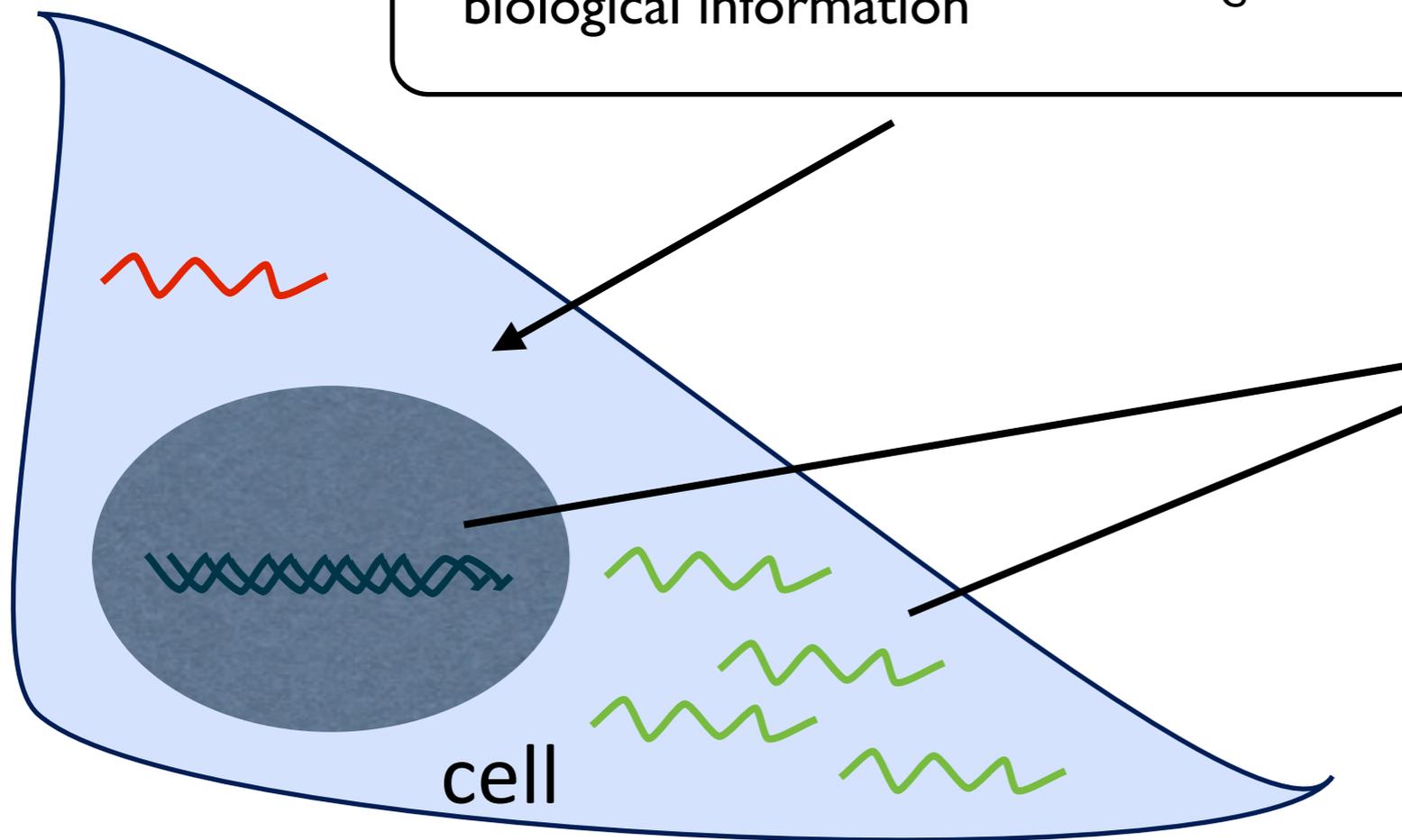
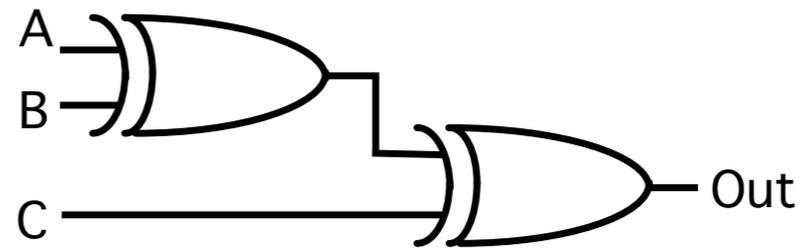


Module 5: Logic circuits with DNA strand displacement (part 1)

CSE590: Molecular programming and neural computation.

Goal: Engineering embedded controllers for biochemical systems

A cell-based “computer” needs to be biocompatible, and sense, analyze and act on biological information



Biological Information is encoded in the sequences and amounts of biomolecules (DNA, RNA, proteins, etc.)

```
ugagguaguagguuguauaguu  
ugagguaguagguugugugguu  
ugagguaguagguuguauugguu  
agagguaguagguugcauaguu  
ugagguaggagguuguauaguu  
ugagguaguagauuguauaguu  
ugagguaguaguuguacaguu  
ugagguaguaguuguugcuguu
```

Logic circuits using DNA strand displacement

Q: Why digital logic? Biology is not digital.

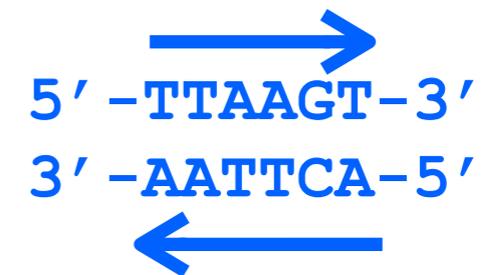
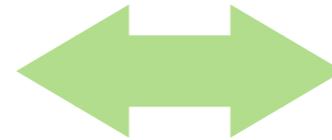
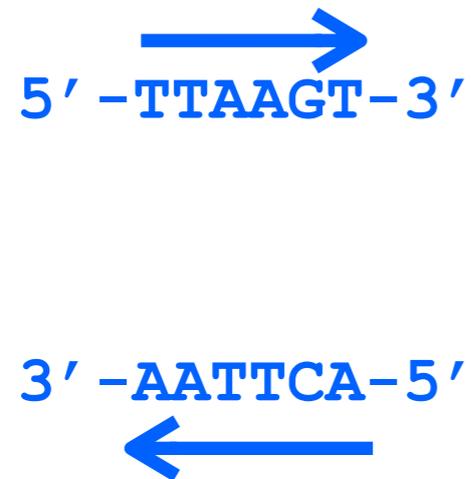
A: Because adherence to digital logic design has enabled incredibly complex, manmade information technology. We don't need to do exactly what biology does.

Q: Why DNA strand displacement?

A: Because it's a surprisingly powerful building block.

Basic rules

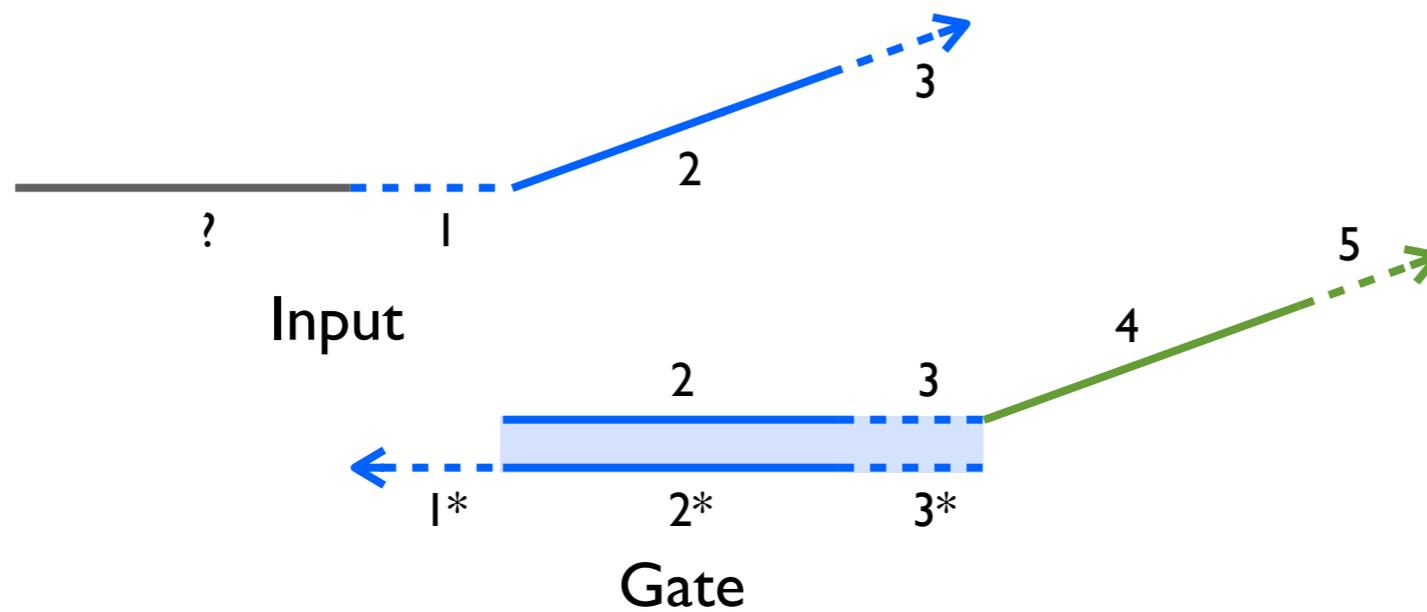
Short domains bind **reversibly**



Long domains bind **irreversibly**



DNA strand displacement mechanism



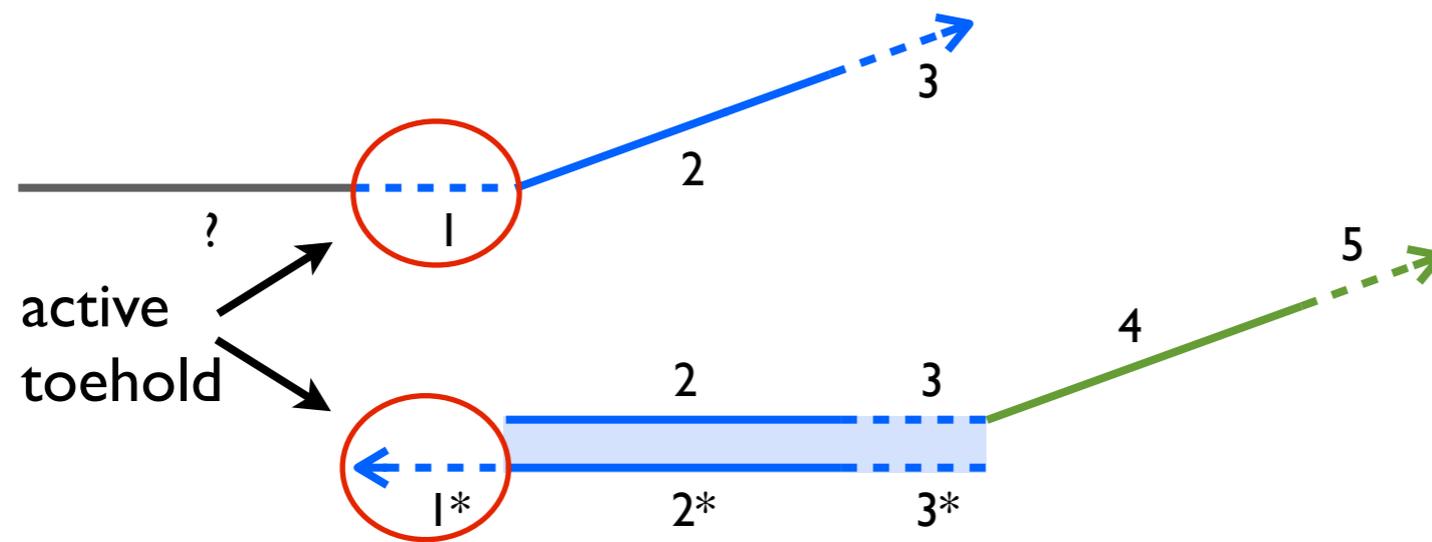
RNA sequence:

5' -AAUUCAGAUCCACCCAAAGAG-3'



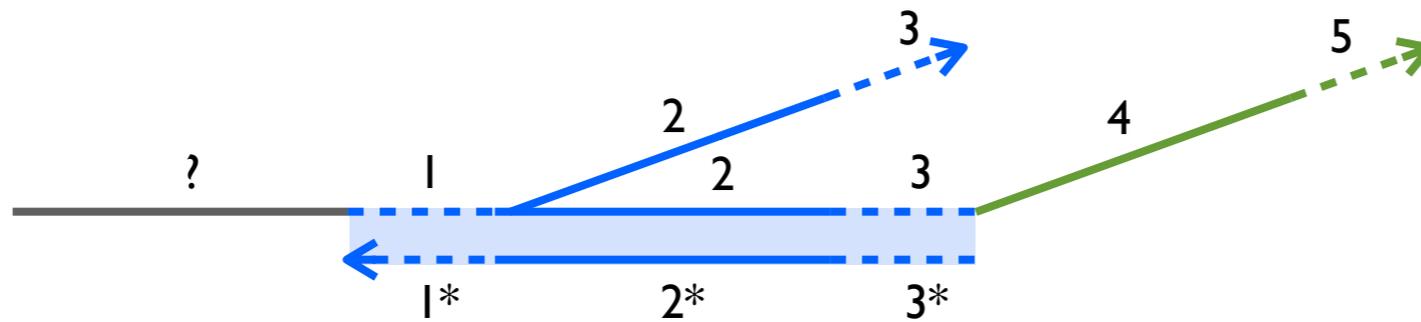
For a review see D.Y. Zhang and G. Seelig, Nature Chemistry (2011)

DNA strand displacement mechanism



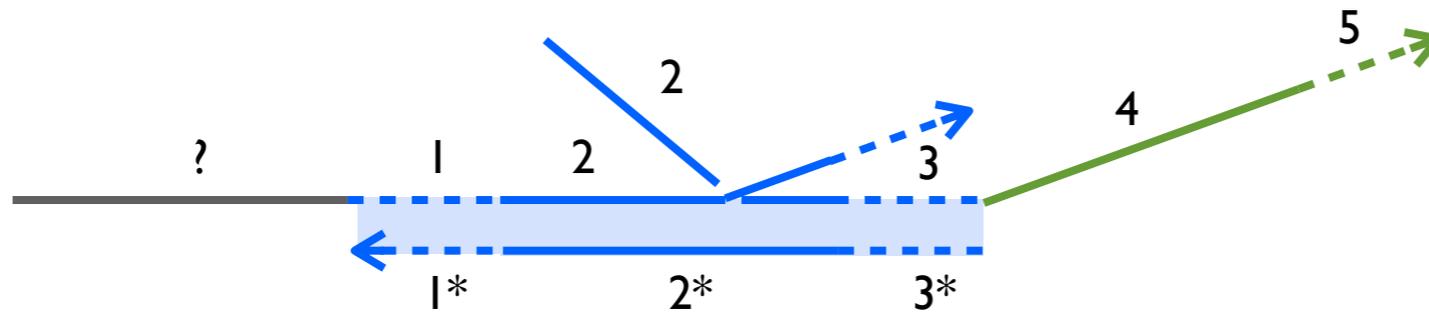
For a review see D.Y. Zhang and G. Seelig, Nature Chemistry (2011)

