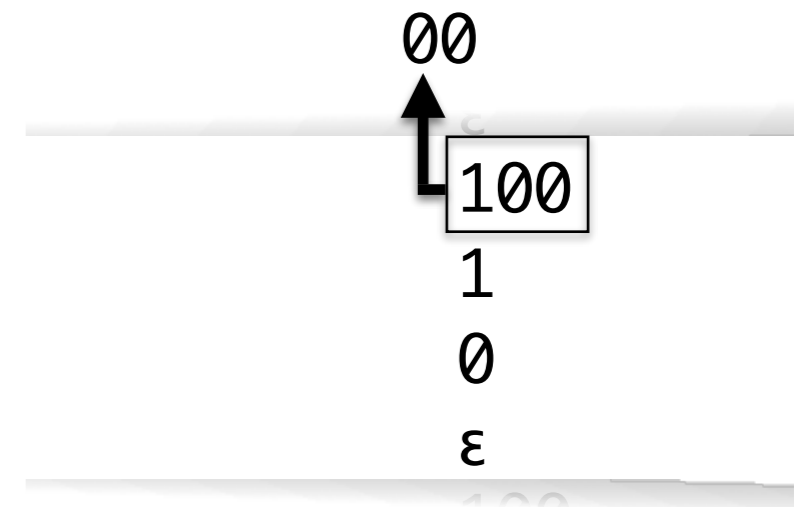
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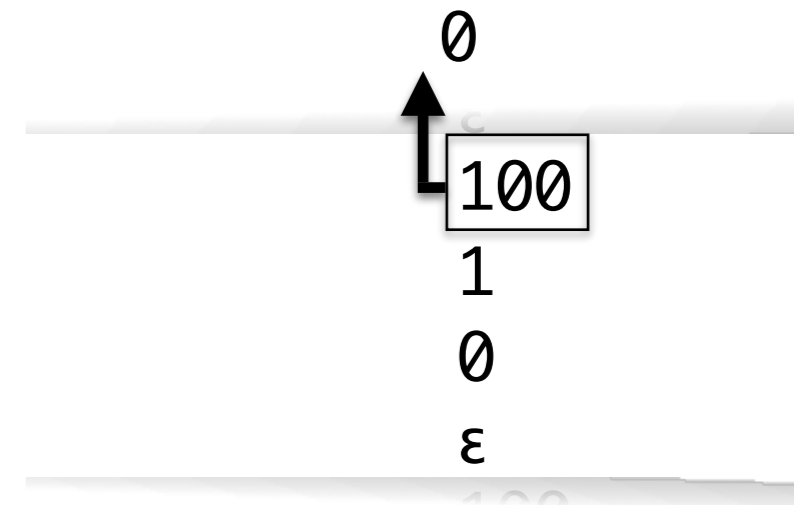
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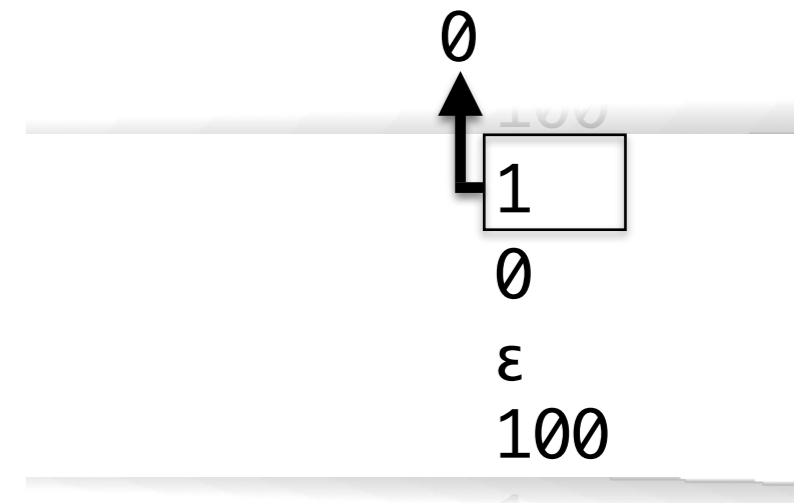
## Example.



# 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 ( $\varepsilon$ ): halt*
  - *If the 1st letter of the tape word is 0: delete the 0 and increment the pointer  $p$*
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## Example.

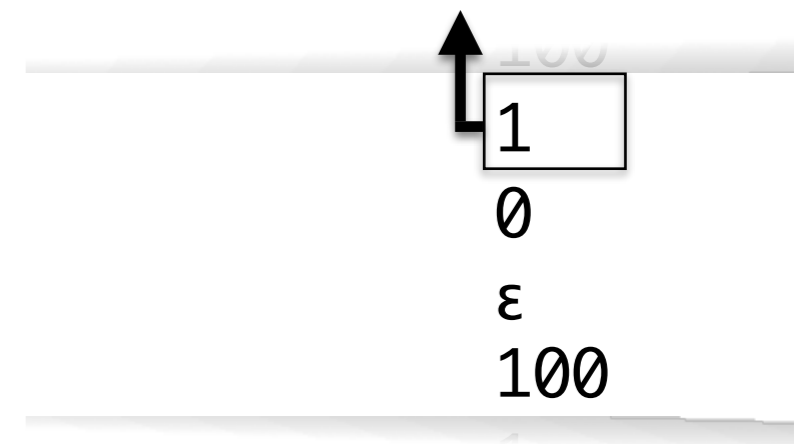




# Skipping Cyclic Tag Systems

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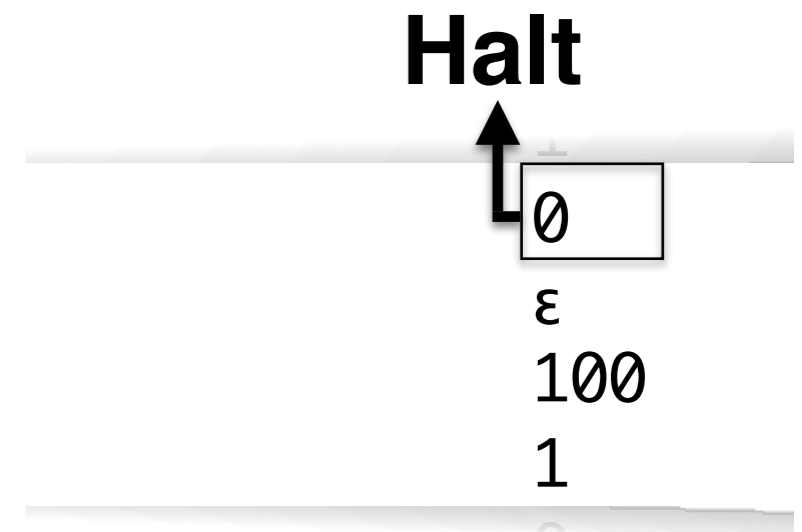
## Example.



# 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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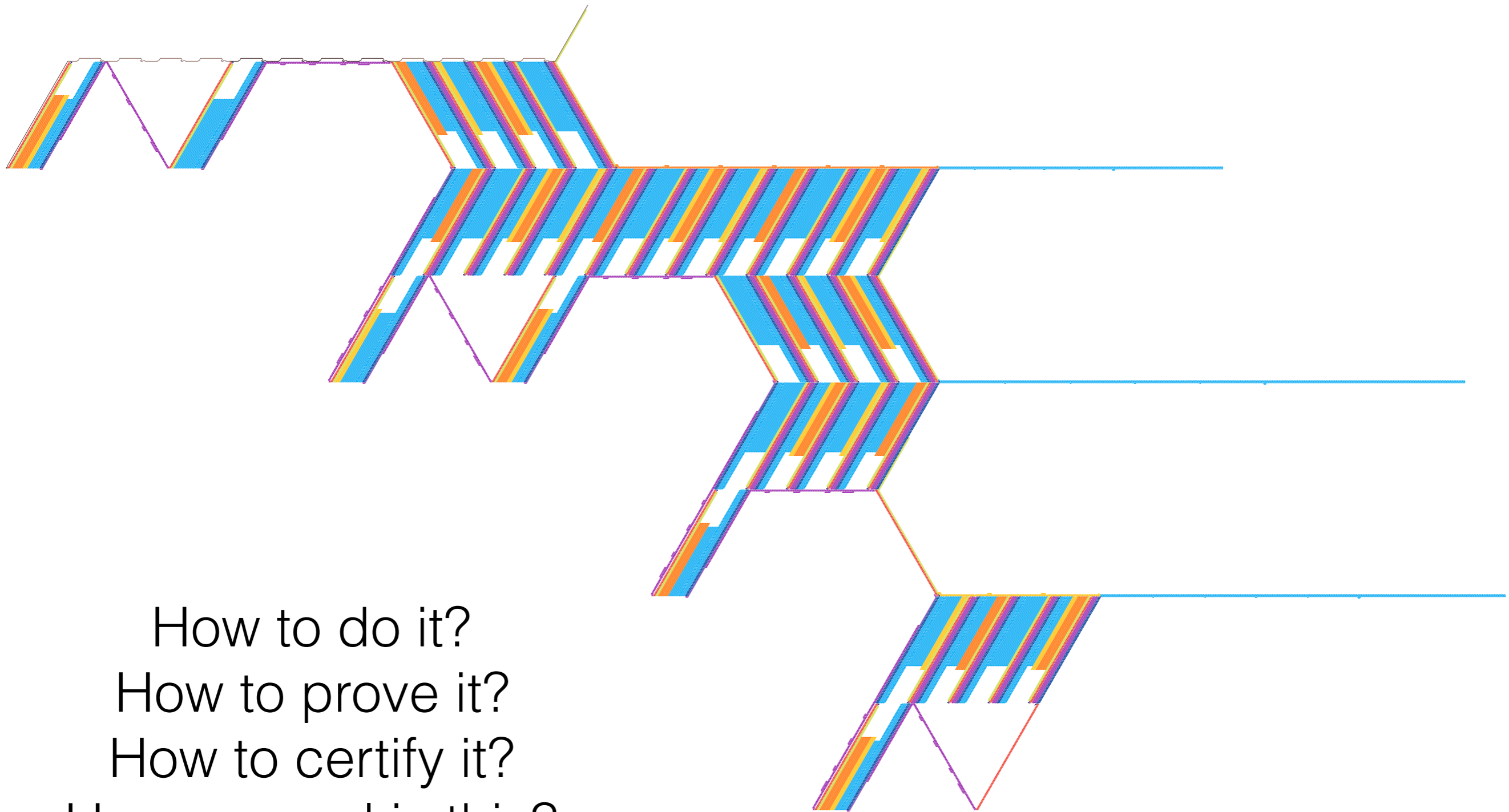
**Example.**



# 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 ( $\varepsilon$ ): 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  $+2$*
- **Theorem** [Neary, Woods, 2006]  
Cyclic tag systems simulate any Turing machine with only a **quadratic** slow down