DNA strand displacement mechanism



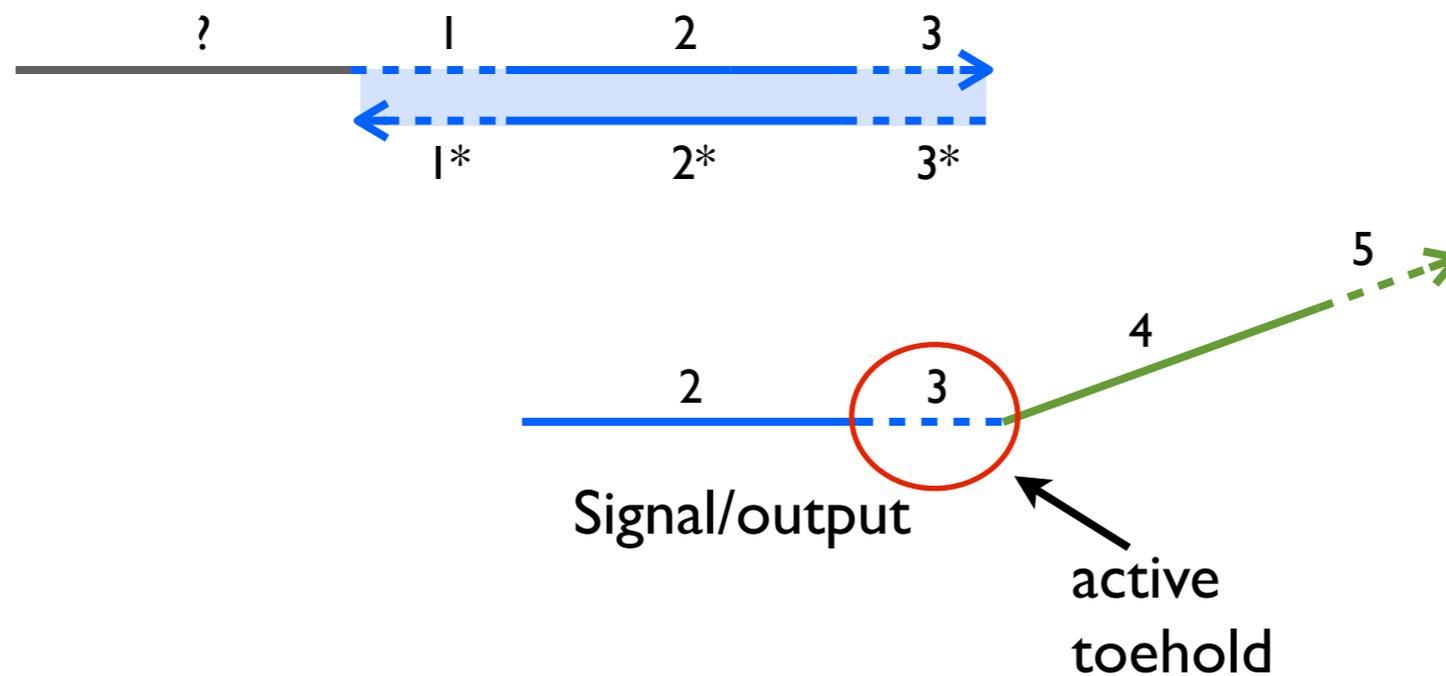
Strand displacement is initiated at the single-stranded toeholds. Toehold binding is a reversible process.

DNA strand displacement mechanism



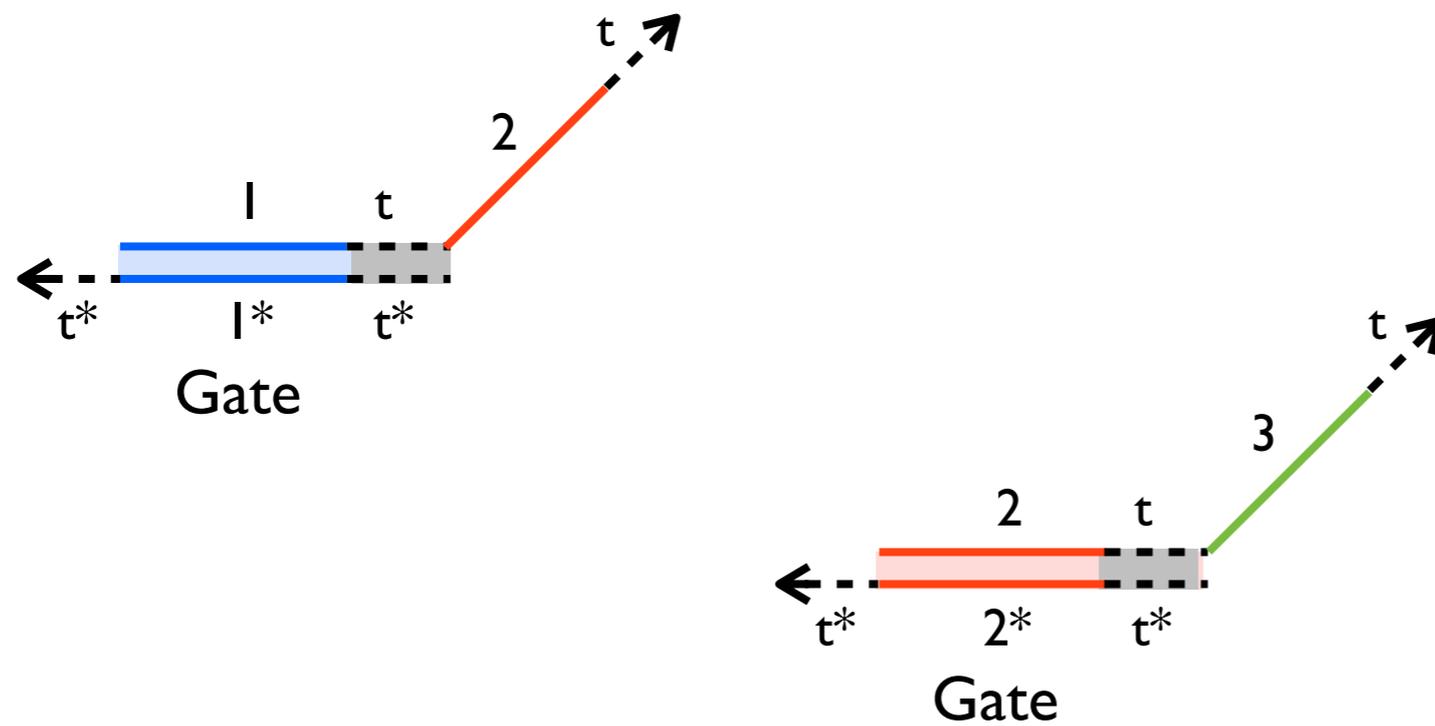
Strand displacement proceeds through a branch migration. Branch migration is a random walk.

DNA strand displacement mechanism



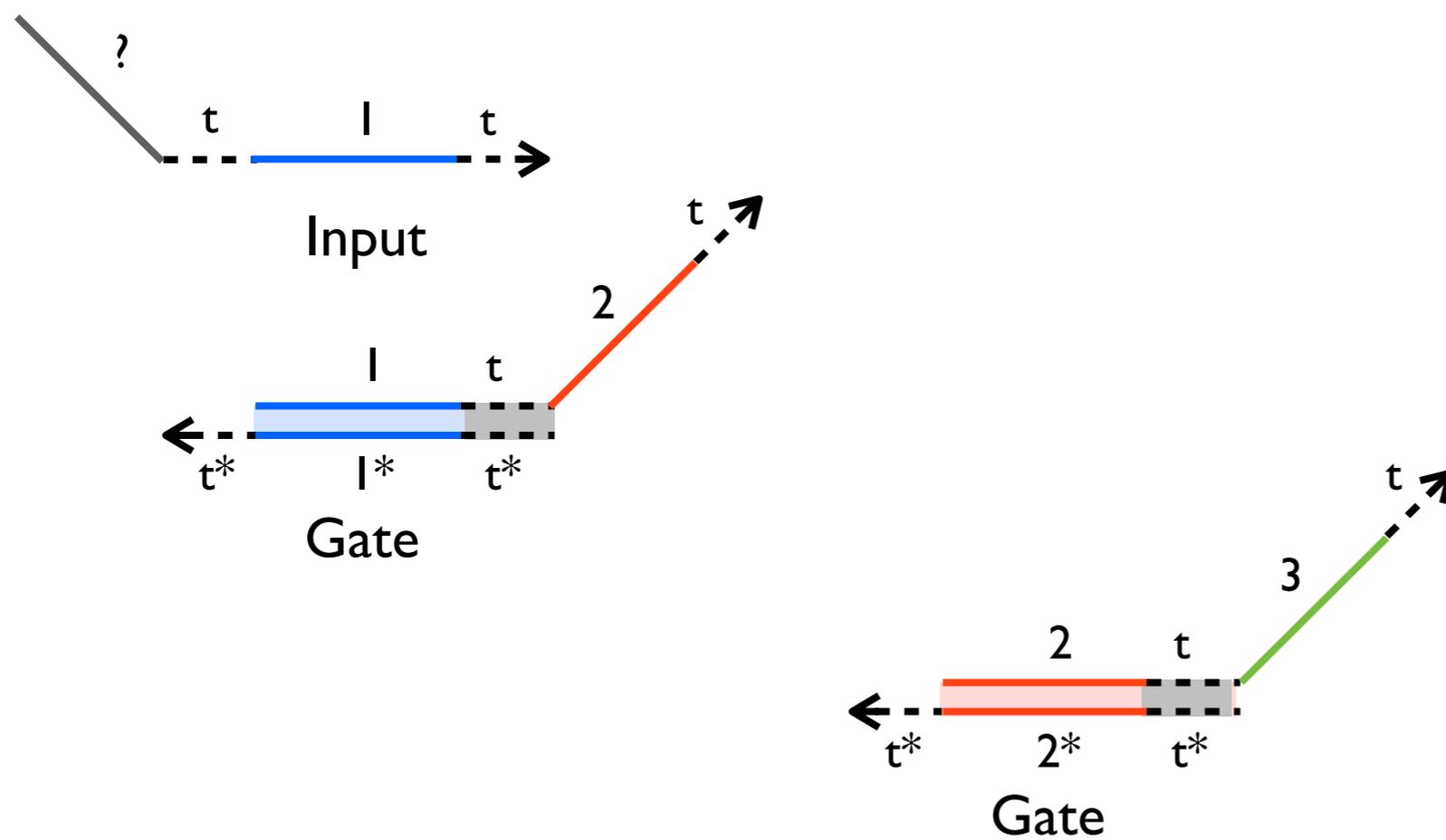
Release of the output strand is (almost) irreversible in the absence of a toehold for the reverse reaction.

Signals can propagate through multiple layers



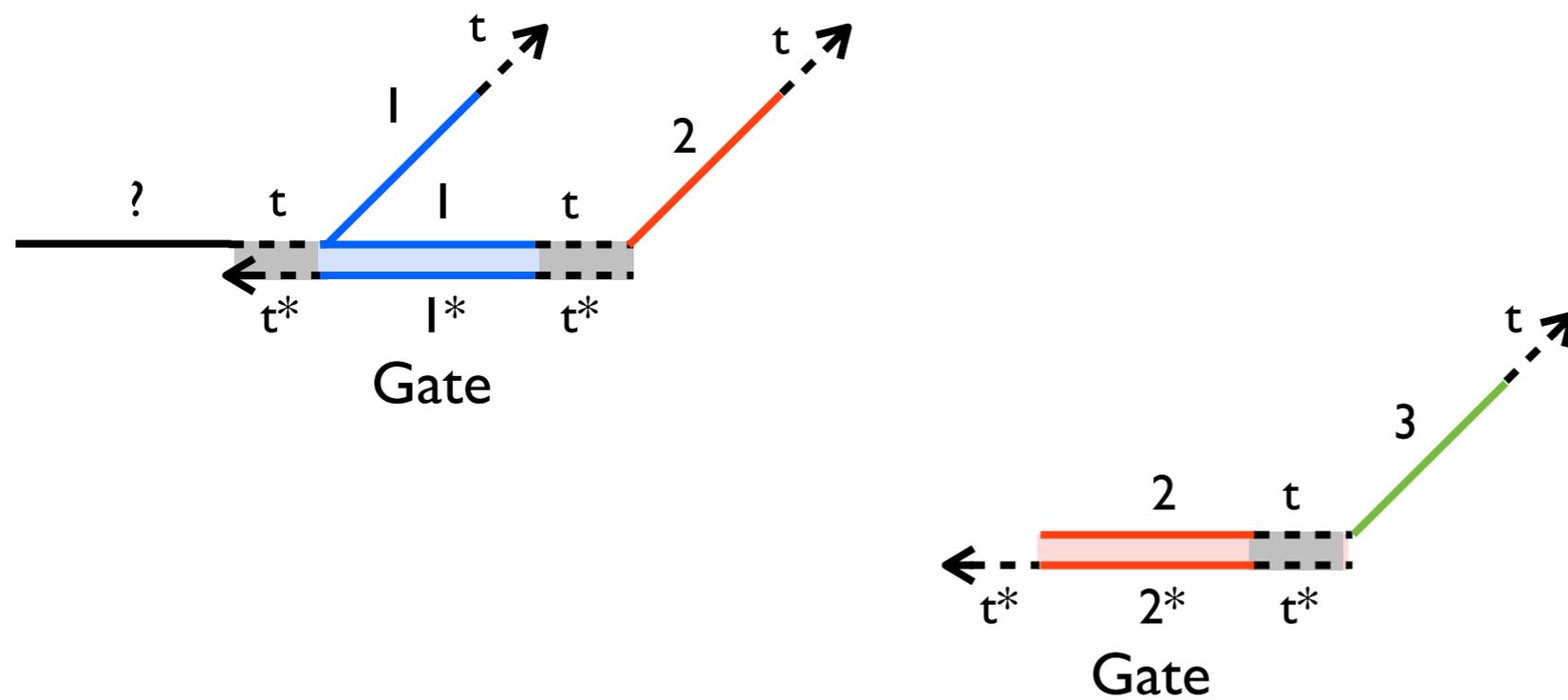
The sequences of inputs and outputs can be completely independent.

Signals can propagate through multiple layers



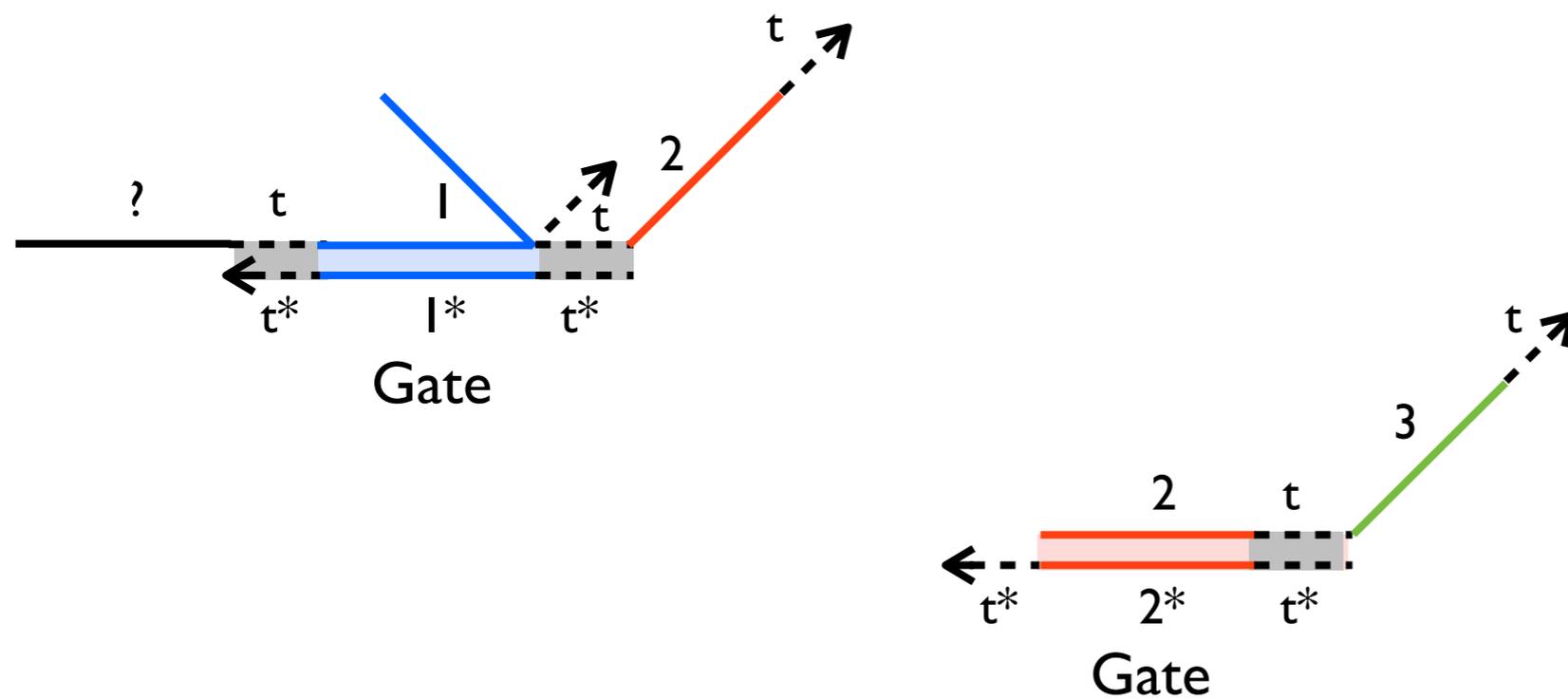
The sequences of inputs and outputs can be completely independent.

Signals can propagate through multiple layers



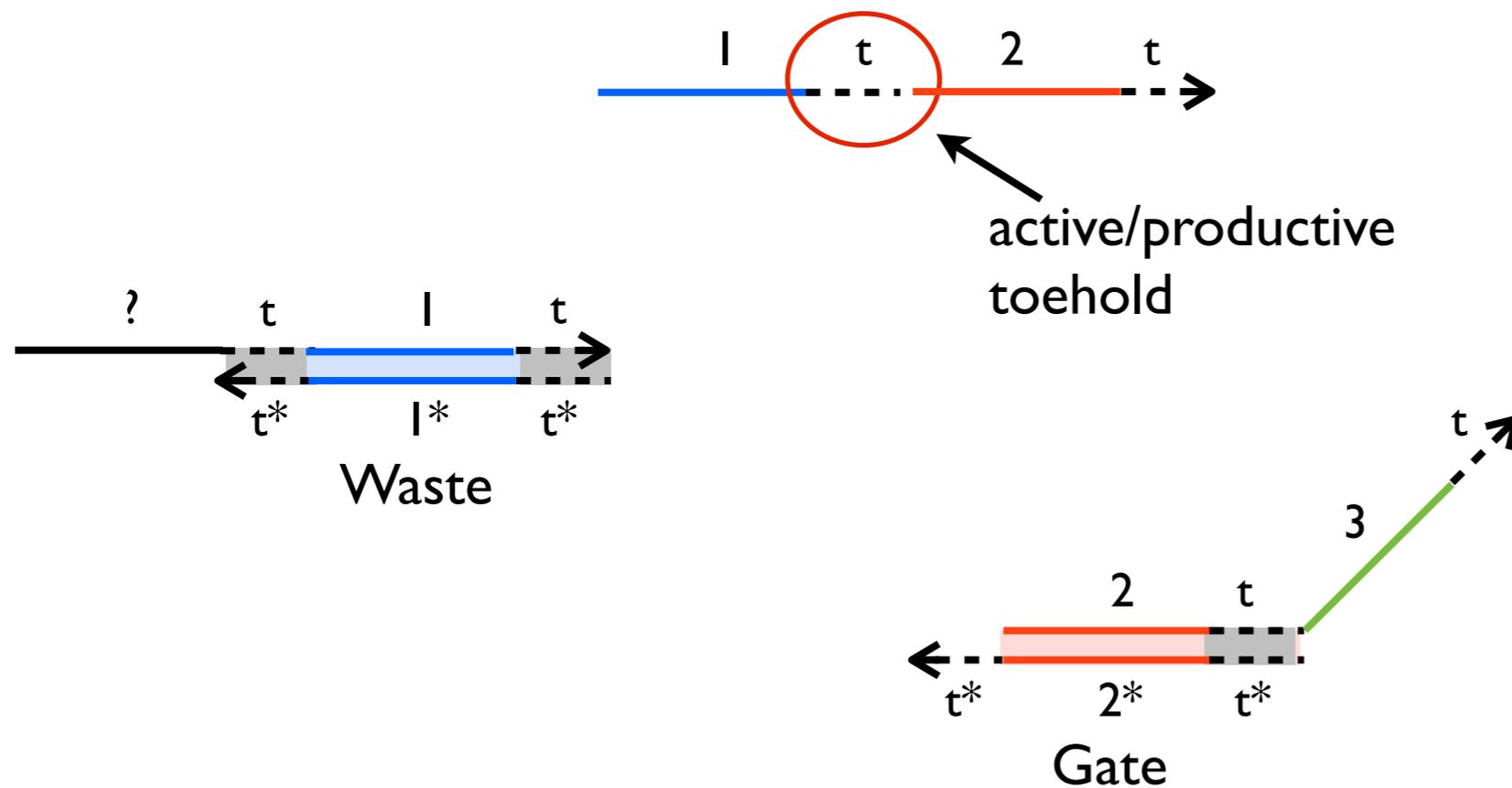
The sequences of inputs and outputs can be completely independent.

Signals can propagate through multiple layers



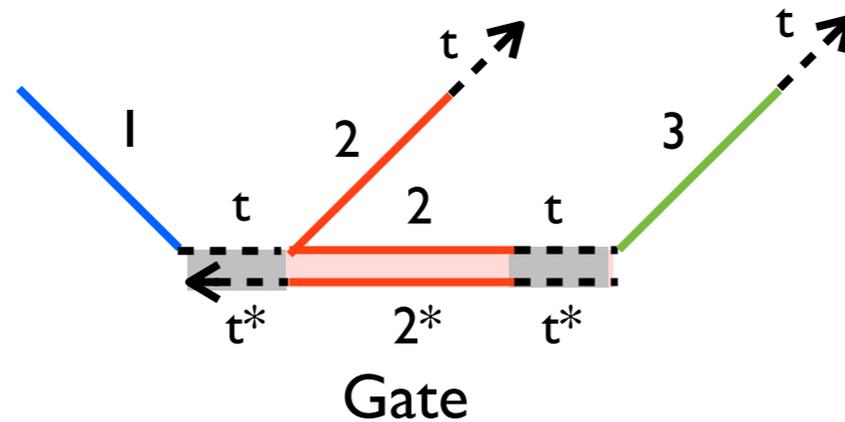
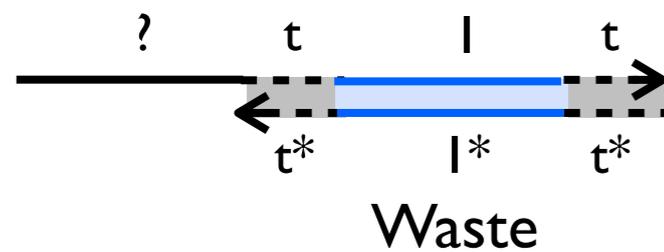
The sequences of inputs and outputs can be completely independent.

Signals can propagate through multiple layers



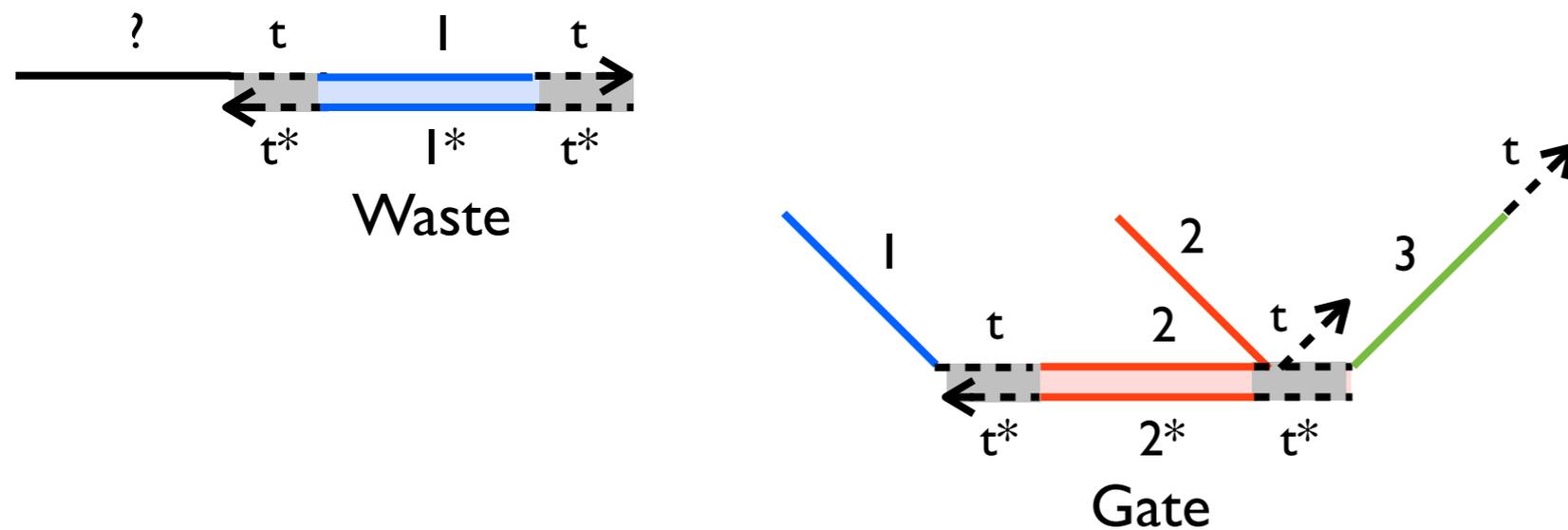
The sequences of inputs and outputs can be completely independent.

Signals can propagate through multiple layers



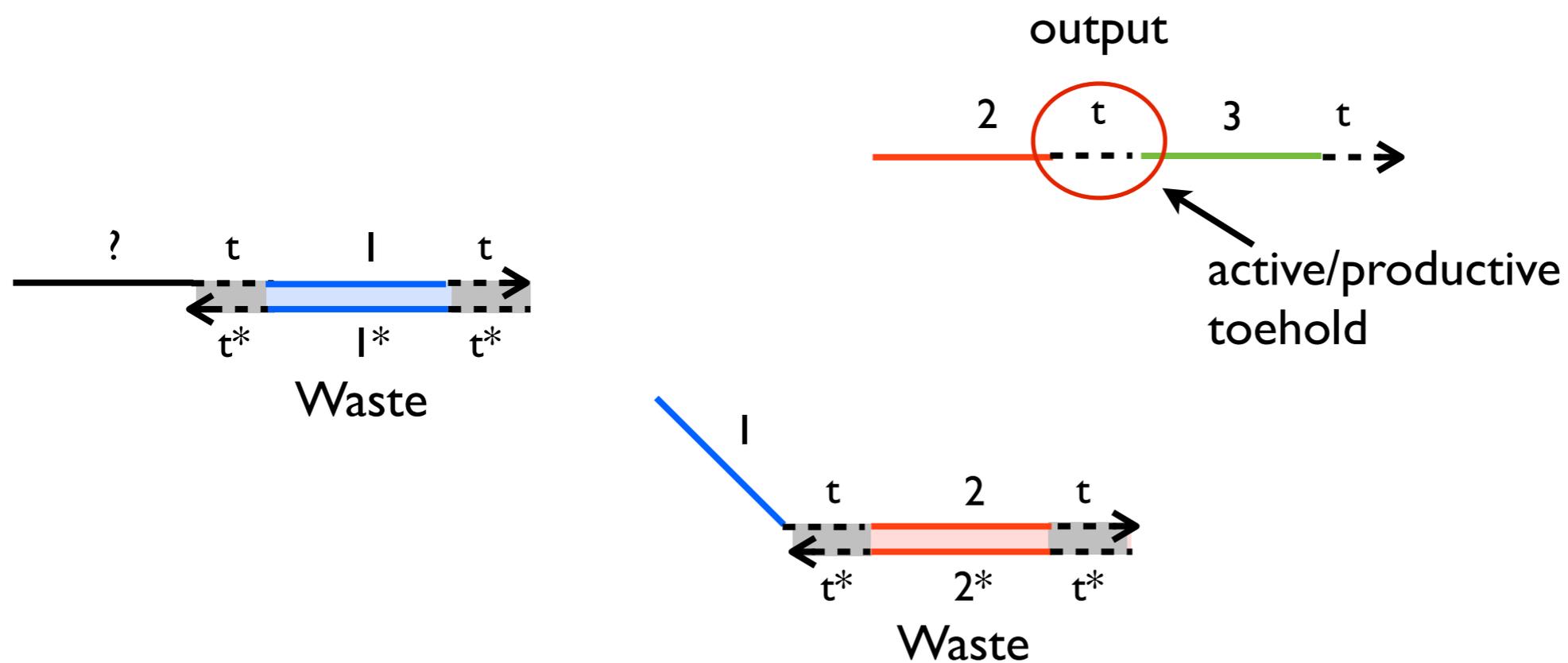
The sequences of inputs and outputs can be completely independent.

Signals can propagate through multiple layers



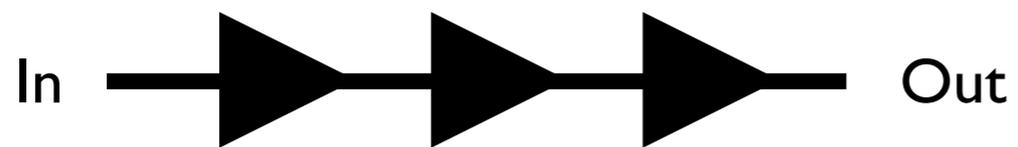
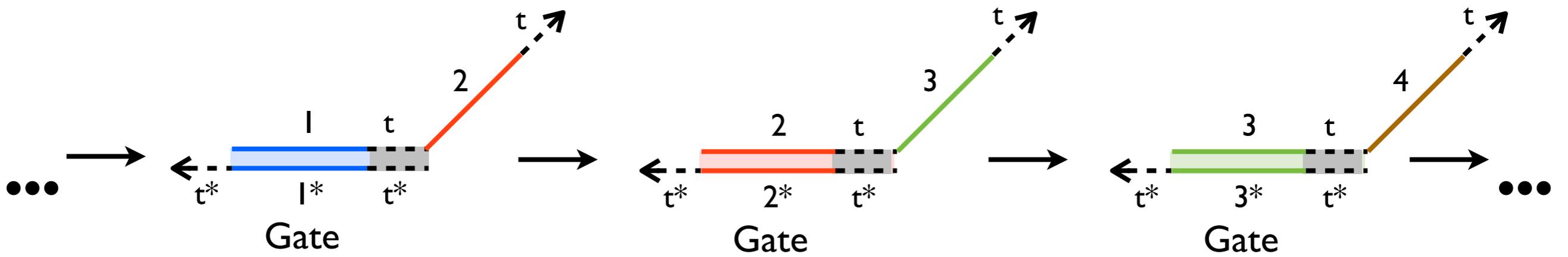
The sequences of inputs and outputs can be completely independent.