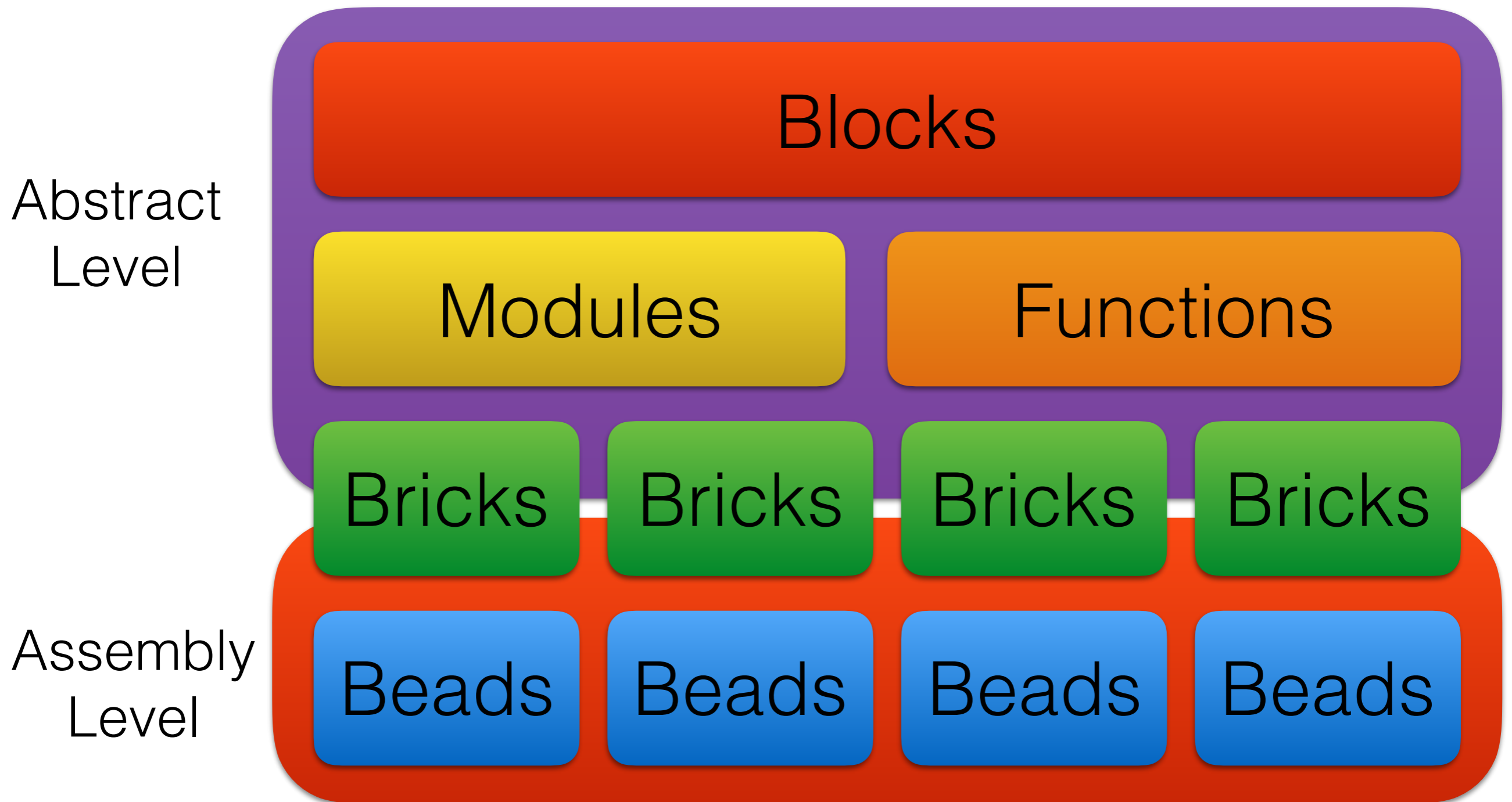
# The simulation



How to do it?  
How to prove it?  
How to certify it?  
How general is this?



# A general programming framework



# A general programming framework

Prove here correctness of algorithm

Blocks

Abstract Level

Modules

Functions

Bricks

Bricks

Bricks

Bricks

Assembly Level

Beads

Beads

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:  $p = \langle \overset{[0]}{1}\overset{[1]}{1}\overset{[2]}{0}, \epsilon, \overset{[2]}{1}\overset{[3]}{1}, \overset{[3]}{0} \rangle$

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

# Trimmed space-time diagram

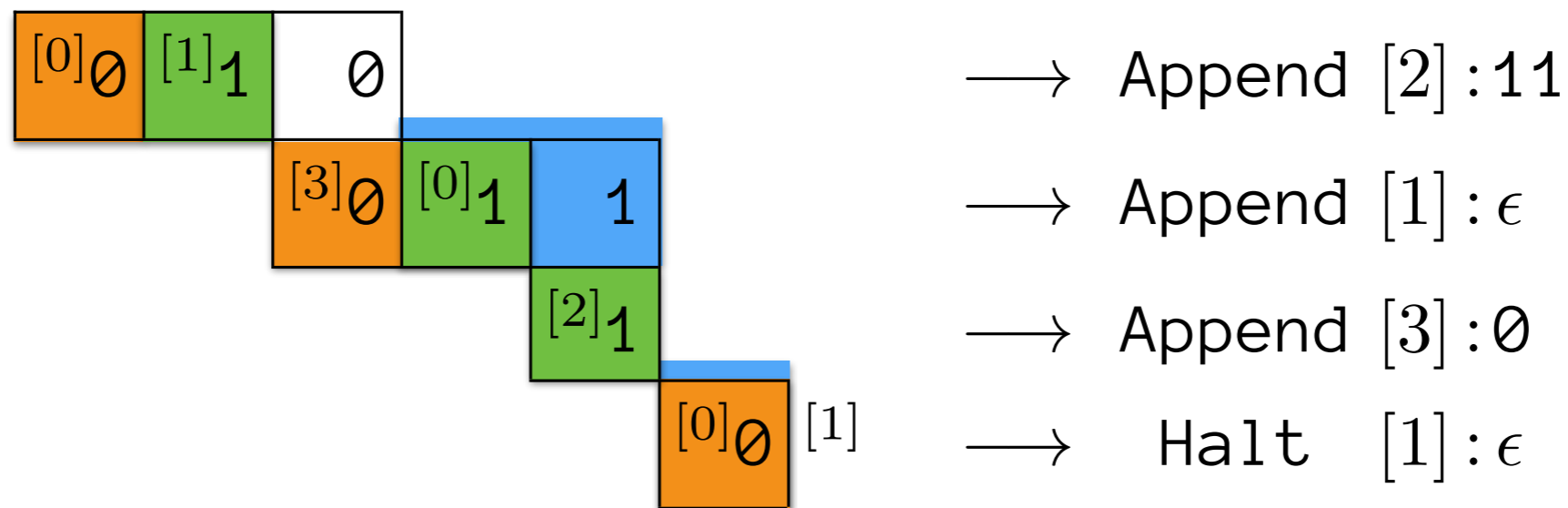
Consider the following productions:  $p = \langle \overset{[0]}{1}\overset{[1]}{1}\overset{[2]}{0}, \epsilon, \overset{[2]}{1}\overset{[3]}{1}, \overset{[3]}{0} \rangle$

$[0] \overset{\text{orange}}{0}1\emptyset \rightarrow [1] \overset{\text{green}}{1}\emptyset \xrightarrow[\text{[2]:11}]{\text{Append}} [3] \overset{\text{orange}}{0}\overset{\text{blue}}{1}\overset{\text{blue}}{1} \rightarrow [0] \overset{\text{green}}{1}1 \xrightarrow[\text{[1]:}\epsilon]{\text{Append}} [2] \overset{\text{green}}{1} \xrightarrow[\text{[3]:0}]{\text{Append}} [0] \overset{\text{orange}}{0} \rightarrow [1] \text{Halt}$

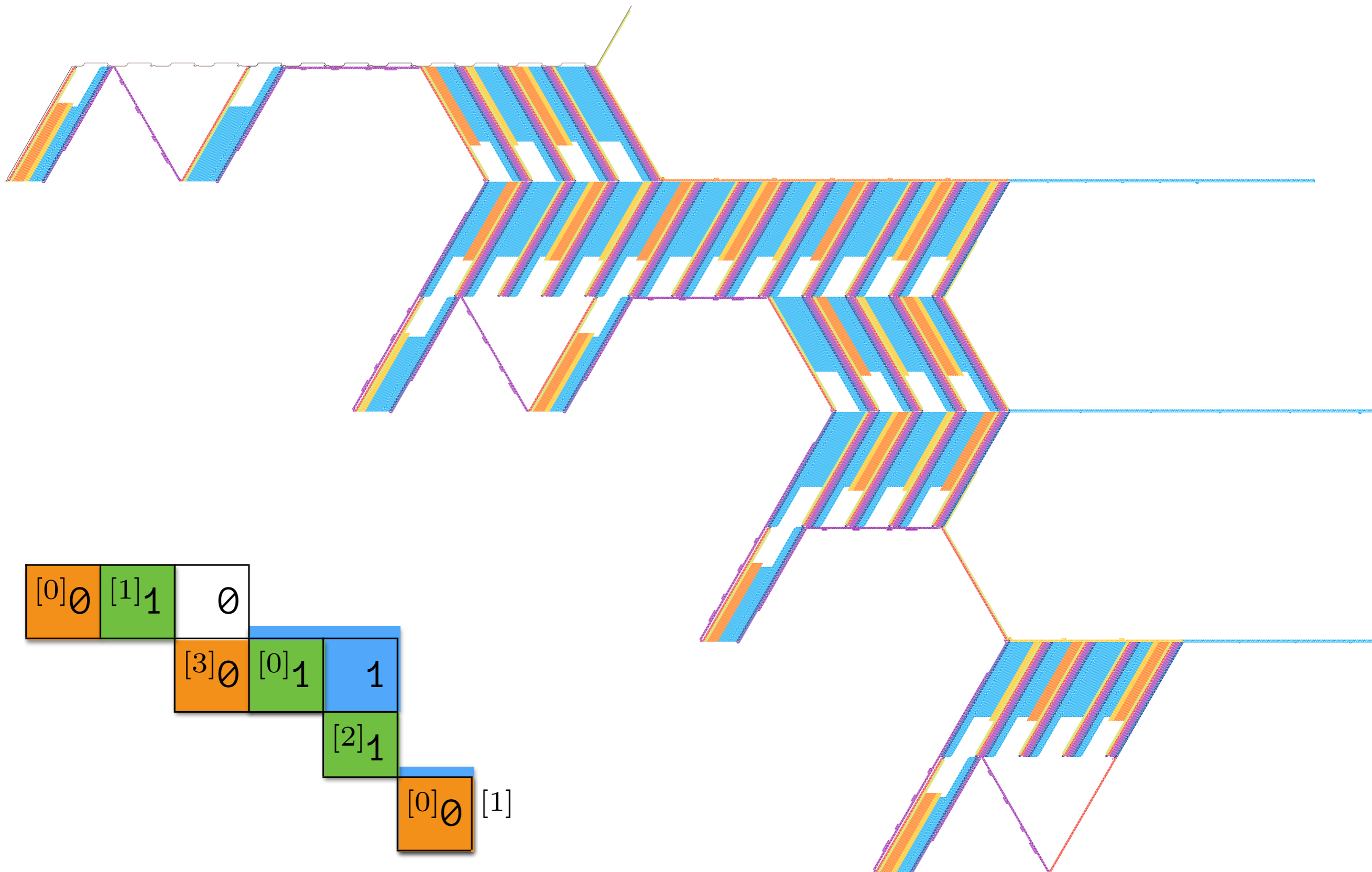
# Trimmed space-time diagram

Consider the following productions:  $p = \langle \overset{[0]}{1}\overset{[1]}{1}\overset{[2]}{\emptyset}, \epsilon, \overset{[2]}{1}\overset{[3]}{1}, \emptyset \rangle$

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

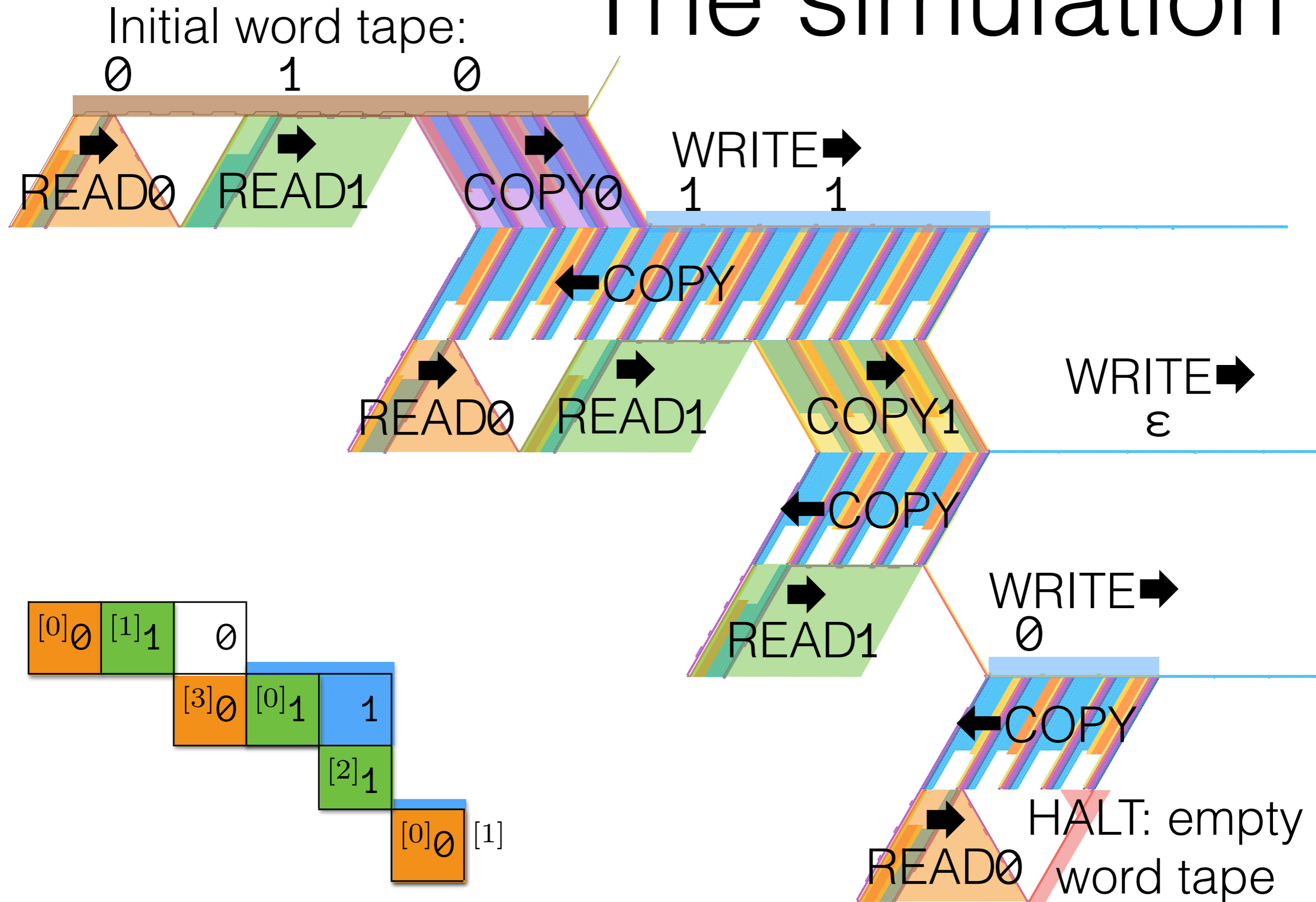


# The simulation

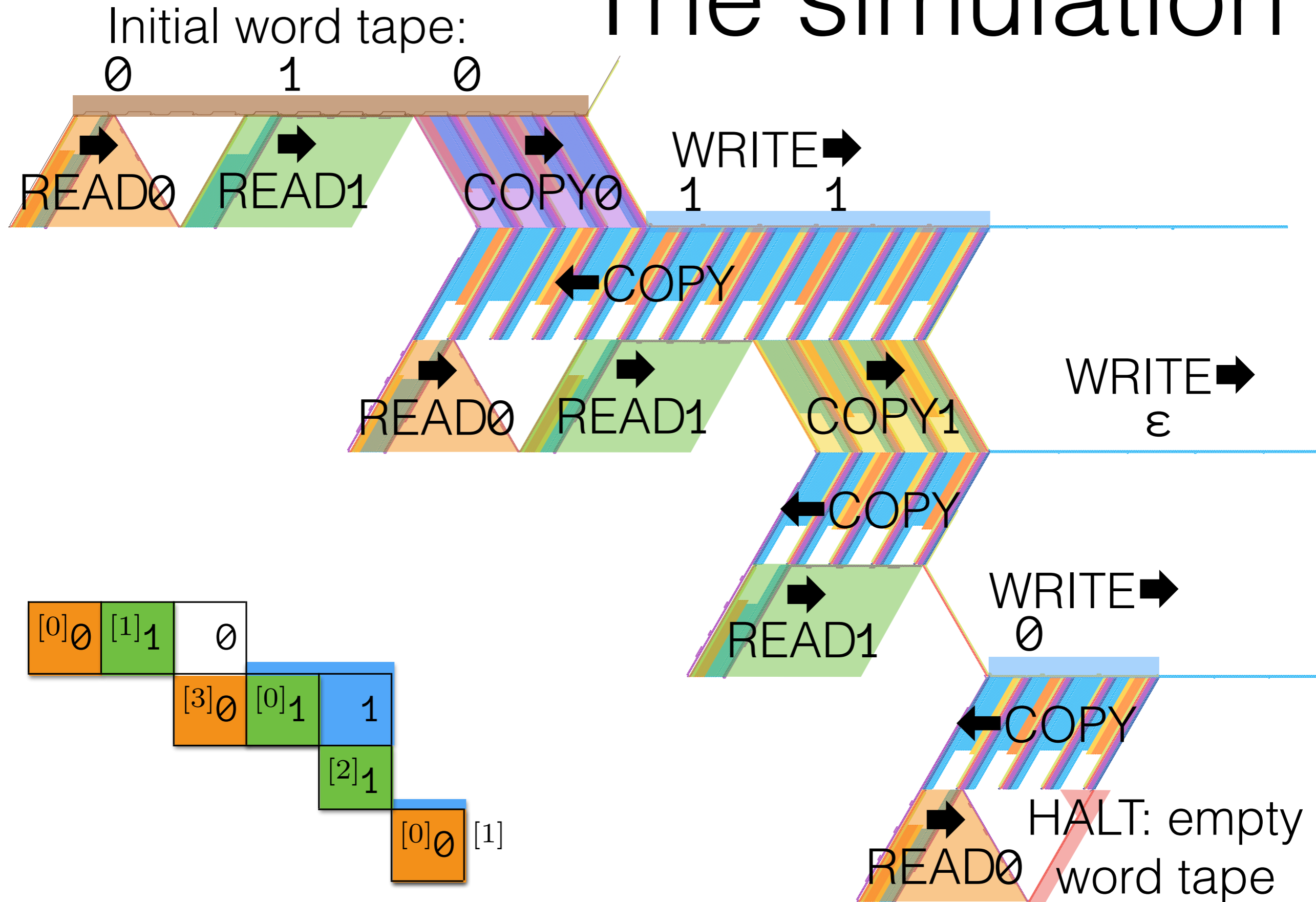




# The simulation

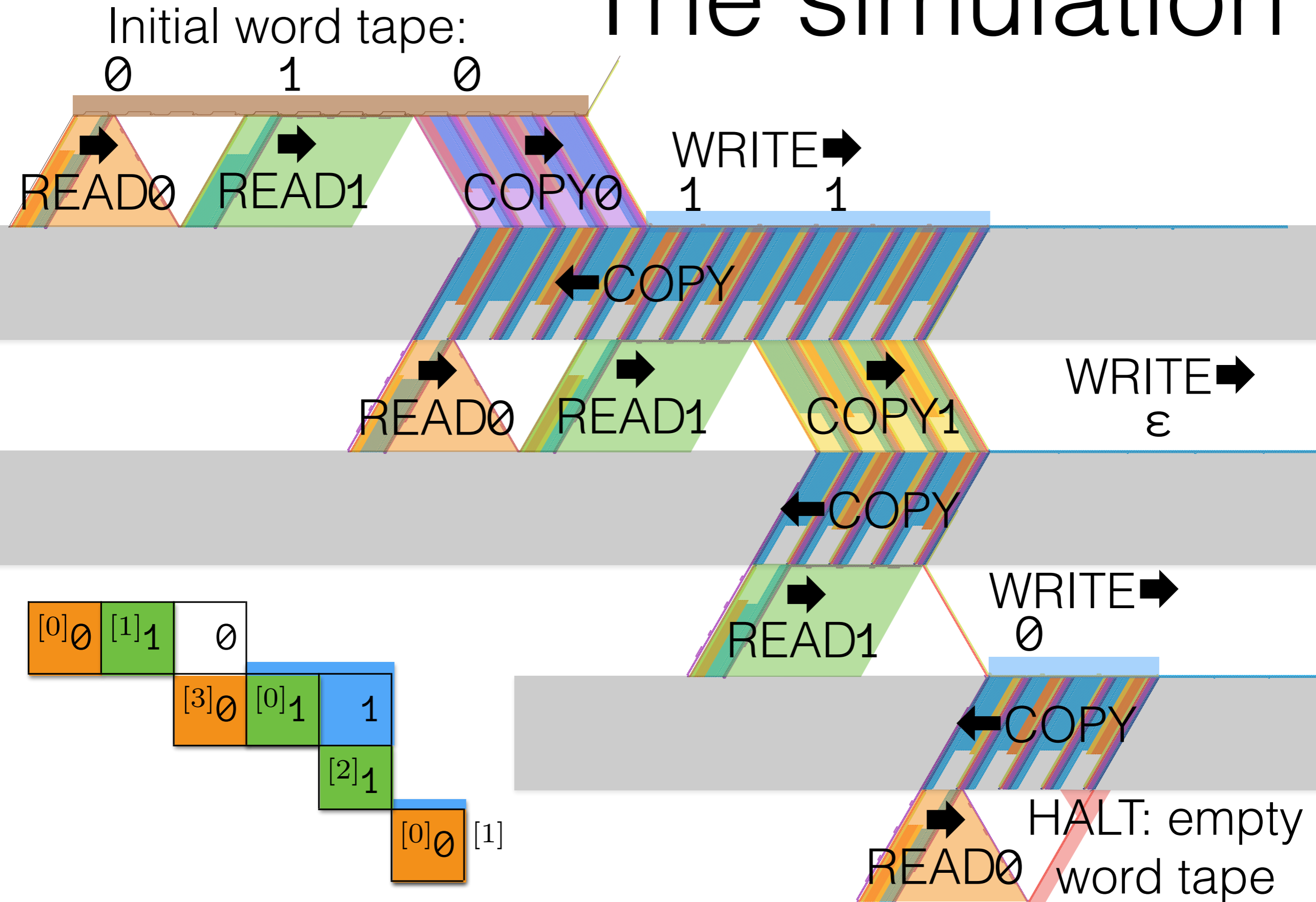


# The simulation

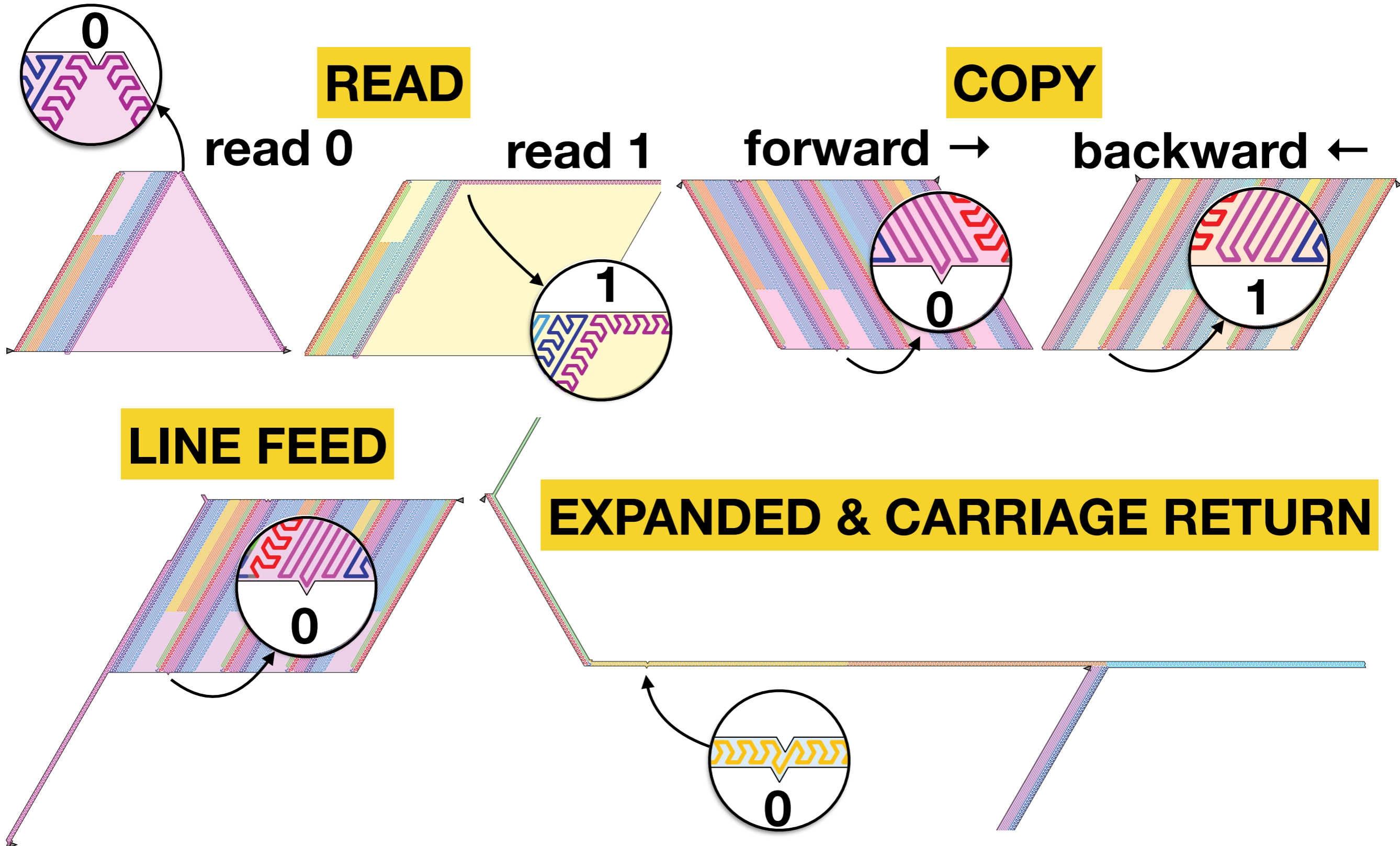




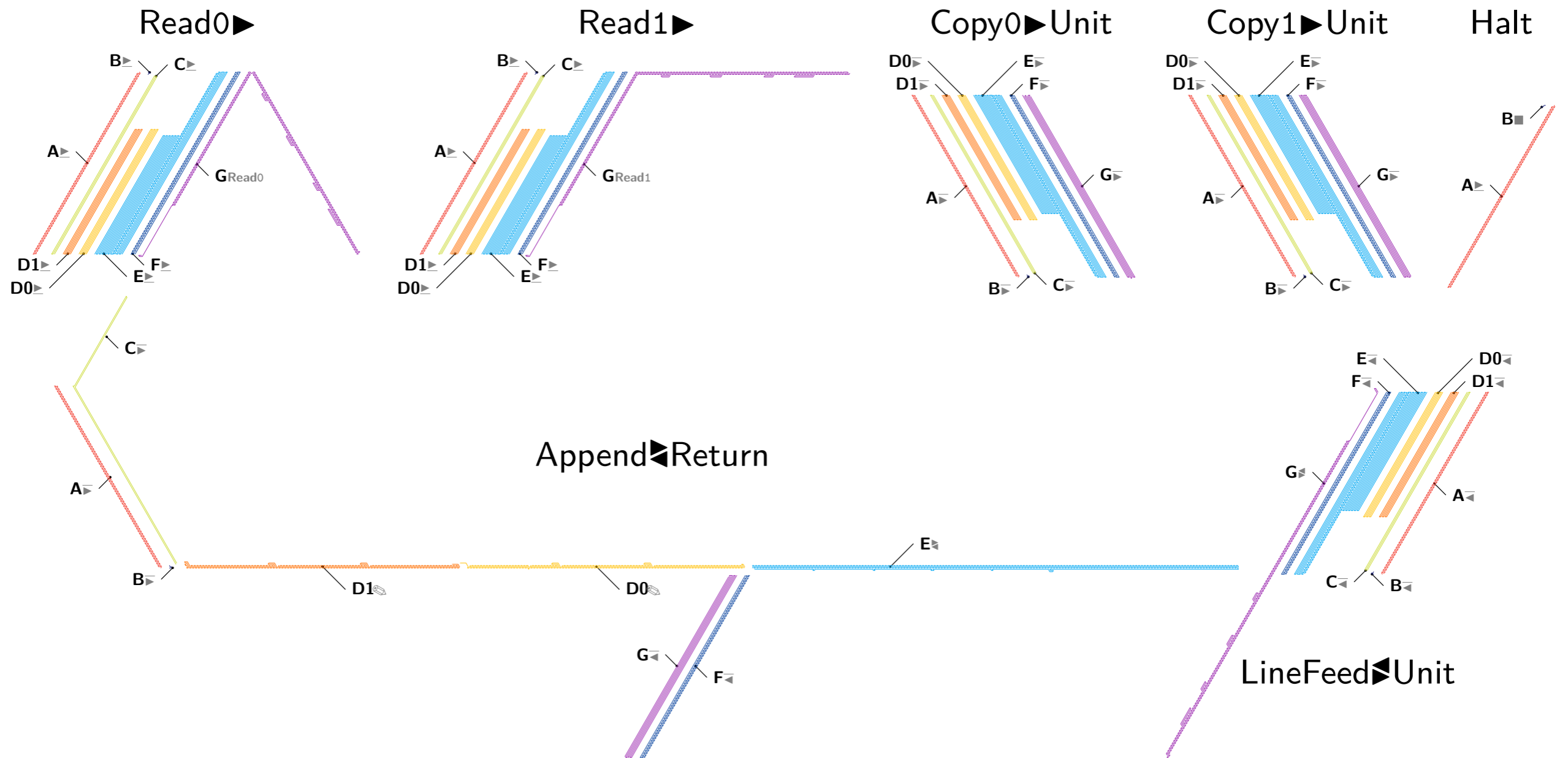
# The simulation



# The blocks



# The bricks inside each block





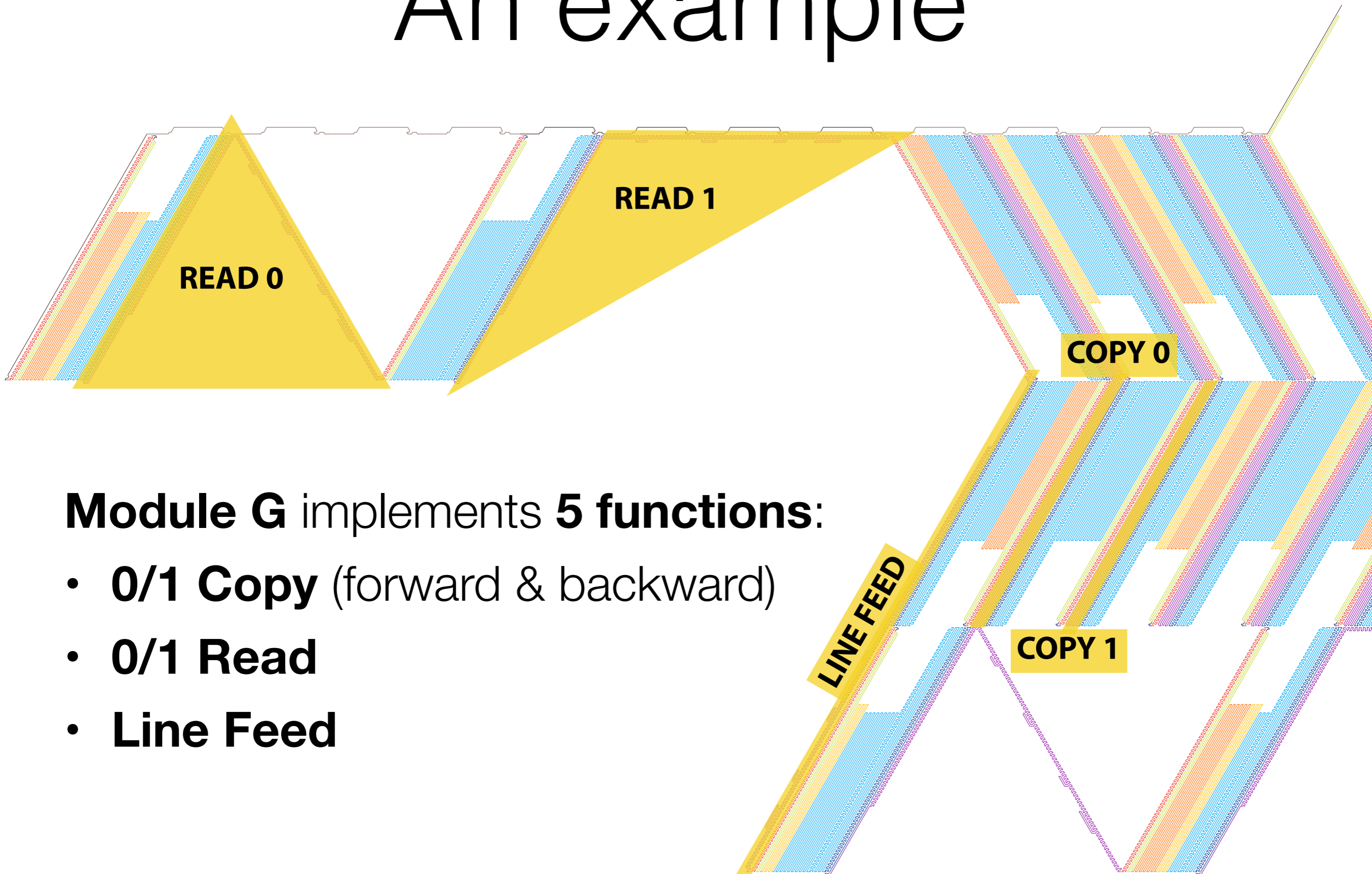
How do we implement  