Signals can propagate through multiple layers



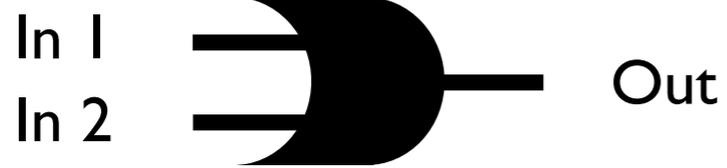
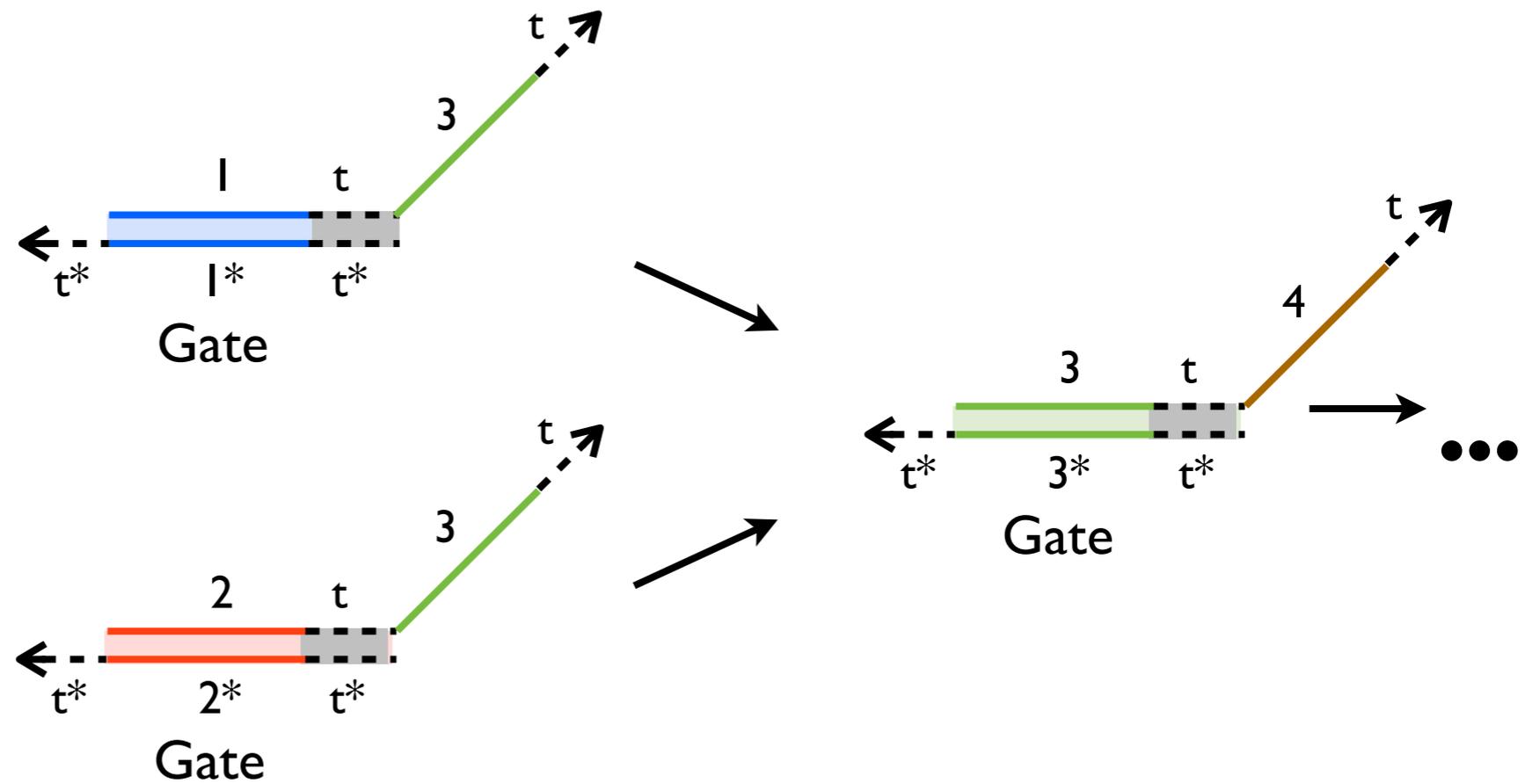
The sequences of inputs and outputs can be completely independent.

Signals can propagate through multiple layers



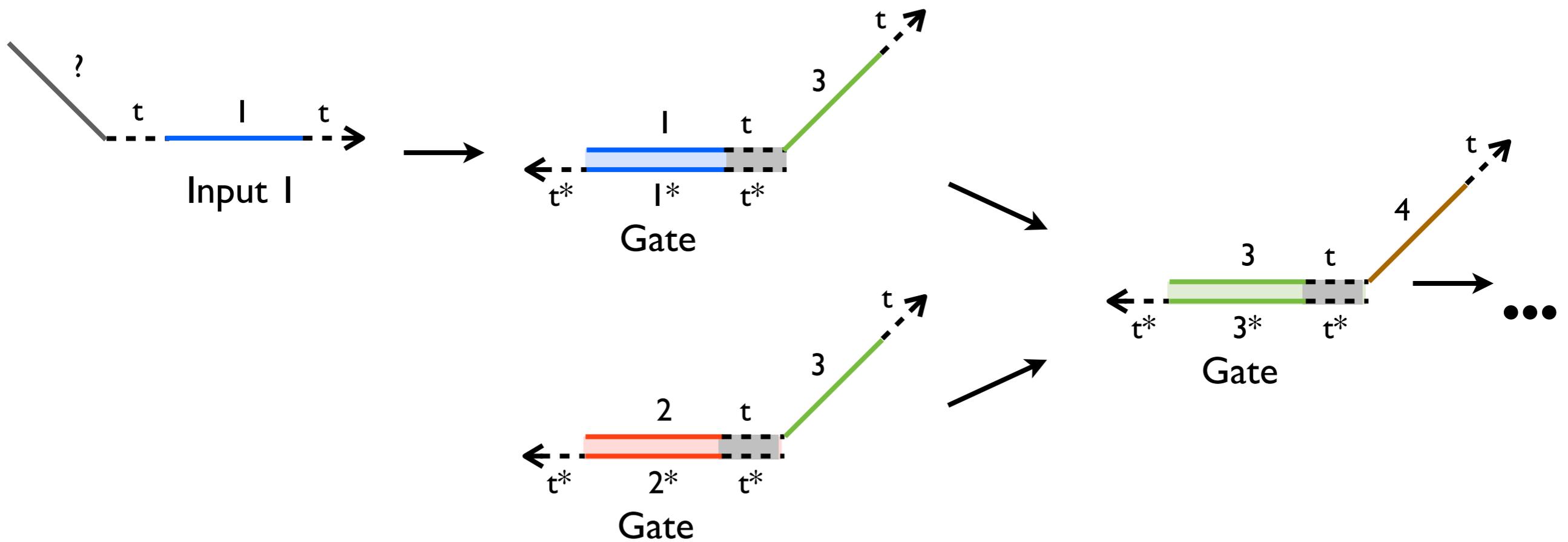
The sequences of inputs and outputs can be completely independent.

OR logic / fan-in



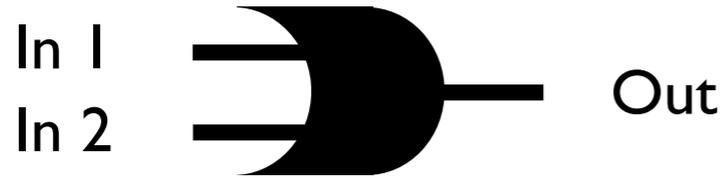
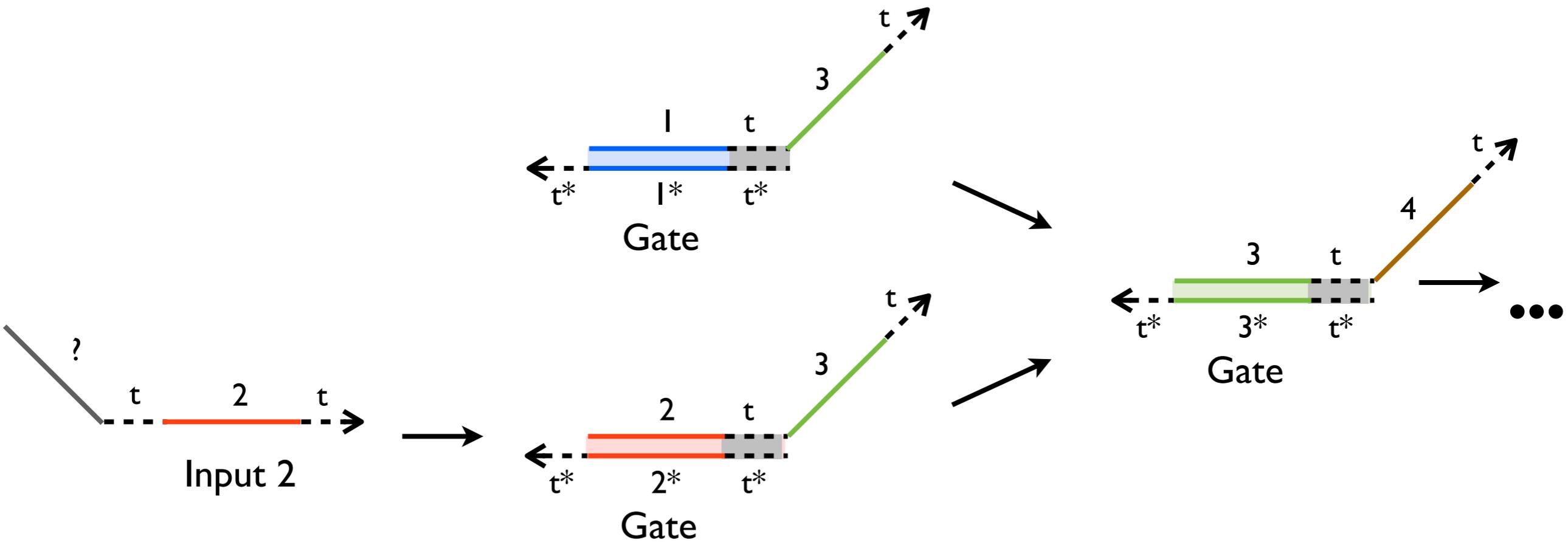
In 1	In 2	Out
0	0	0

OR logic / fan-in



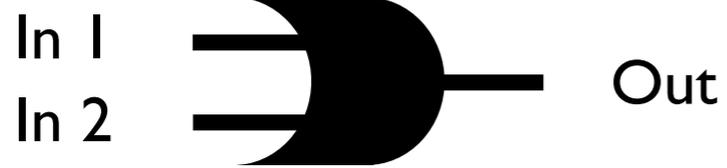
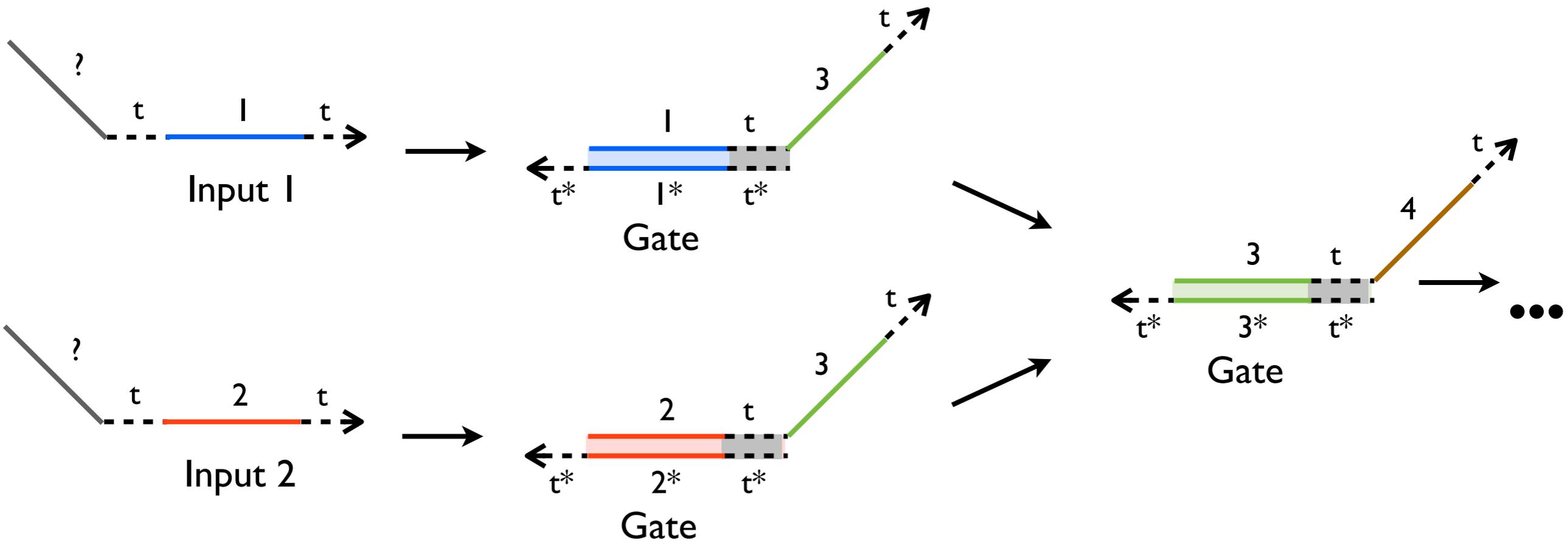
In 2	In 1	Out
0	0	0
0	1	1

OR logic / fan-in



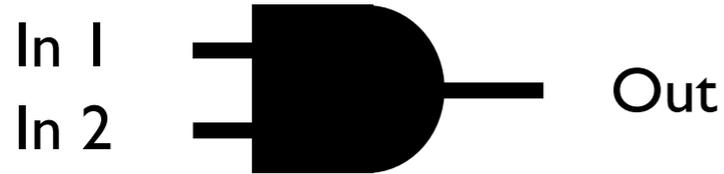
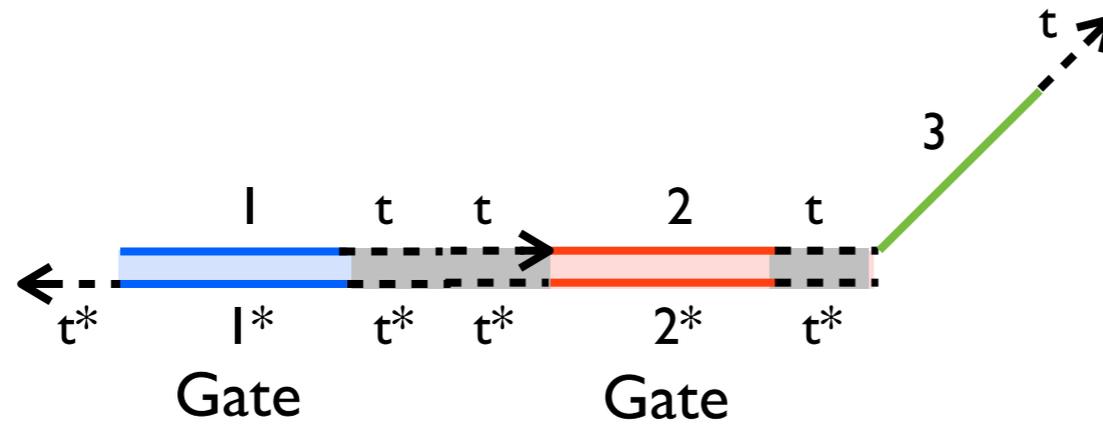
In 2	In 1	Out
0	0	0
0	1	1
1	0	1

OR logic / fan-in



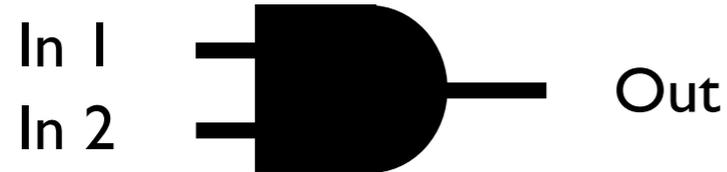
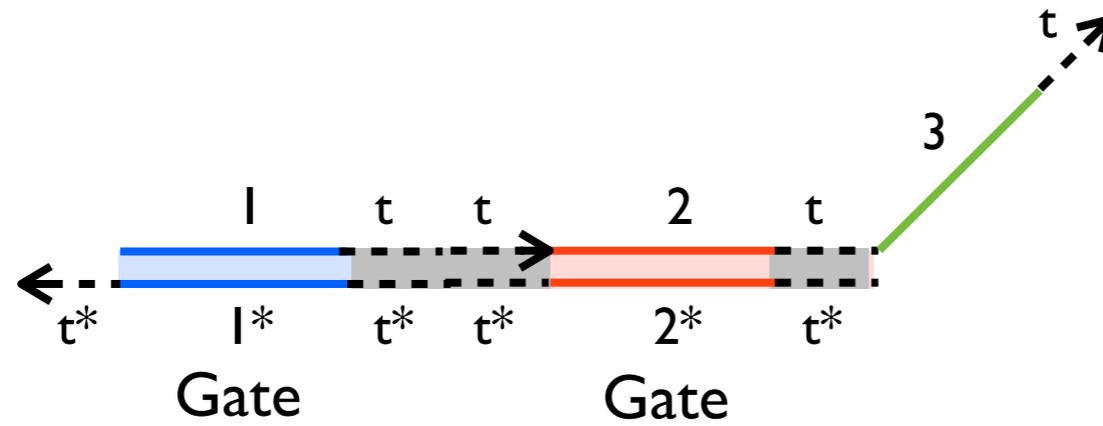
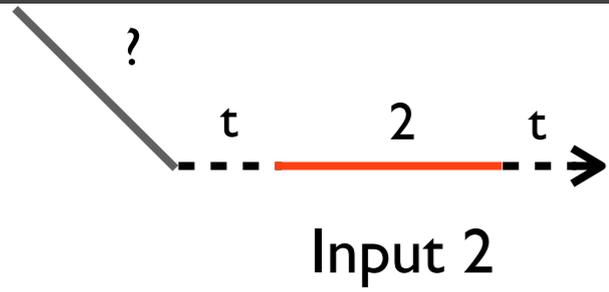
In 2	In 1	Out
0	0	0
0	1	1
1	0	1
1	1	1

AND logic



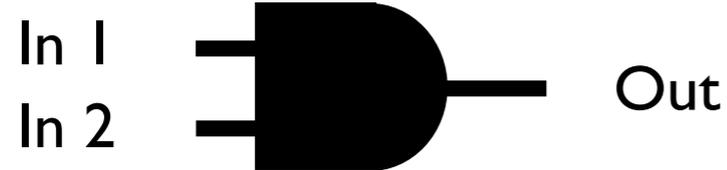
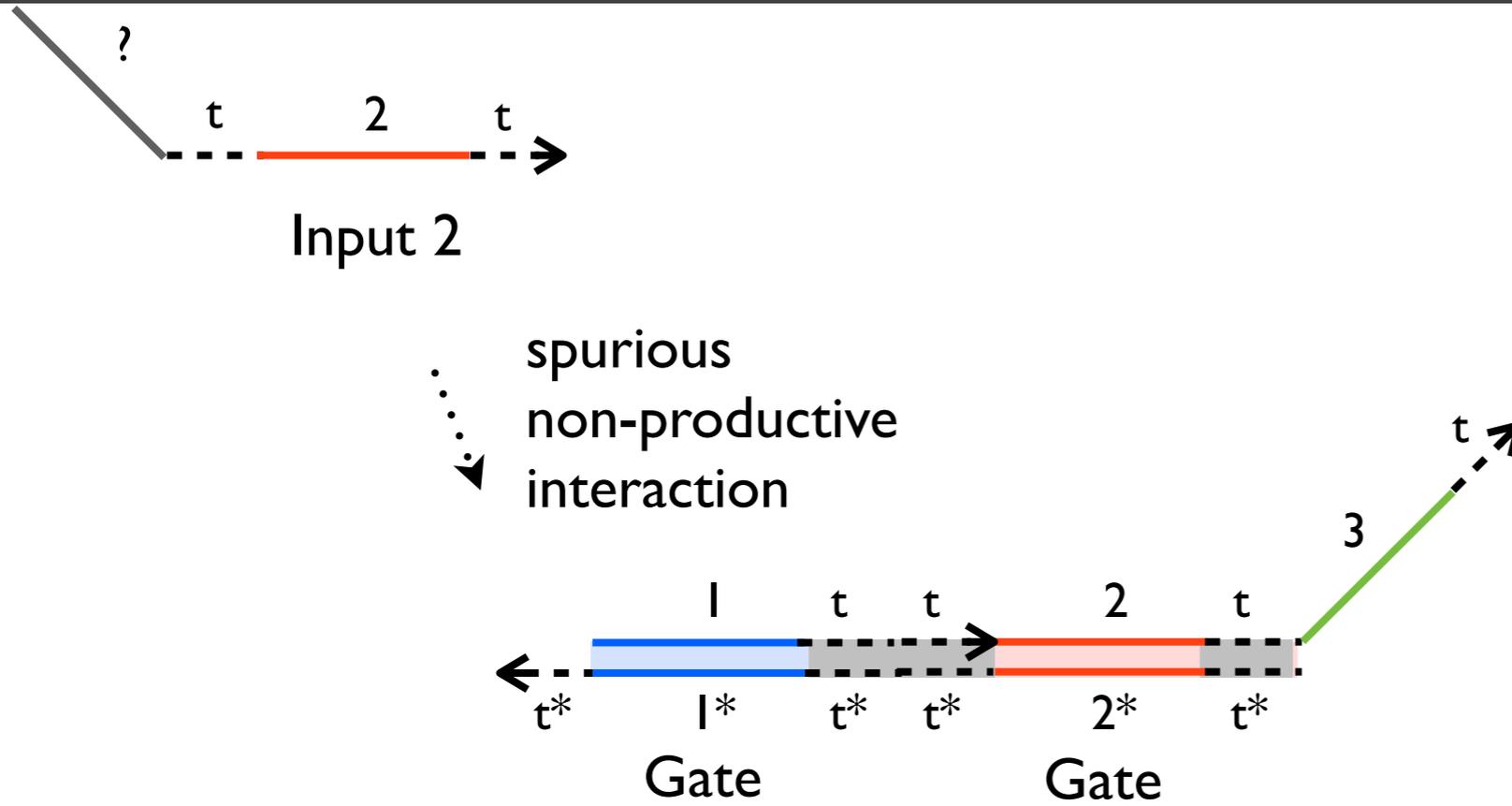
In 2	In 1	Out
0	0	0

AND logic



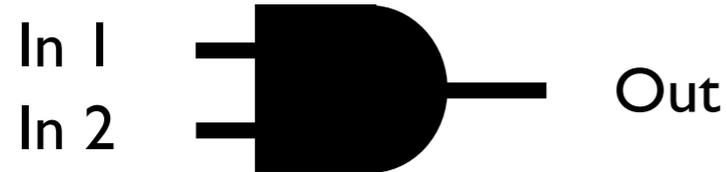
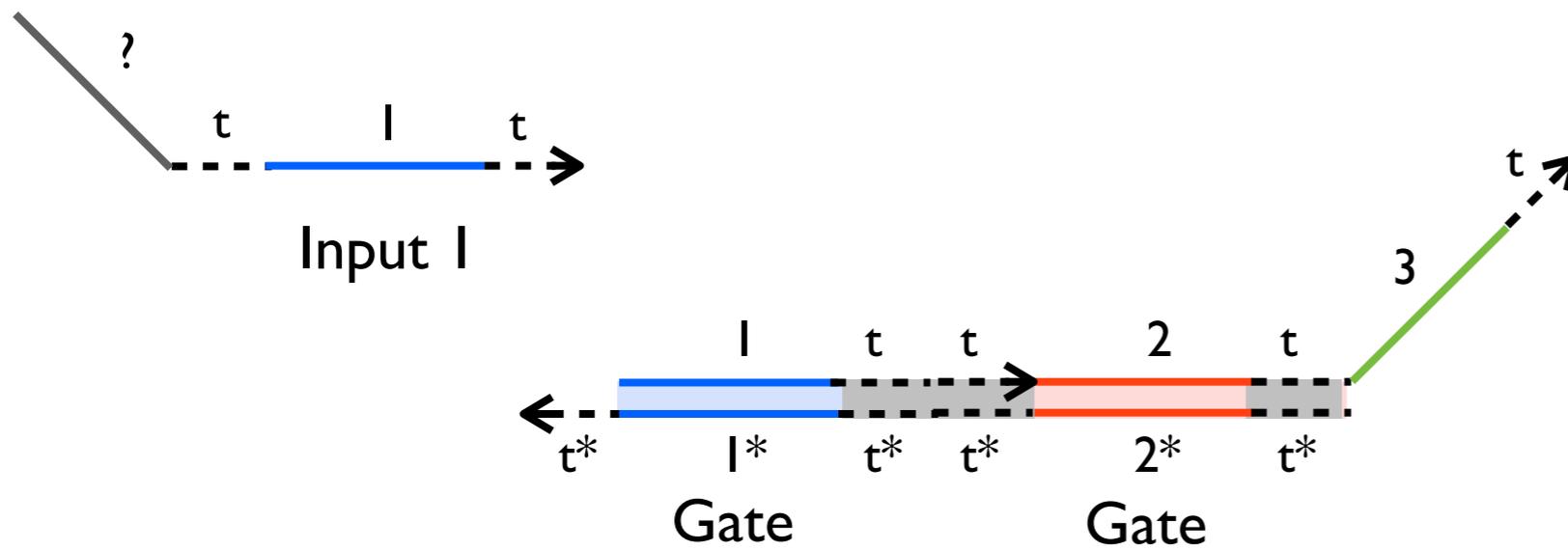
In 2	In 1	Out
0	0	0

AND logic



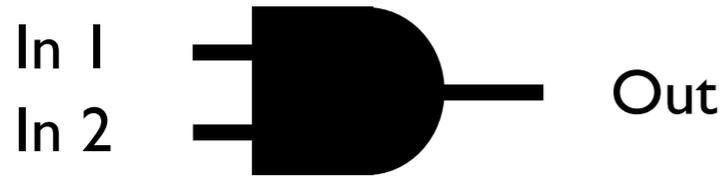
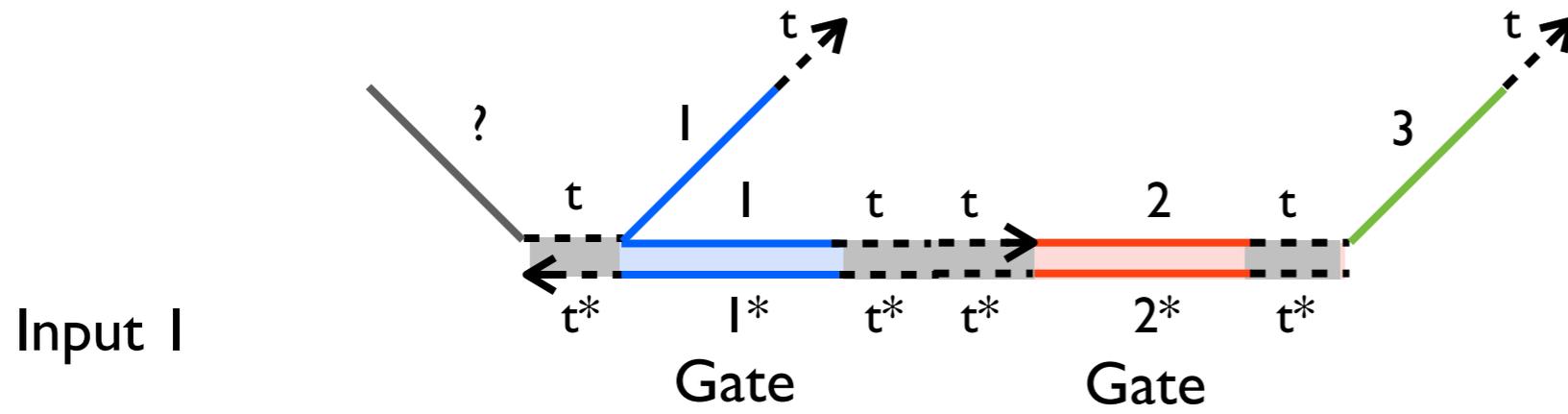
In 2	In 1	Out
0	0	0
1	0	0

AND logic



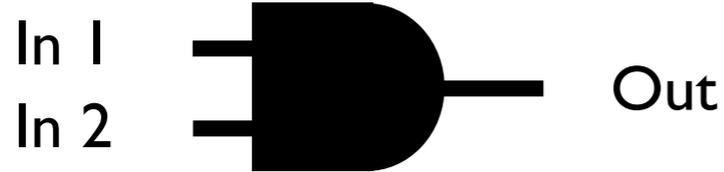
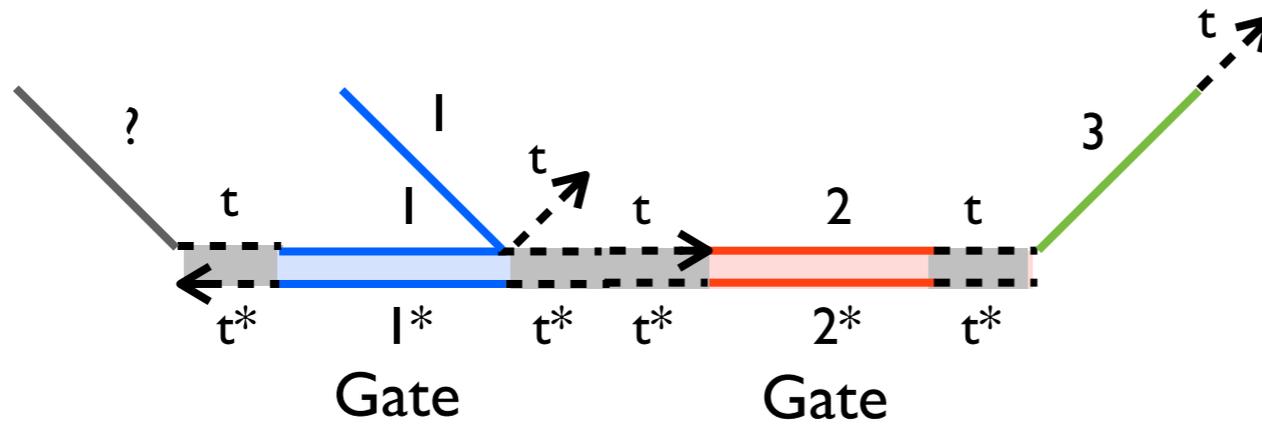
In 2	In 1	Out
0	0	0
1	0	0

AND logic



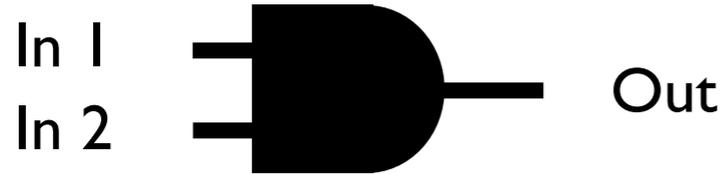
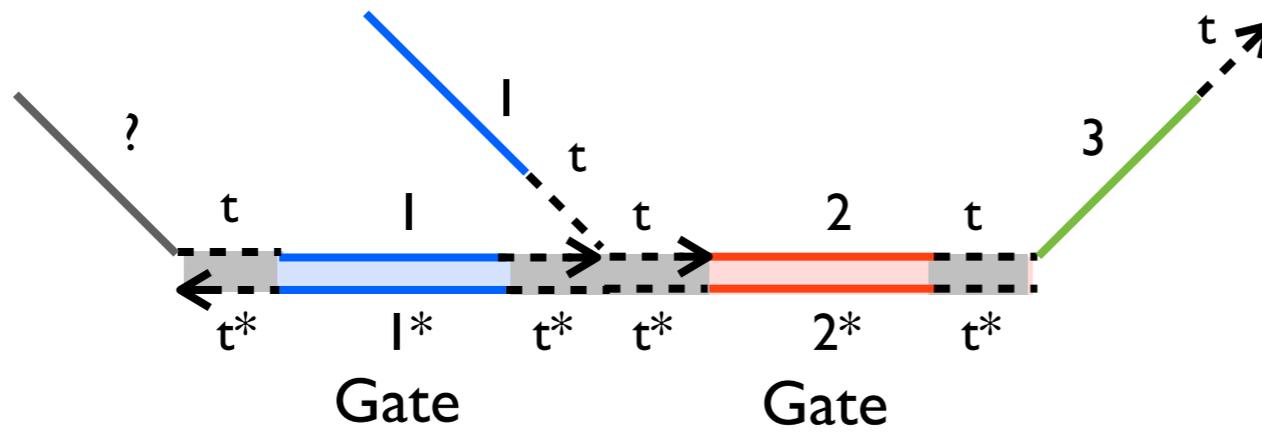
In 2	In 1	Out
0	0	0
1	0	0