several functions

(i.e. folding into different bricks)  
in a given module?

# An example



# An example

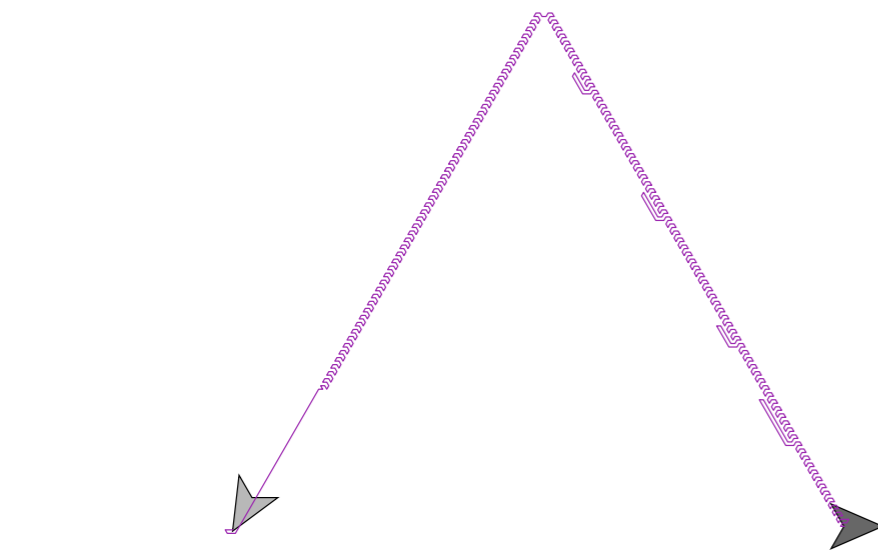


**Module G** implements **5 functions**:

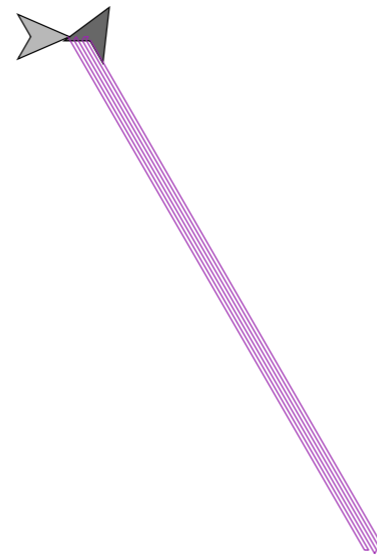
- **0/1 Copy** (forward & backward)
- **0/1 Read**
- **Line Feed**



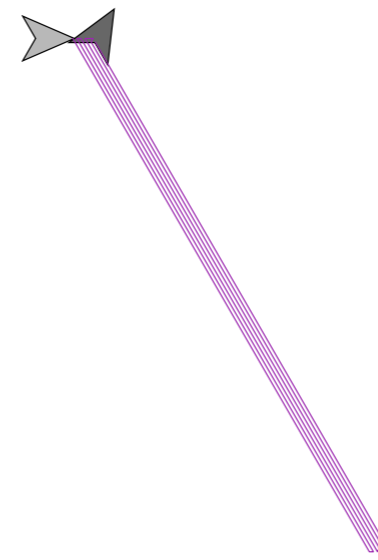
# The various bricks for module G



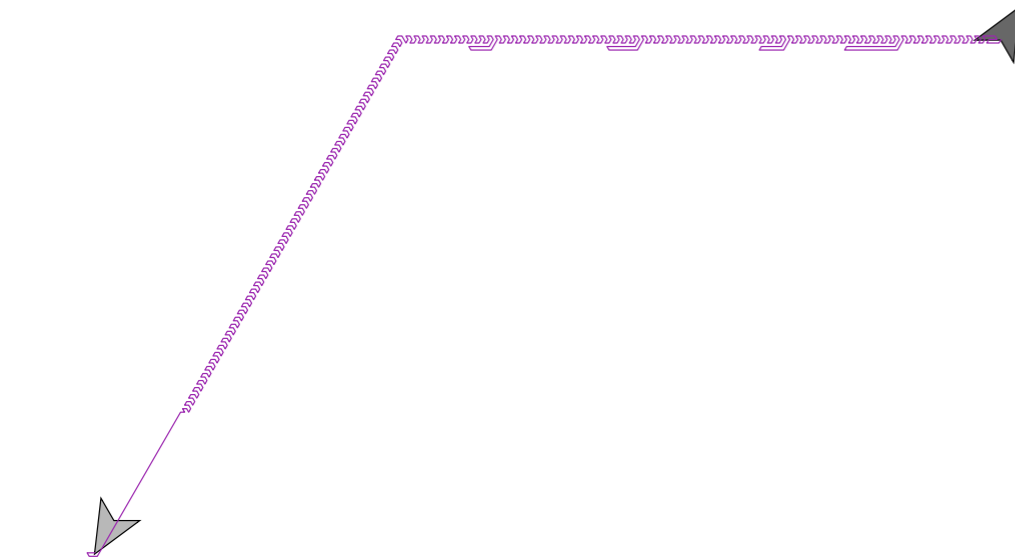
(a) The brick **G  $\triangleright$  Read0**.