AND logic



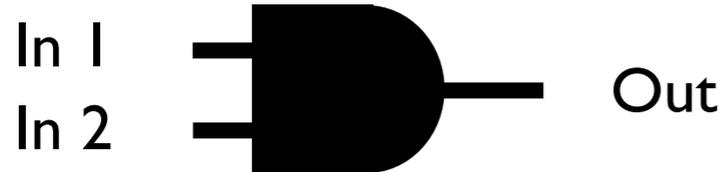
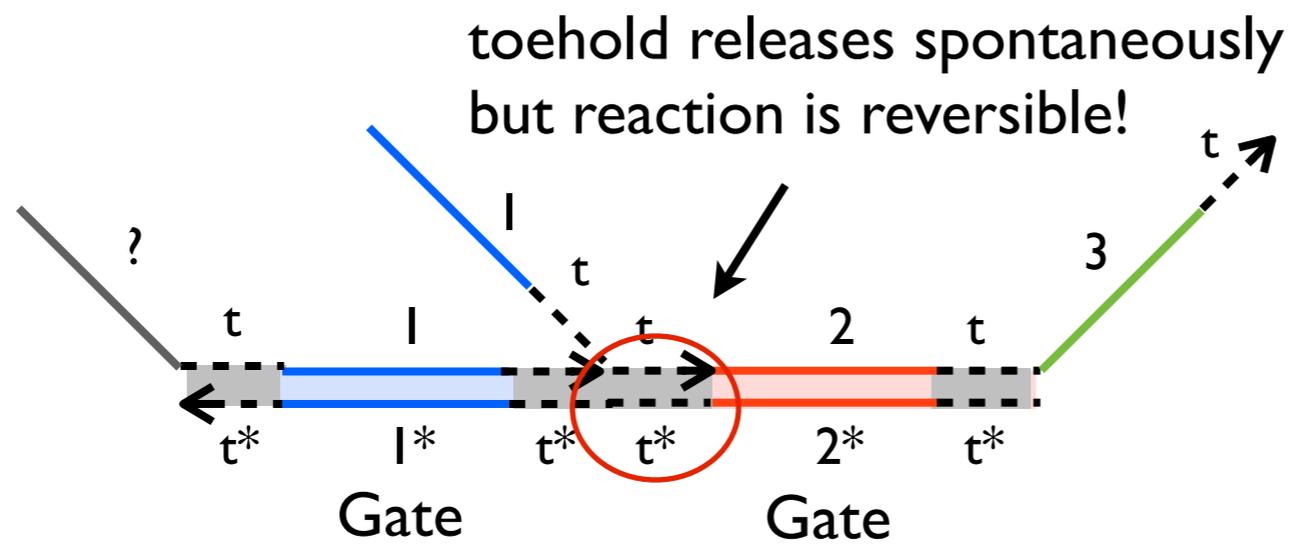
In 2	In 1	Out
0	0	0
1	0	0

AND logic



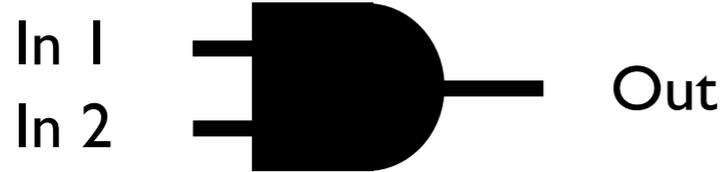
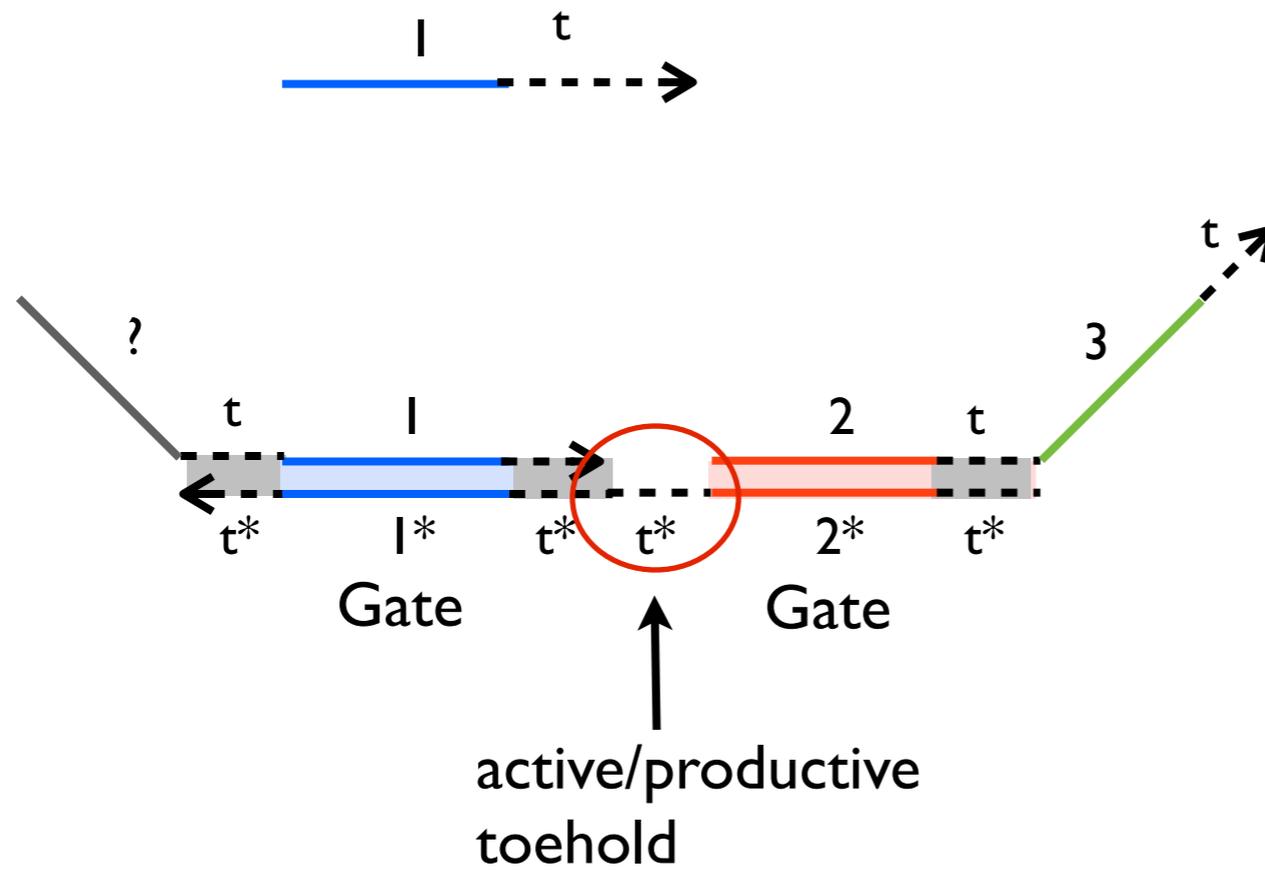
In 2	In 1	Out
0	0	0
1	0	0

AND logic



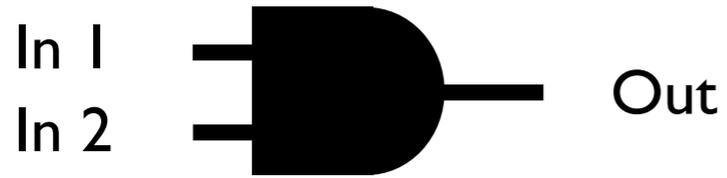
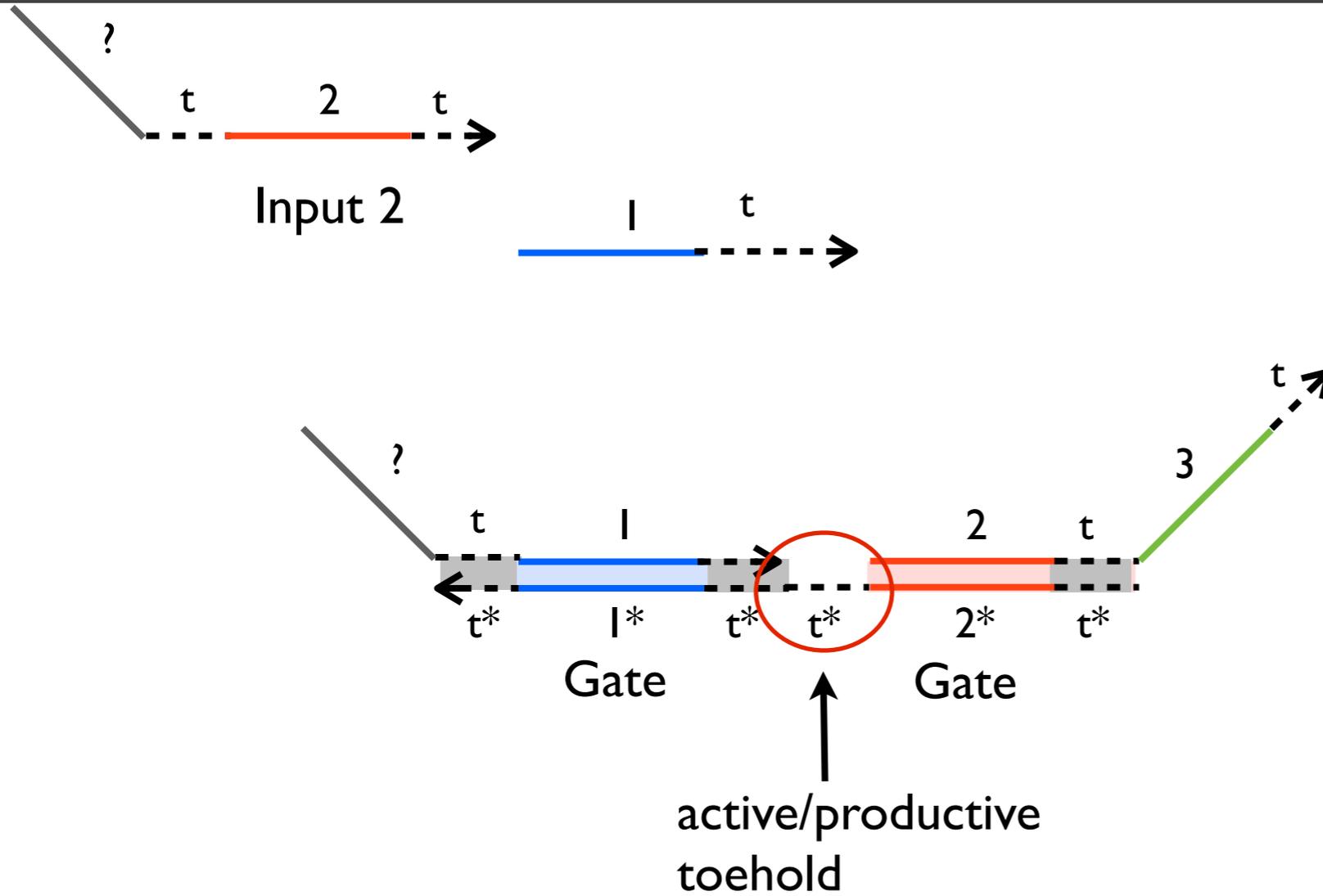
In 2	In 1	Out
0	0	0
1	0	0

AND logic



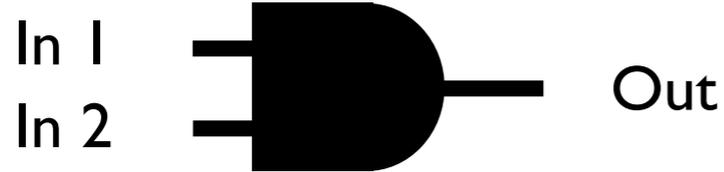
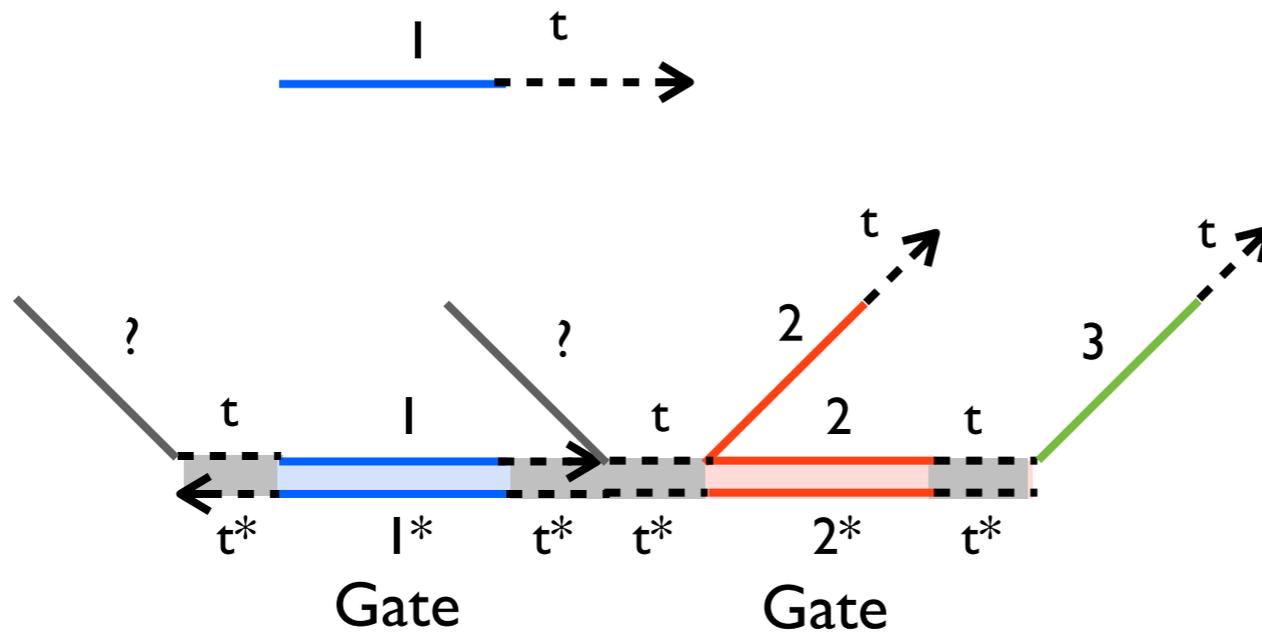
In 2	In 1	Out
0	0	0
0	1	0
1	0	0

AND logic



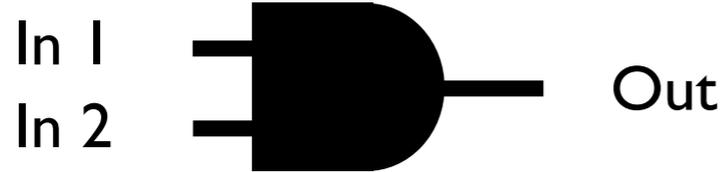
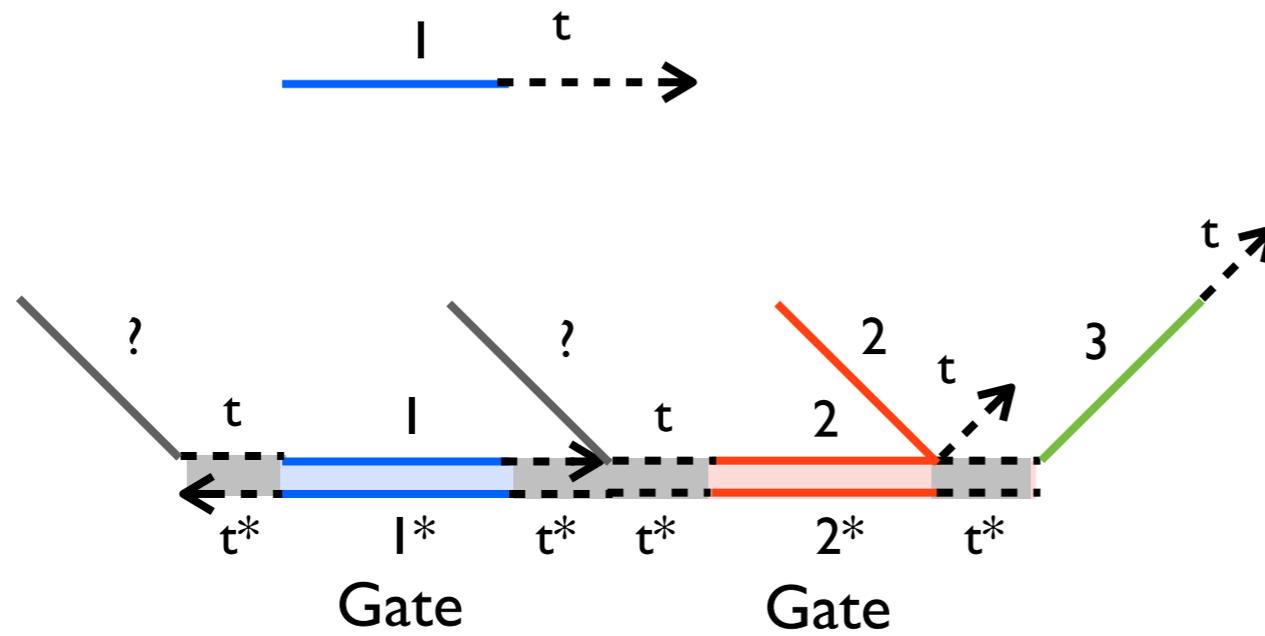
In 2	In 1	Out
0	0	0
0	1	0
1	0	0

AND logic



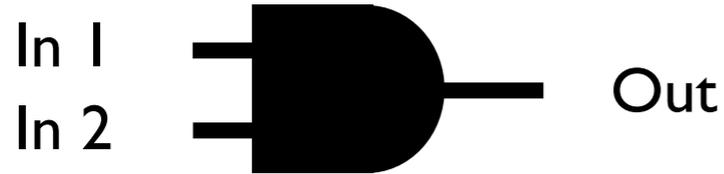
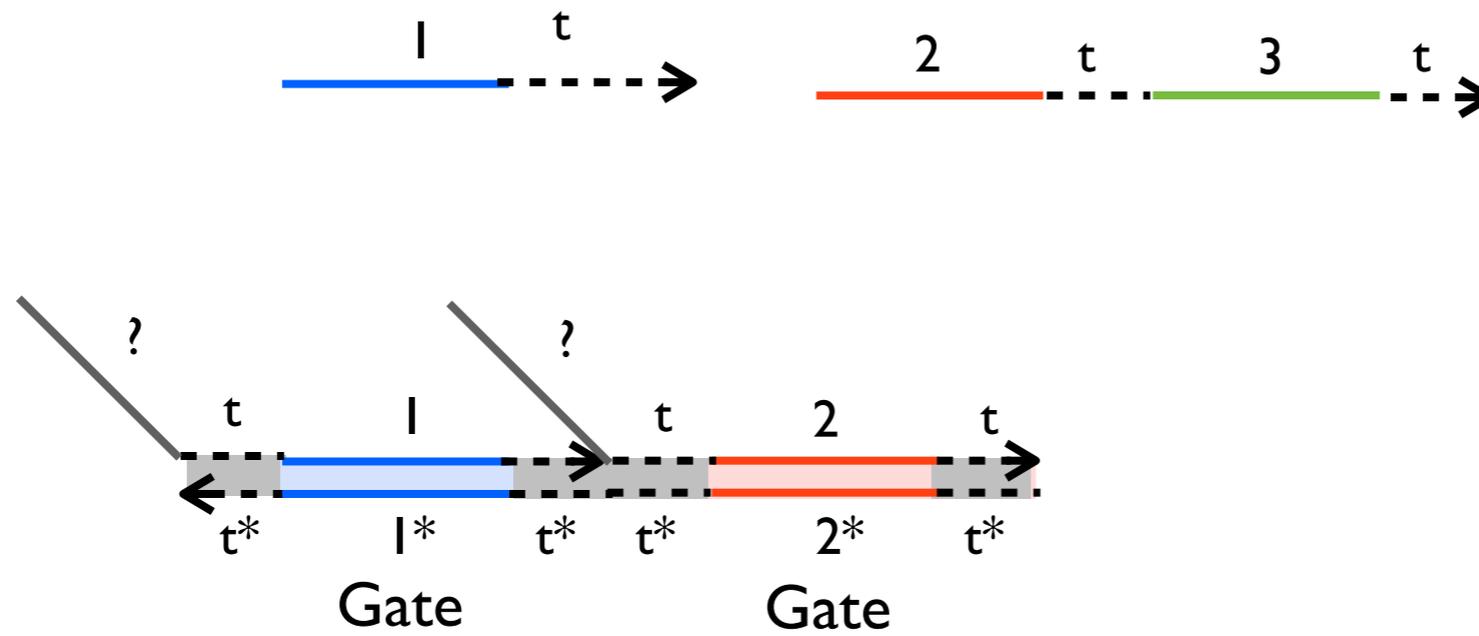
In 2	In 1	Out
0	0	0
0	1	0
1	0	0

AND logic



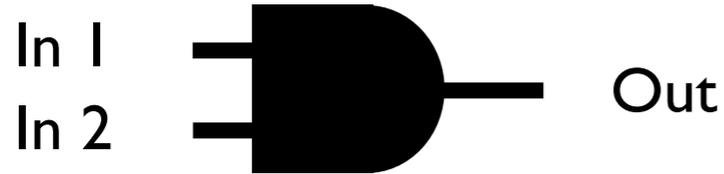
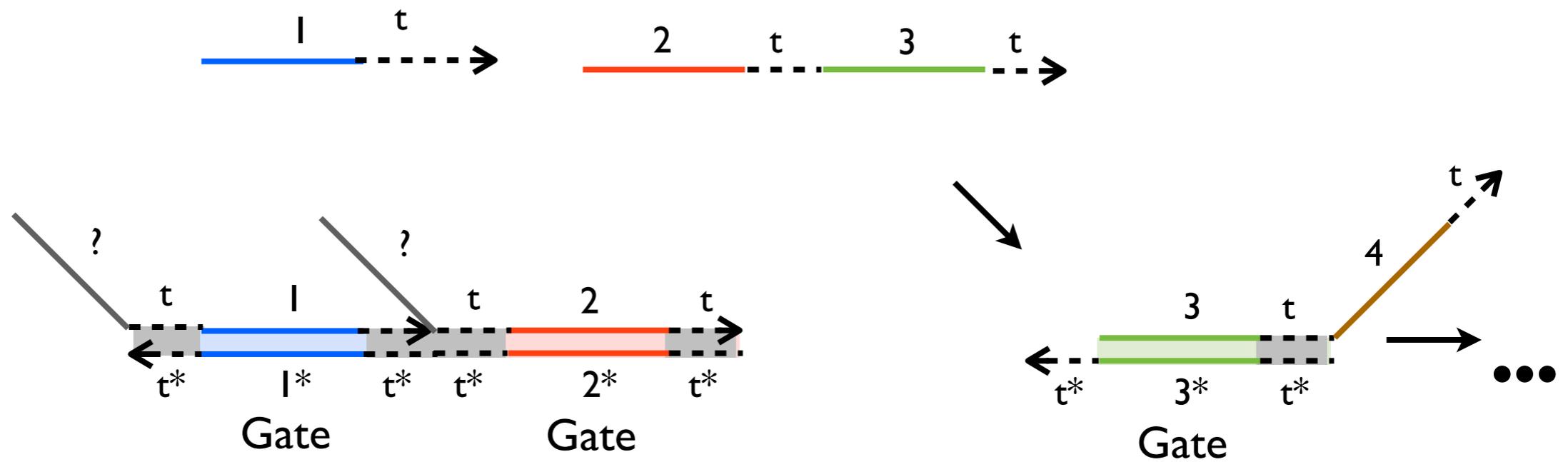
In 2	In 1	Out
0	0	0
0	1	0
1	0	0

AND logic



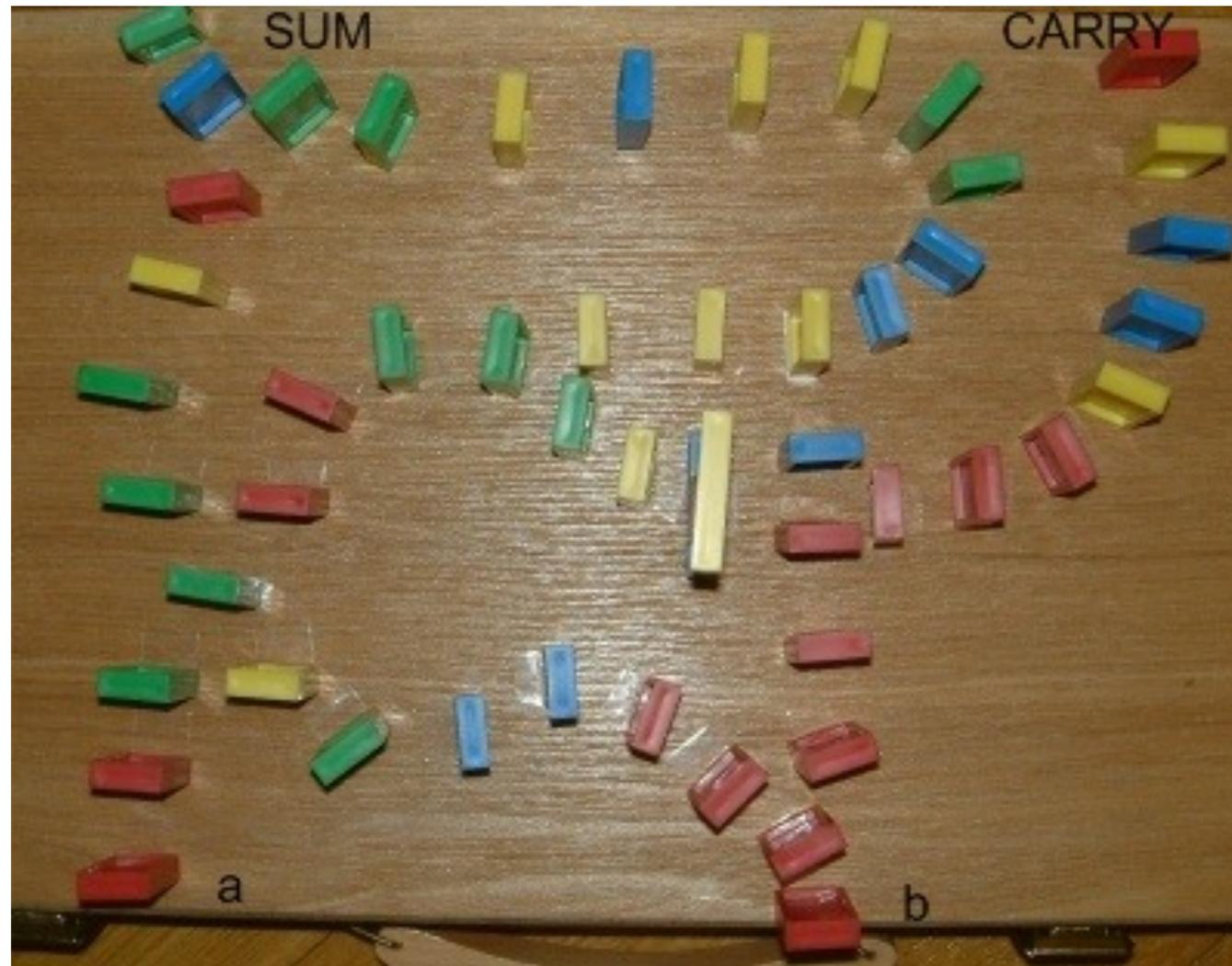
In 2	In 1	Out
0	0	0
0	1	0
1	0	0
1	1	1

AND logic



In 2	In 1	Out
0	0	0
0	1	0
1	0	0
1	1	1

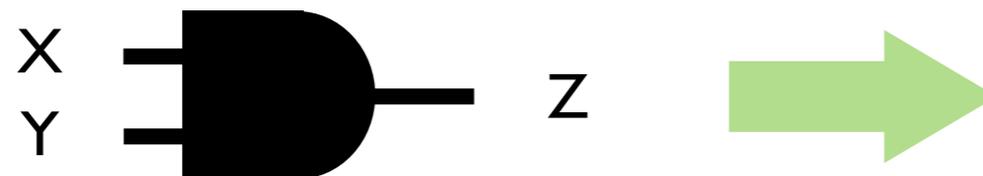
Why is NOT difficult?



Absence of a signal could be “NOT” or could simply mean that computation hasn’t occurred yet.

Dual-rail logic: AND and OR are sufficient for feed-forward digital circuits

Replace X by the pair (X0,X1):

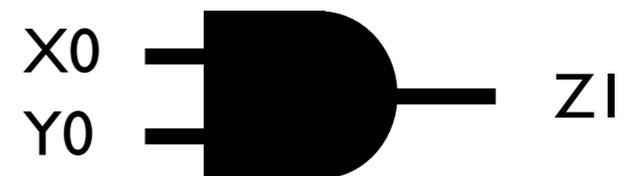
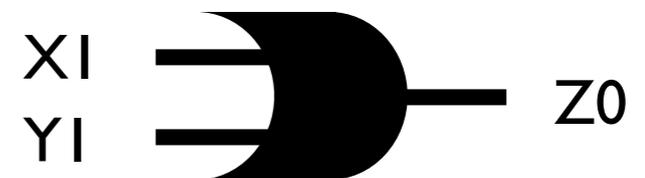
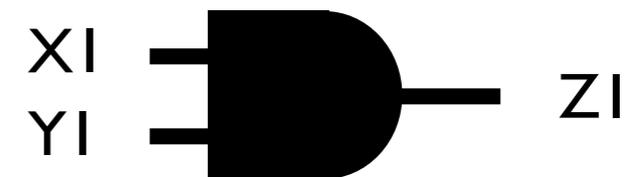
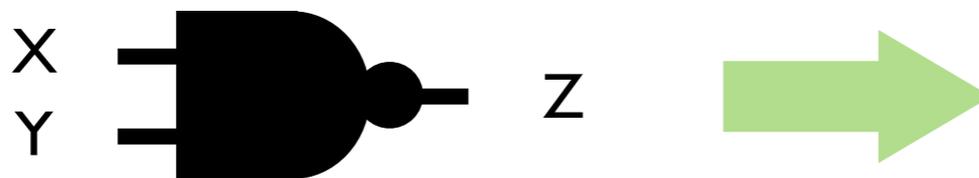


X0 on: logical "0"

X1 on: logical "1"

X0, X1 off:
not yet computed

X0, X1 on:
error



Single wire circuit using NOT, AND, OR, NAND, ... can be replaced by a dual rail representation using AND and OR only. This implementation requires maximally 2x as many gates.