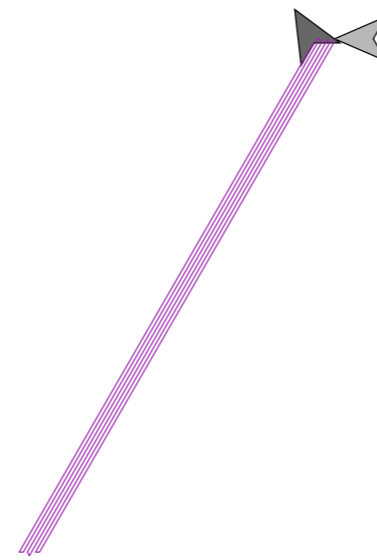
(a) The brick **G  $\triangleright$  Copy0**.



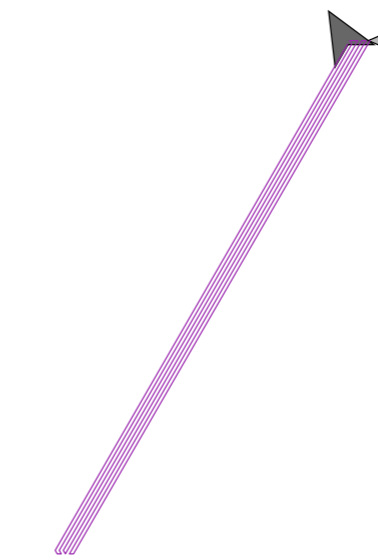
(b) The brick **G  $\triangleright$  Copy1**.



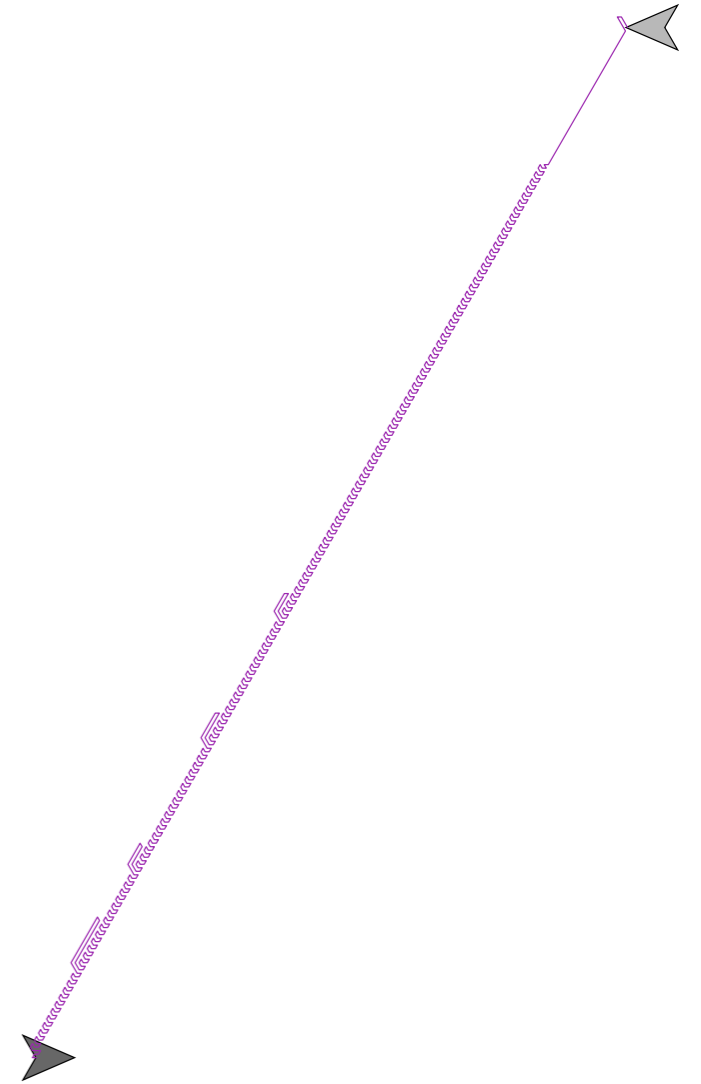
(b) The brick **G  $\triangleright$  Read1**.



(c) The brick **G  $\triangleleft$  Copy0**.



(d) The brick **G  $\triangleright$  Copy1**.



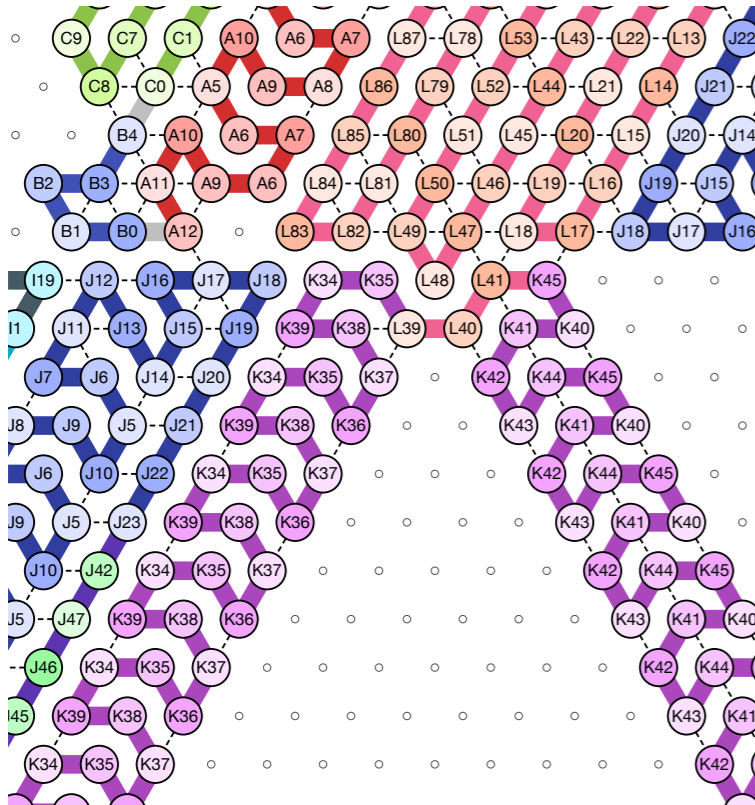
(a) The brick **G  $\blacktriangleright$  LineFeed**.



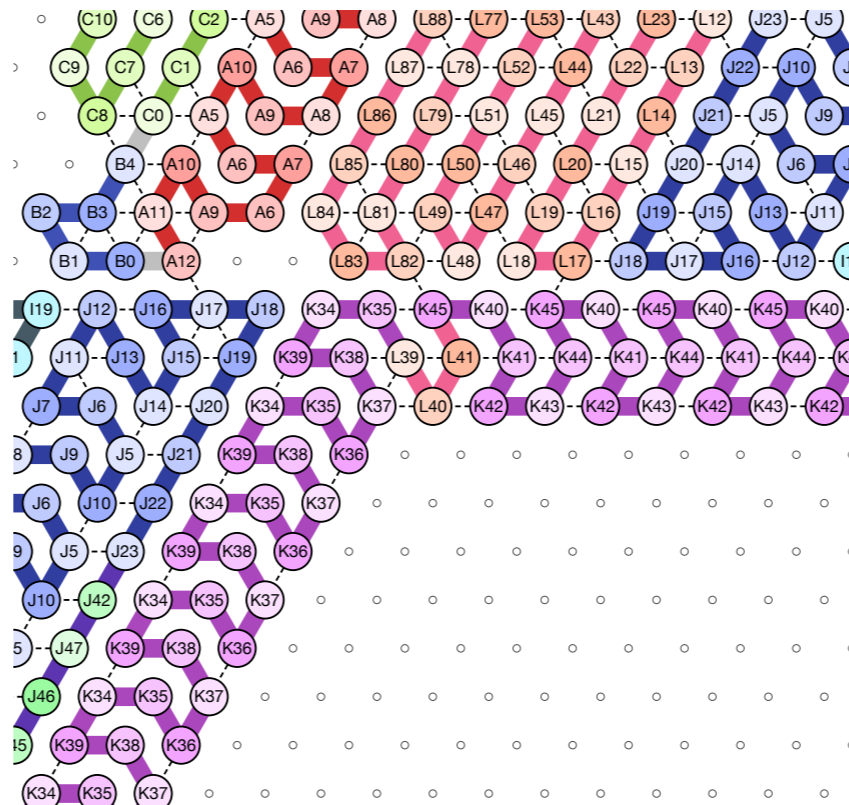




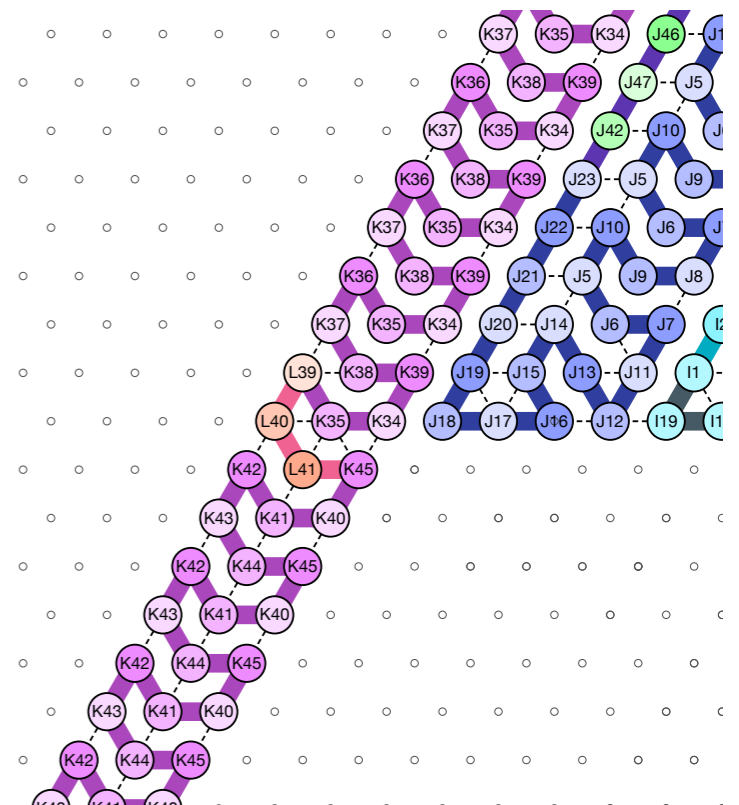
# Glider turns



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



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



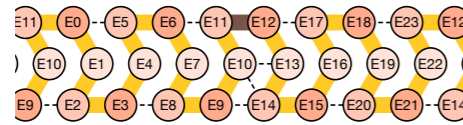
(c) **G** goes straight southwestward in absence of obstacle, and folds into **G  $\blacktriangleright$  LineFeed**.

# Some programming paradigms

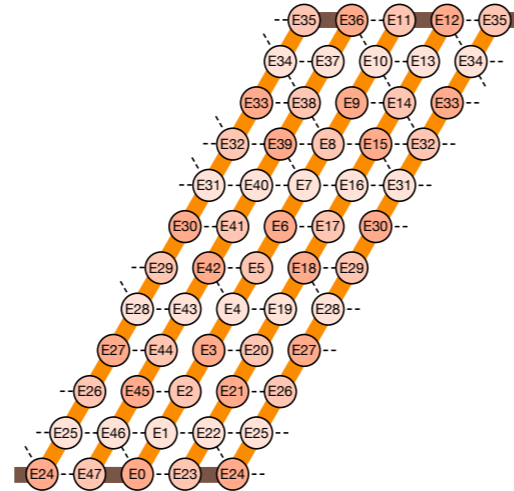


- Switchback expanding in Gliders
- Offset
- Exponential coloring
- Socks

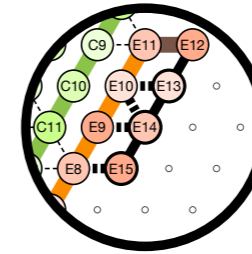
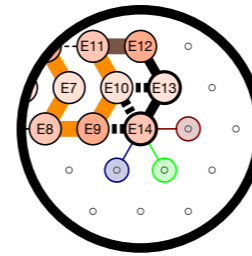
# Switchback expanding into gliders



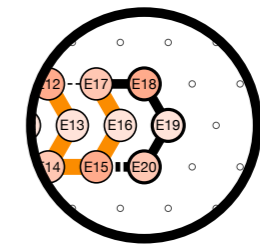
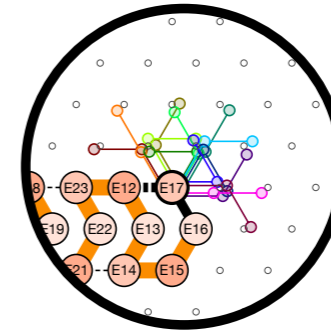
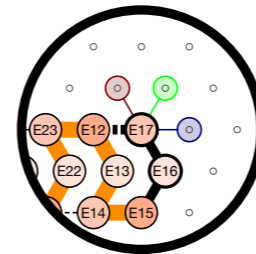
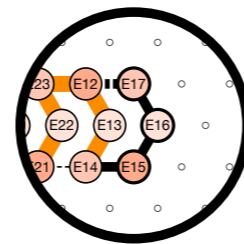
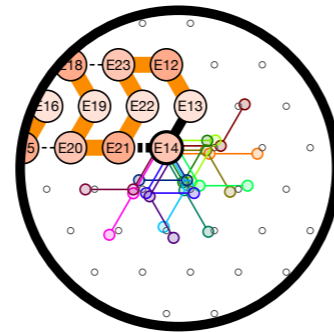
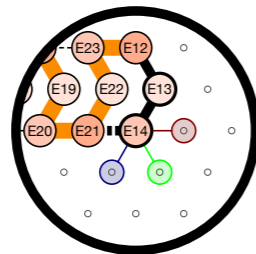
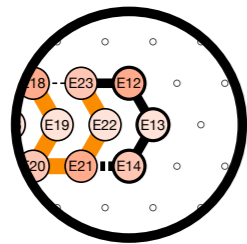
(a) Glider



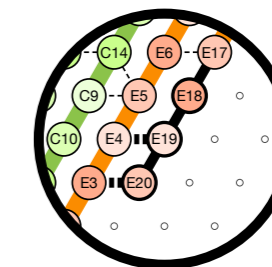
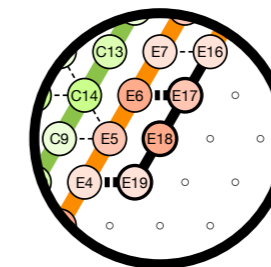
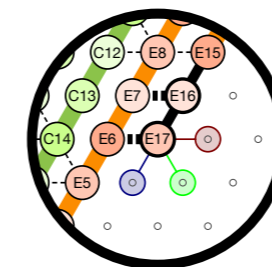
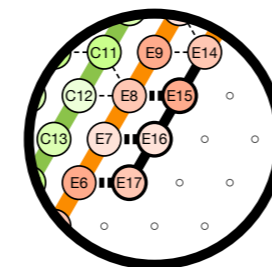
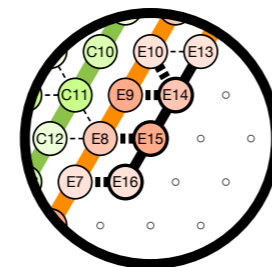
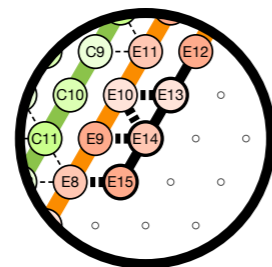
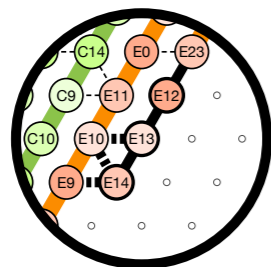
(b) Switchback



(c) Glider/Switchback turn folding compatibility.



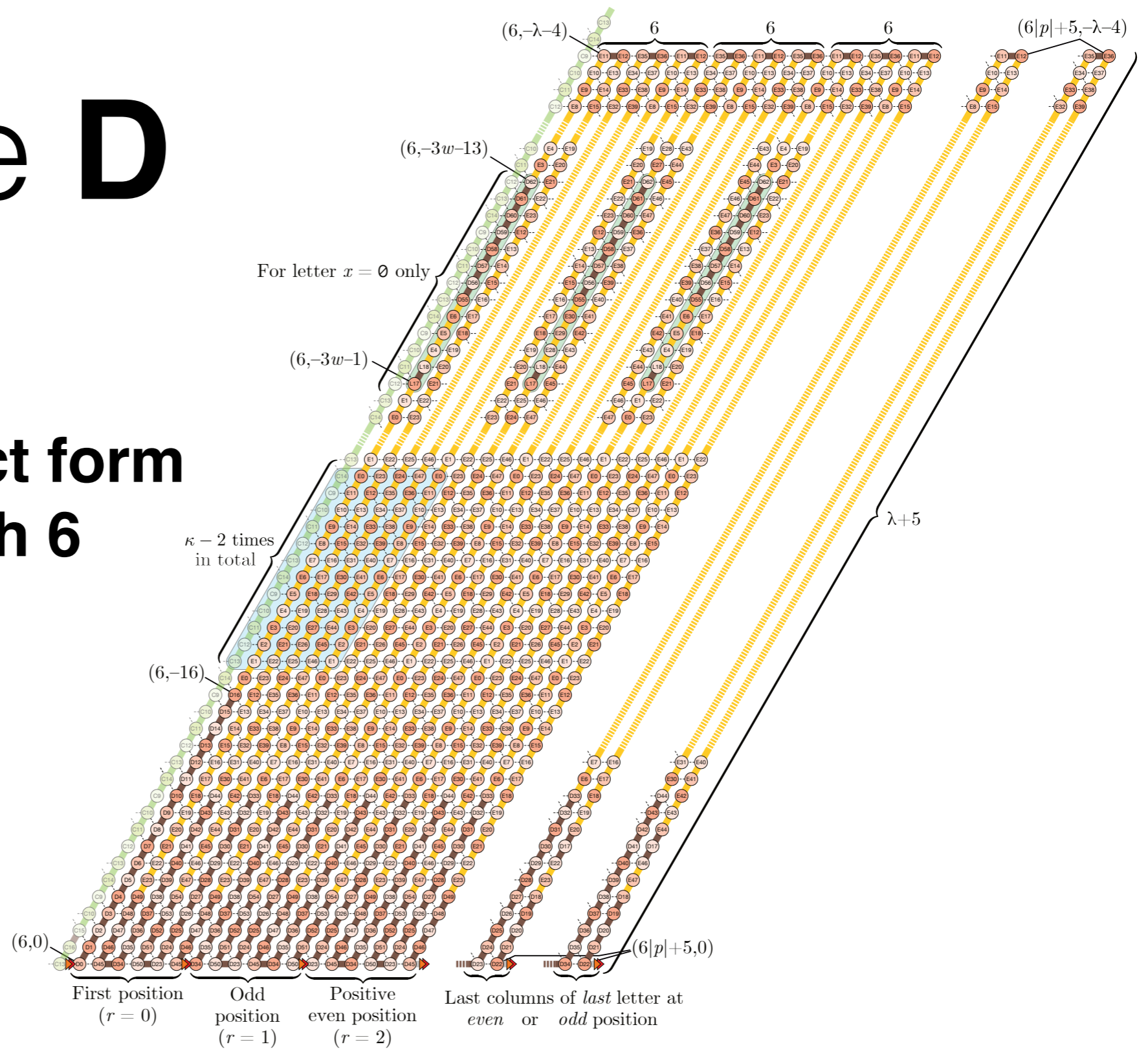
(d) from left to right: the folding of the subsequence as a glider.



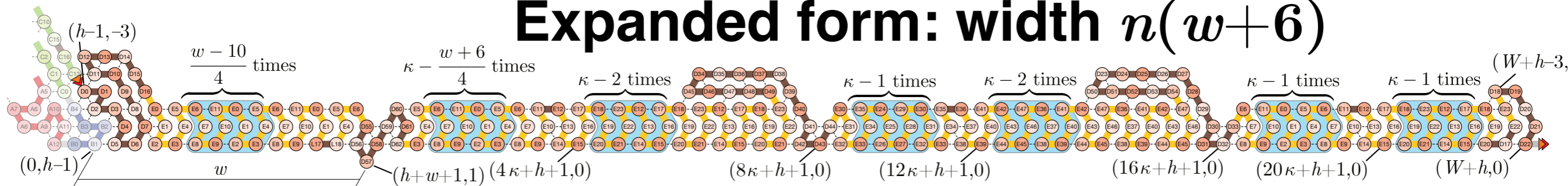
(e) from left to right: the folding of the subsequence as a switchback.

# Module D

**Compact form  
width 6**



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

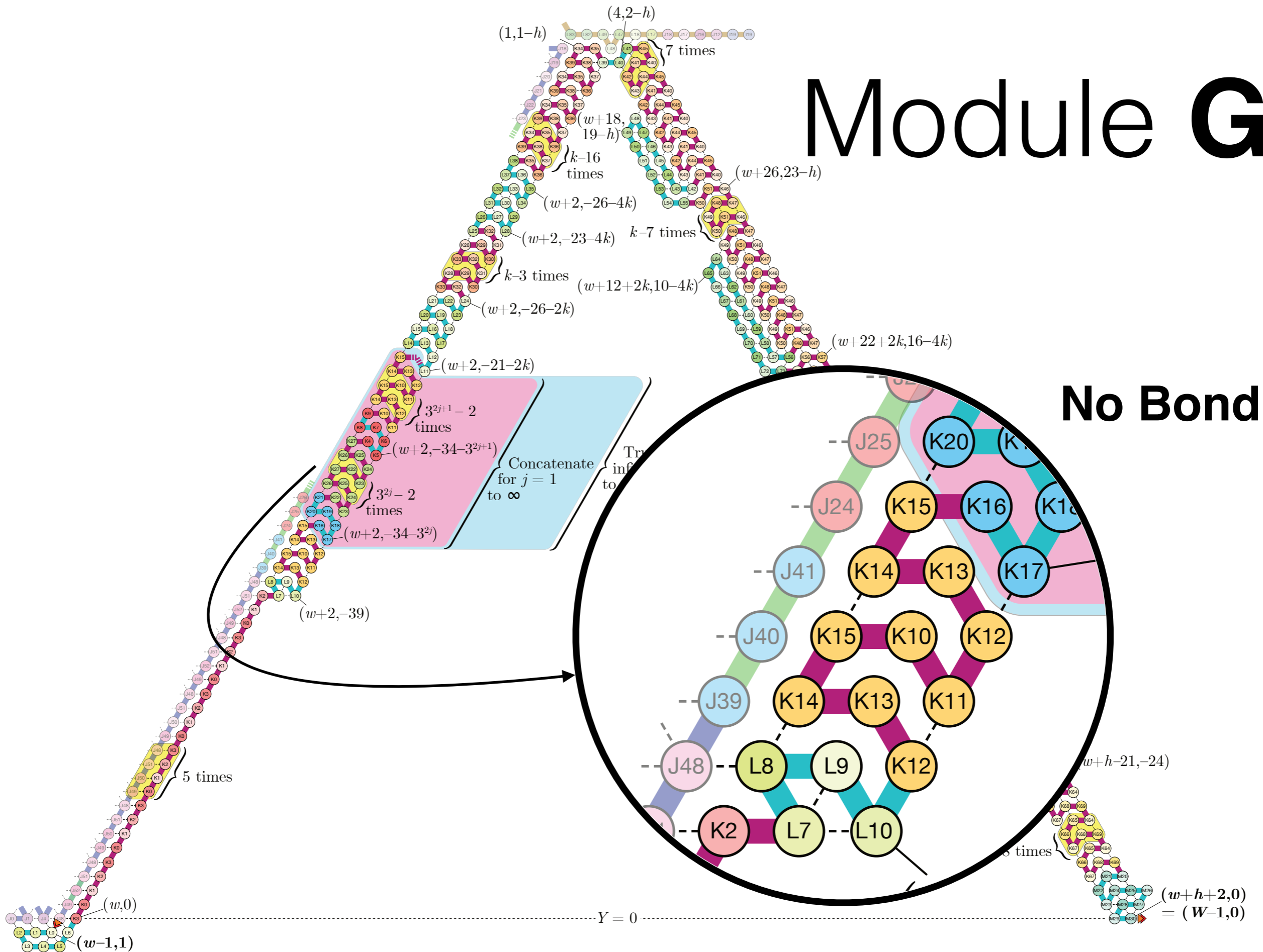


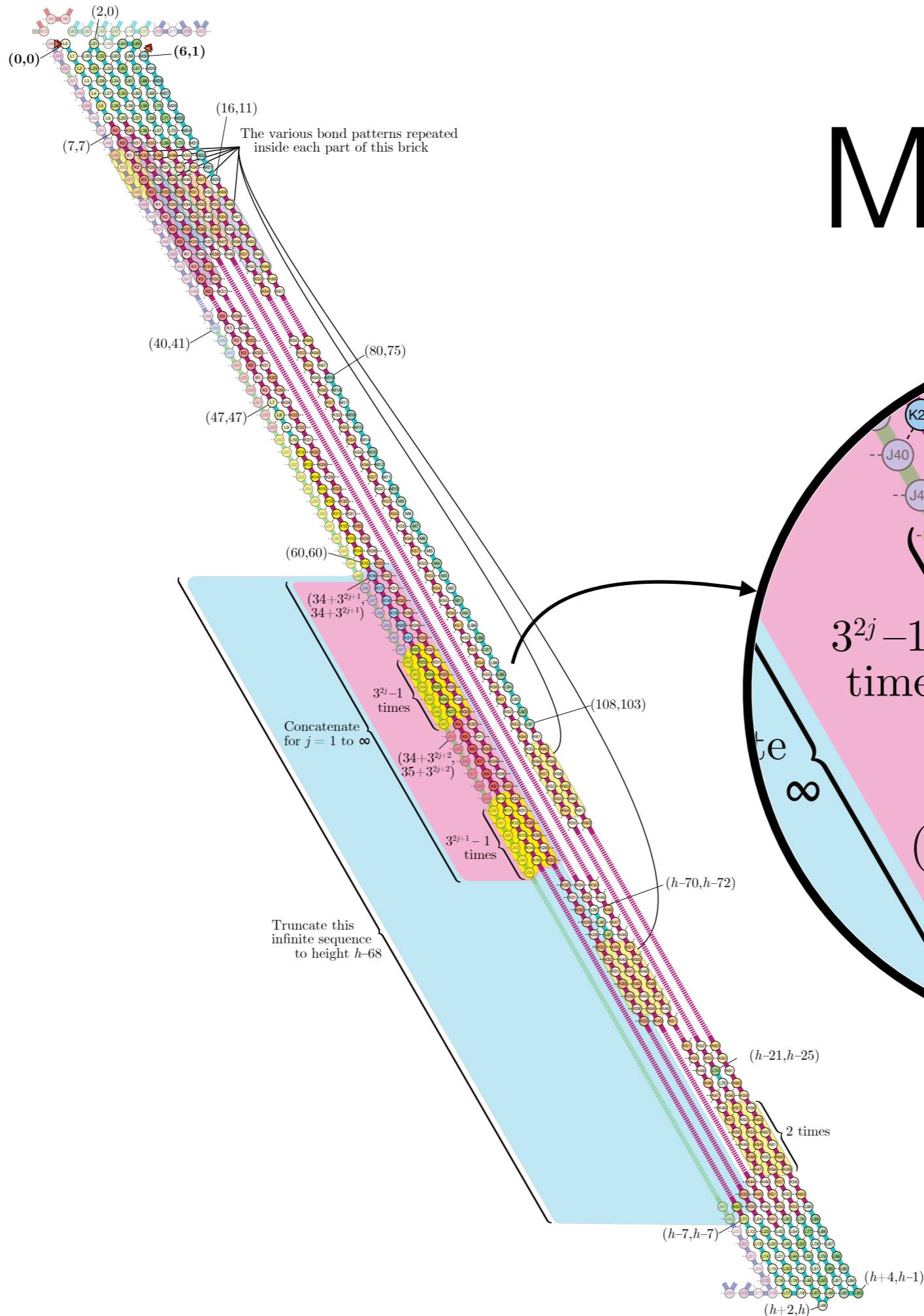
# Exponential coloring

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

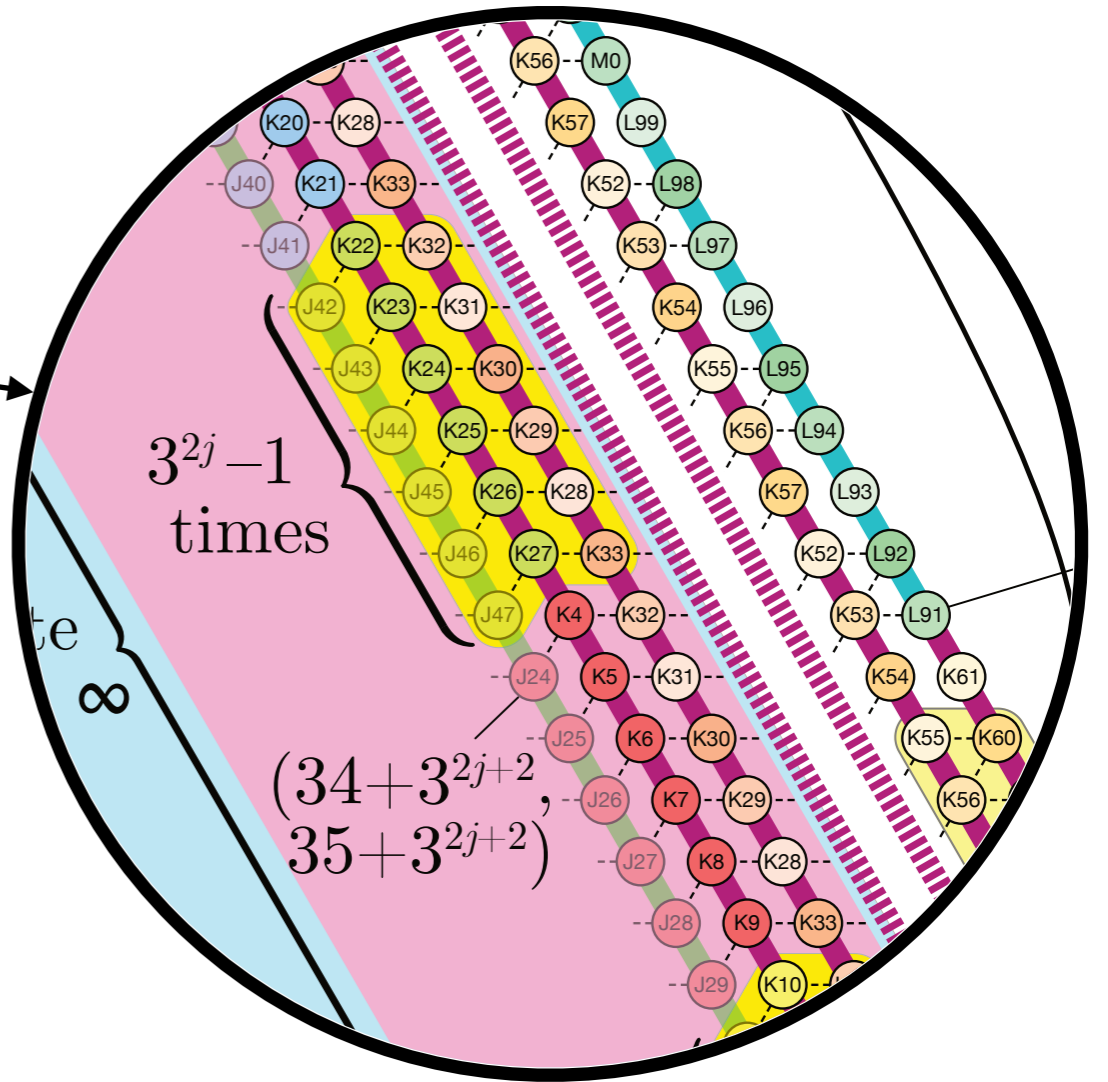


# Module G



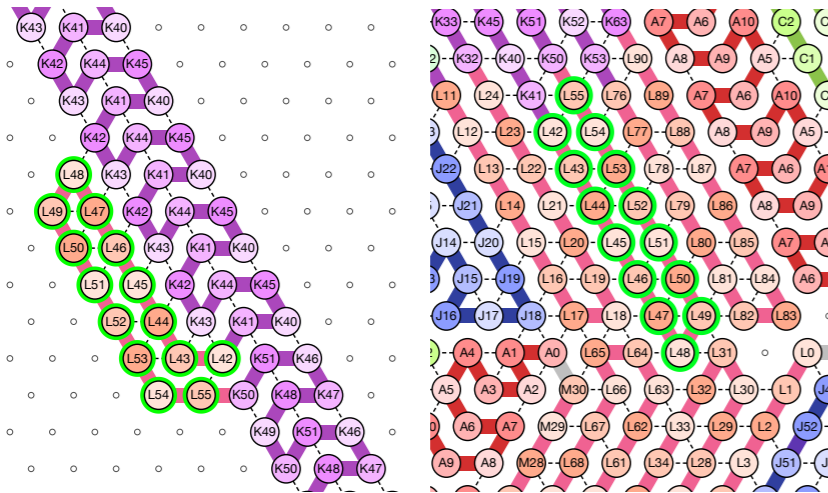


# Module G

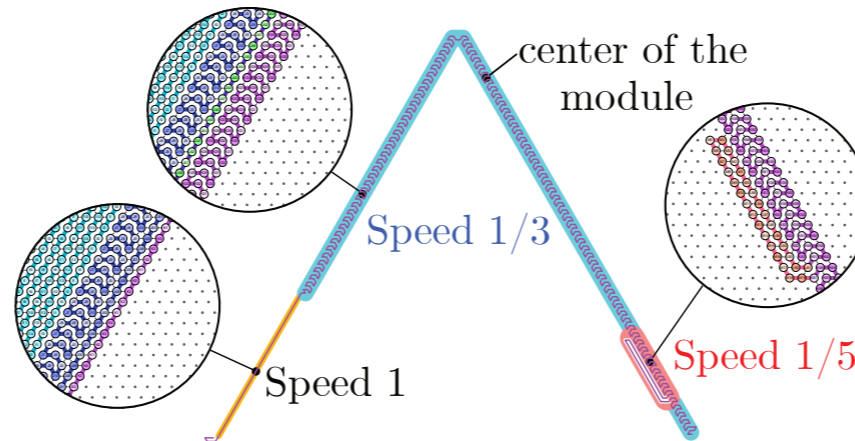


**Bonds everywhere**

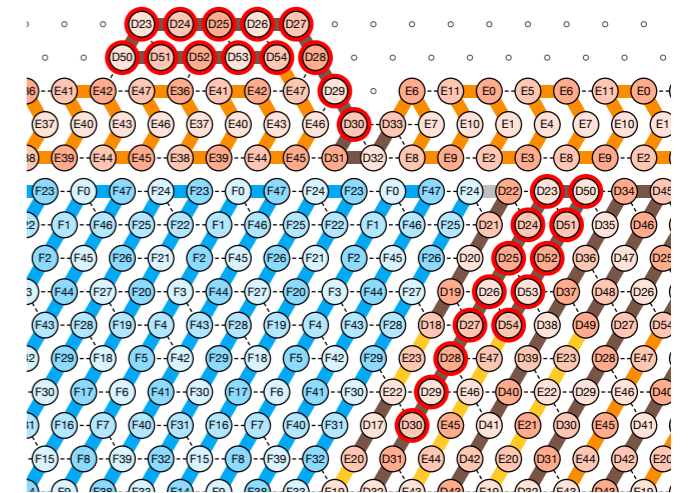
# Socks



(a) Easier bond design



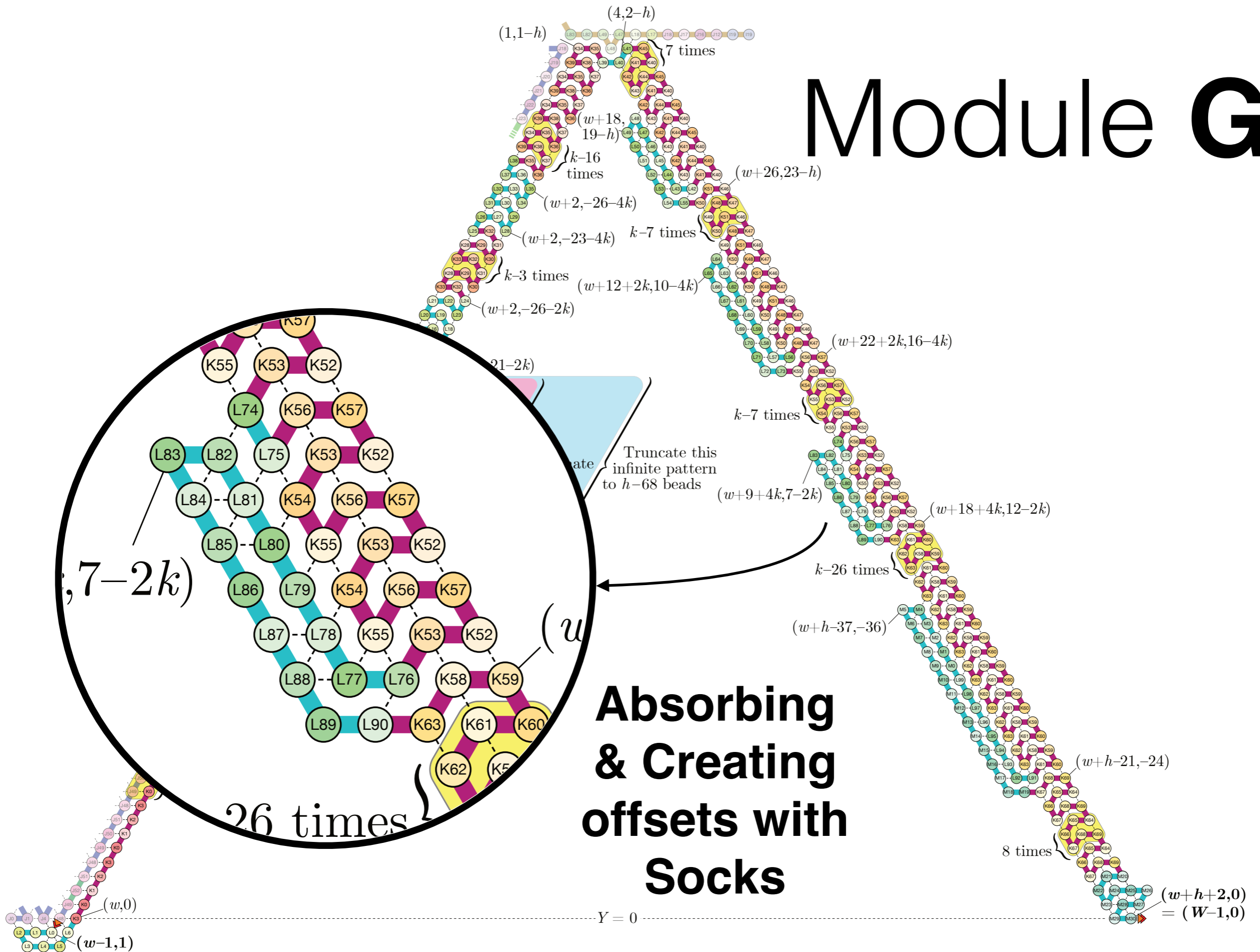
(b) Delaying gliders



(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



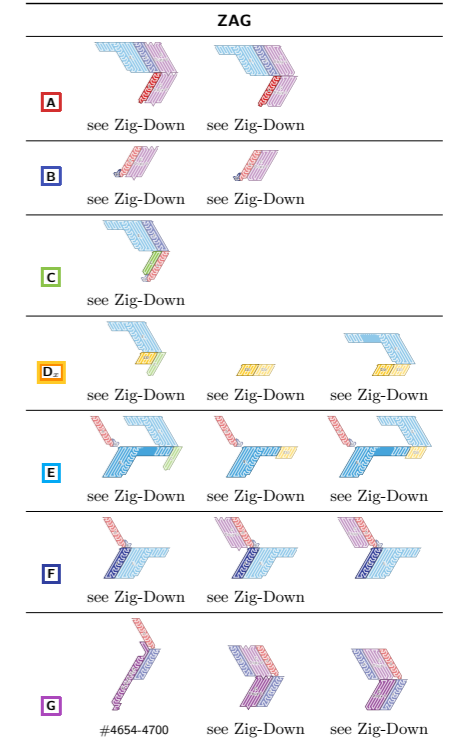


# Proof of correctness

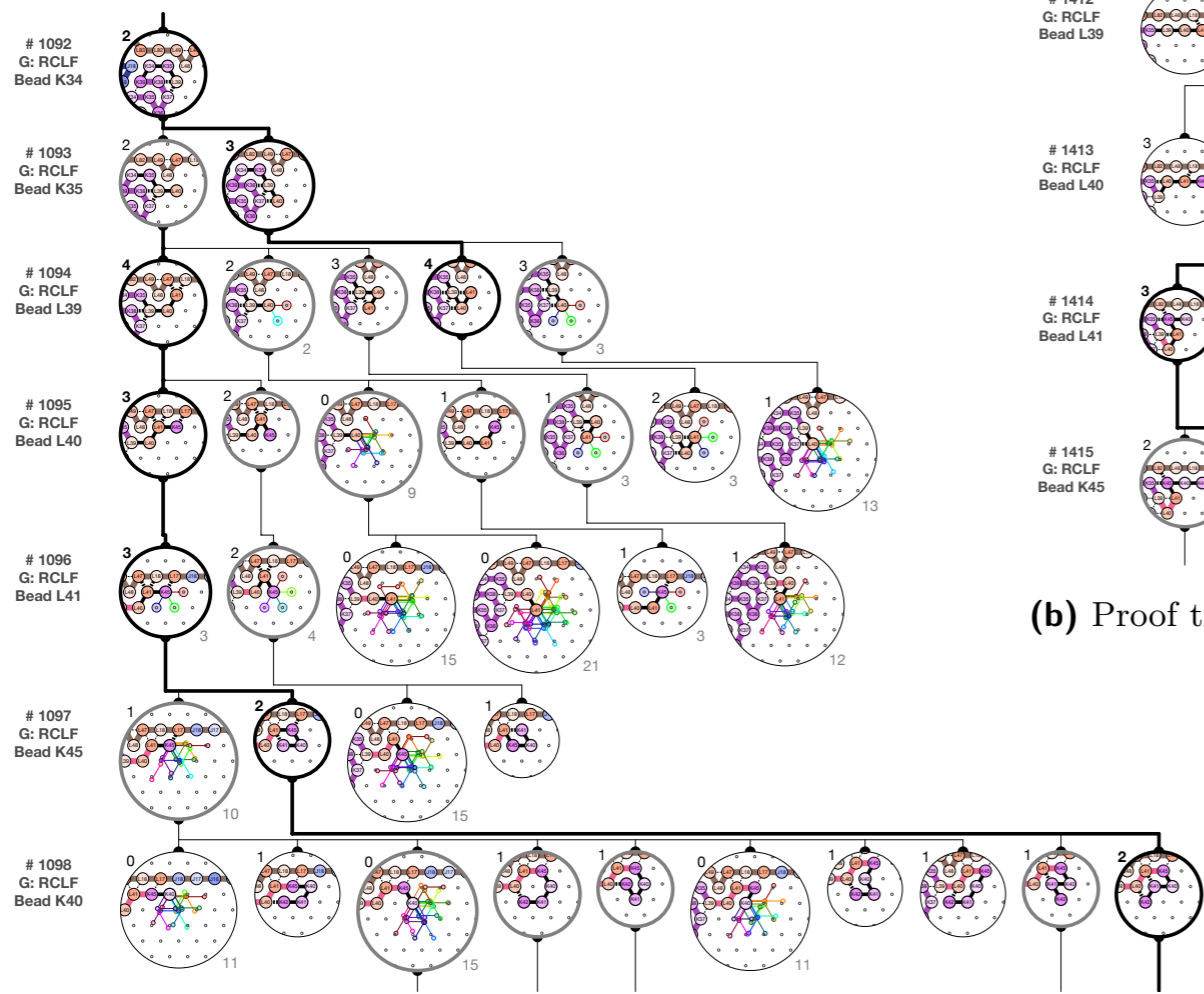
- Enumerate all possible environments for each brick
- Compute proof trees for each brick in all of its fixed environments
- Deal separately with the only three bricks having variable environments



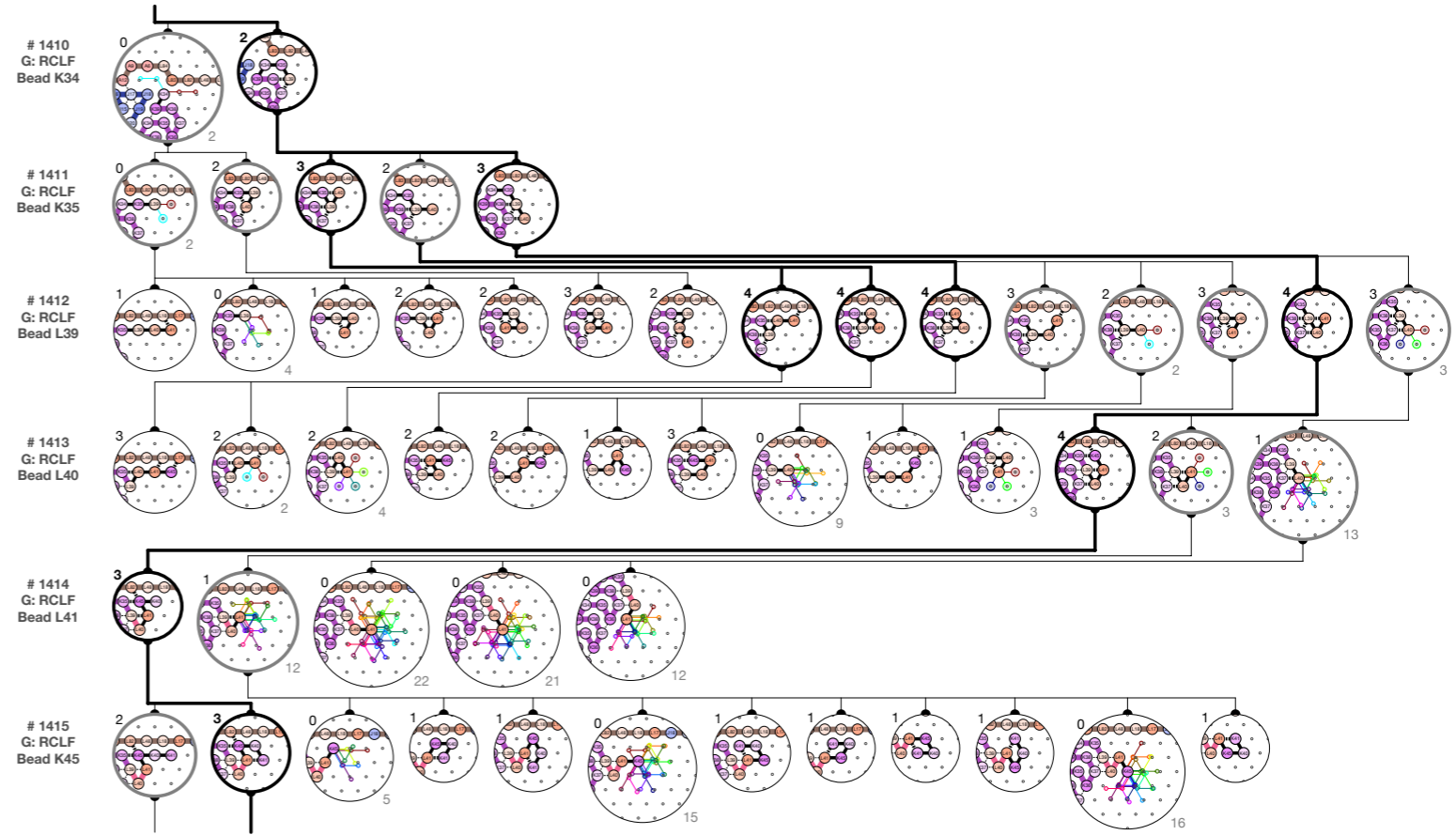
# Listing all environments



# Example: Reading 0/1



(a) Proof tree for the glider turn in **G Read0**.



(b) Proof tree for the glider turn in **G Read1**.

# The rule