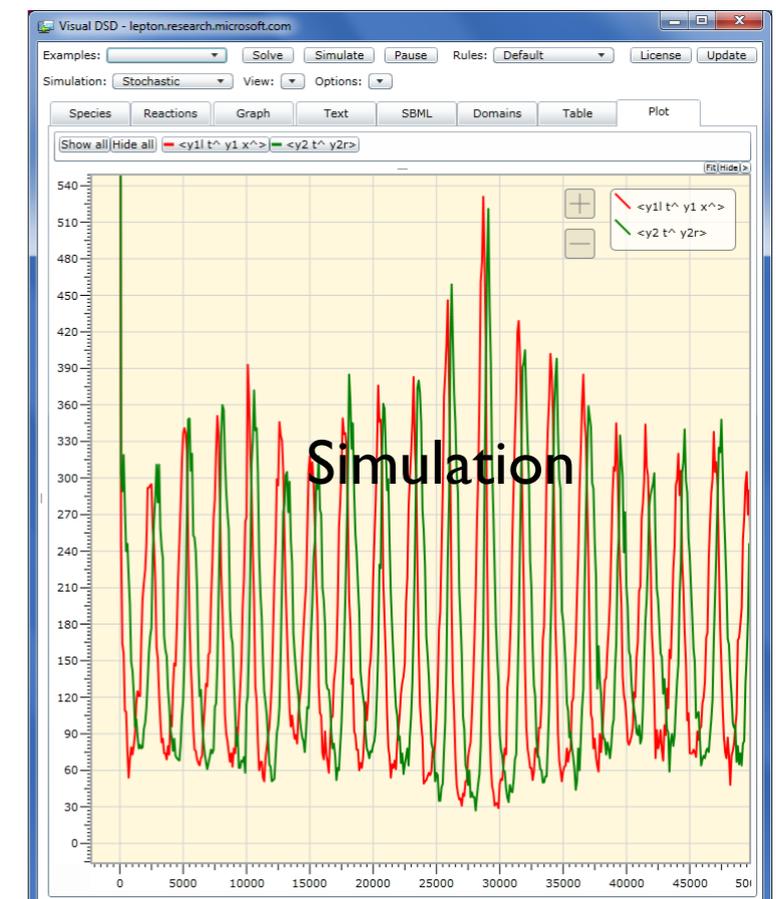
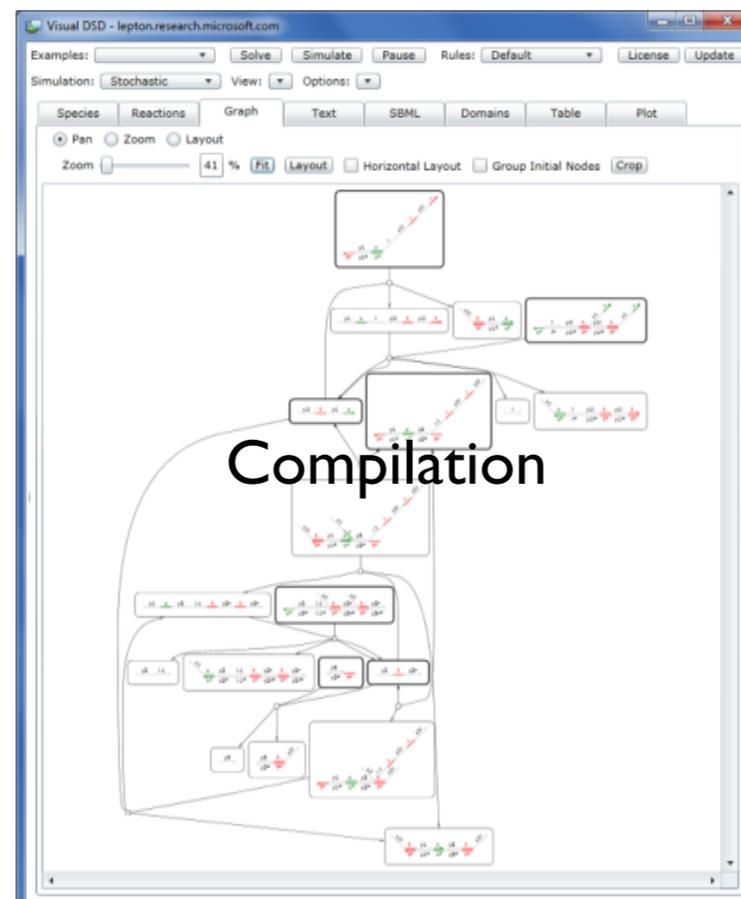
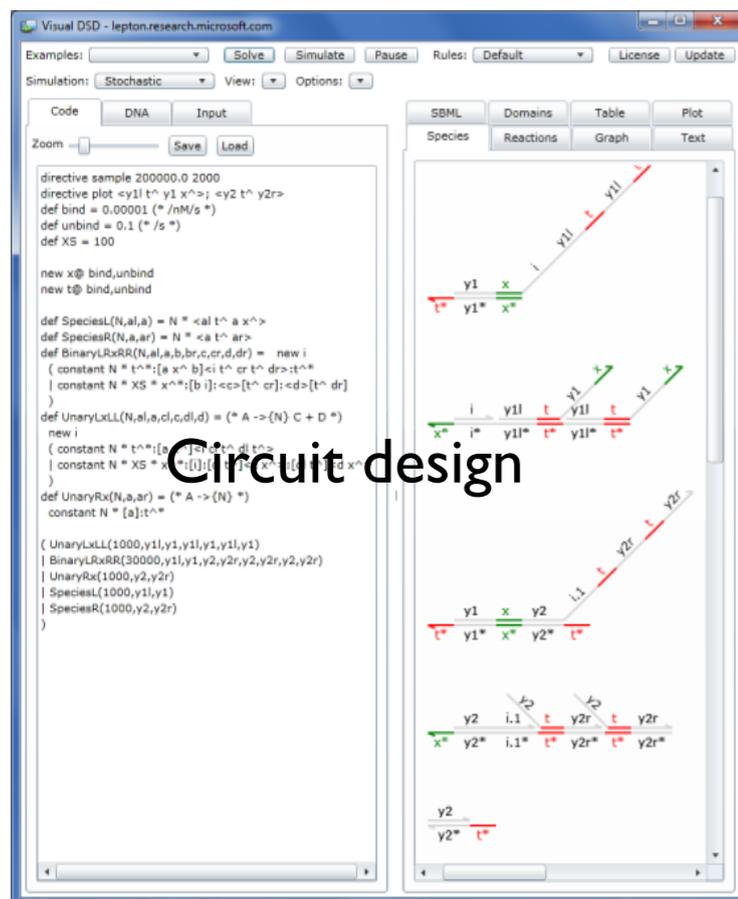
Differences and similarities between electronic and molecular circuits

1. **Lack of spatial isolation:** All gates and signals diffuse in solution and interact stochastically.
2. **Computation energy and non-reusable gates:** Both inputs and gates are consumed as the circuit is evaluated by cascade reactions, so they cannot be reused.
3. **Data encoding:** Information is encoded in the sequences and concentration of biomolecules.
4. **Lack of clear hardware software separation:** Gates and circuits come pre-programmed for the specific computation they are meant to carry out.
5. **Speed of computation:** A circuit's evaluation under typical reaction conditions takes minutes to hours.
6. **Need for dual-rail logic:** NOT is difficult to implement

visual DSD: A tool for simulating DNA strand displacement systems

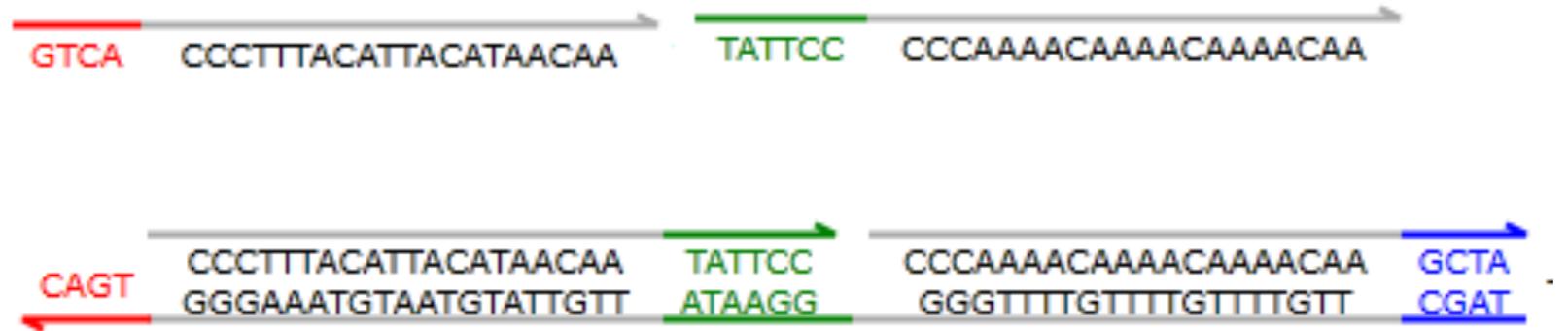
<http://research.microsoft.com/en-us/projects/dna/>

Use links to “web simulator” and “tutorial” for hw.

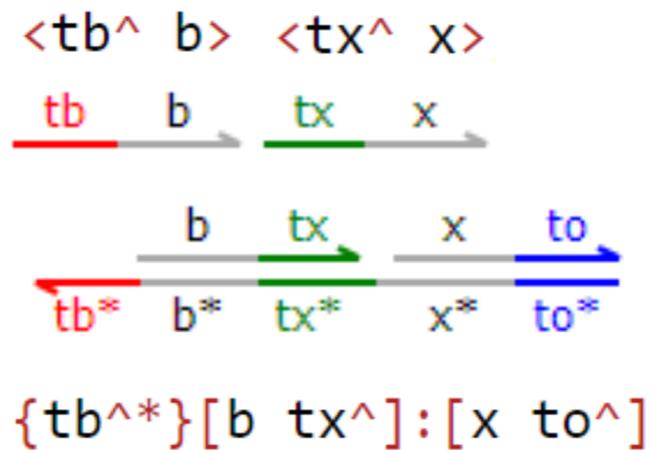


Phillips, Cardelli. Royal Society Interface, 2009
Lakin, Youssef, Polo, Emmott, Phillips. Bioinformatics, 2011

visual DSD: A tool for simulating DNA strand displacement systems



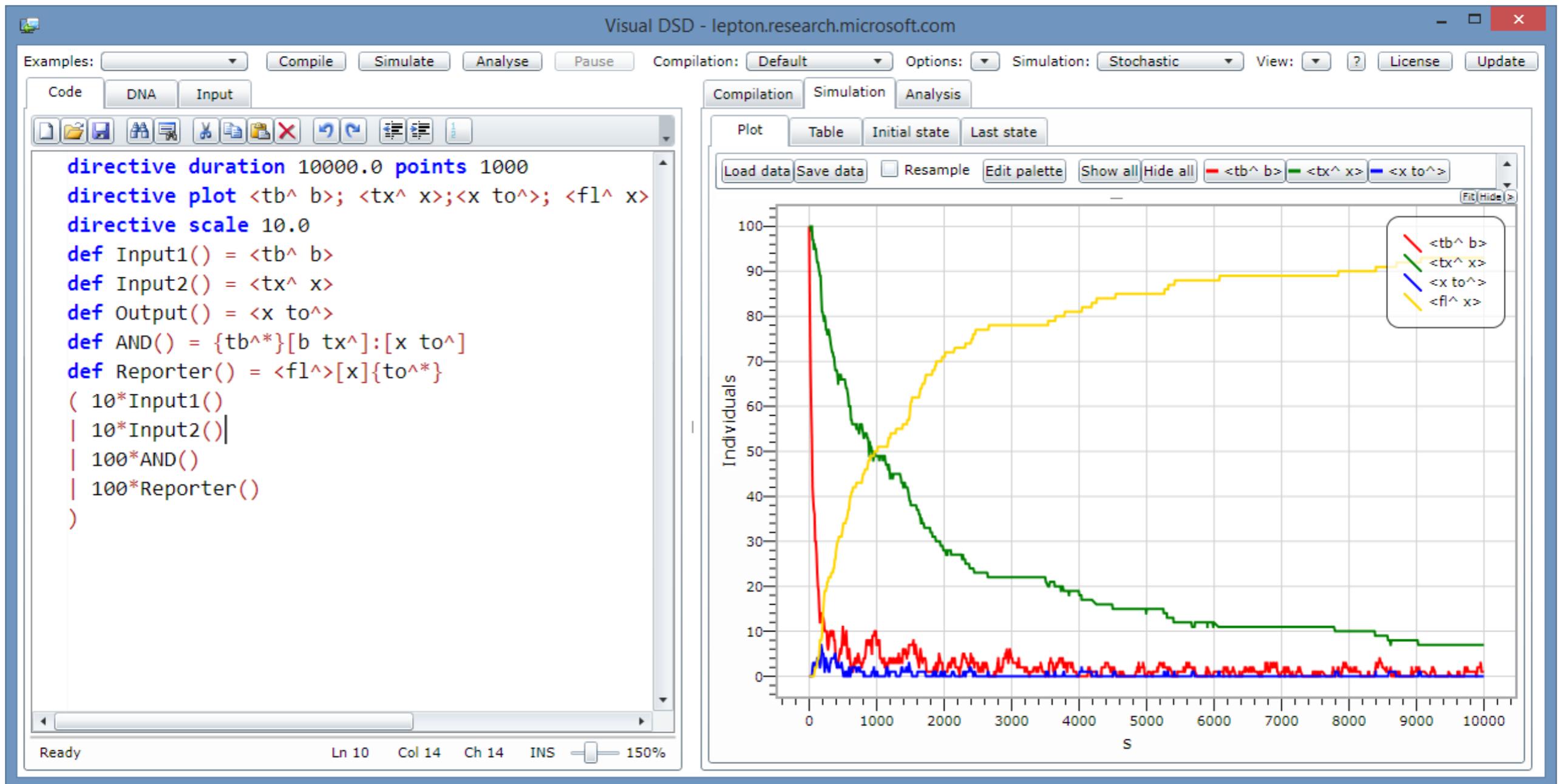
tb --> (5') TACCAA (3')
 tx --> (5') TATTCC (3')
 to --> (5') GTCA (3')
 b --> (5') CCCTTTTCTAAACTAAACAA (3')
 x --> (5') CCCAAAACAAAACAAAACAA (3')



17

Slide credit: Andrew Phillips (MSR)

visual DSD: A tool for simulating DNA strand displacement systems



Slide credit: Andrew Phillips (MSR)

visual DSD: A tool for simulating DNA strand displacement systems

Strand::=

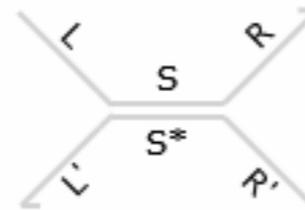


Upper strand



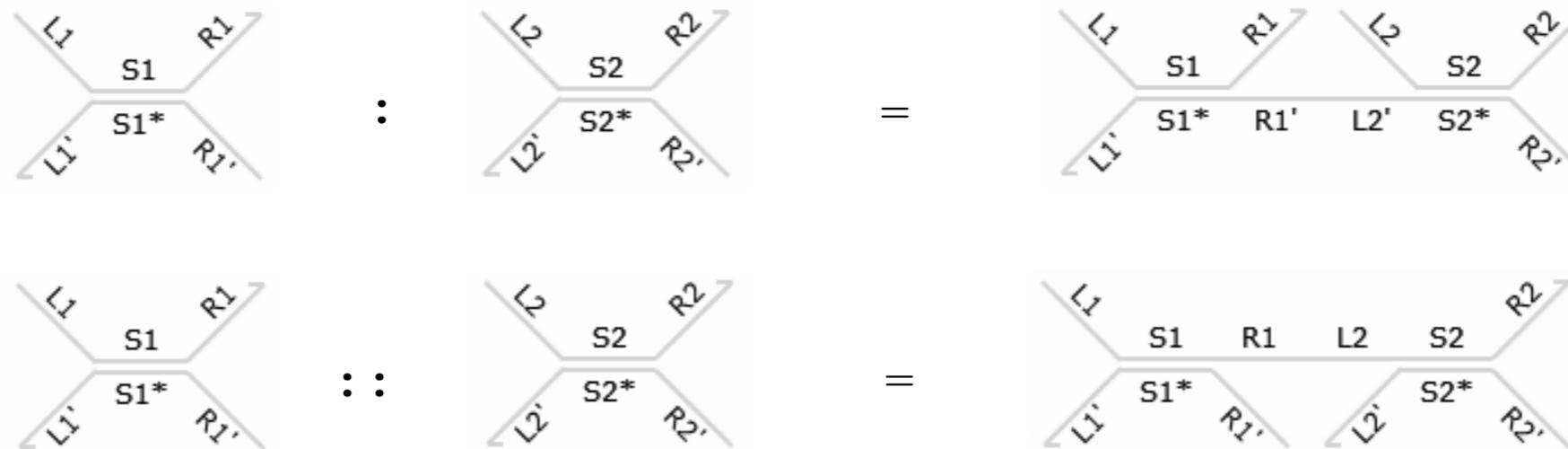
Lower strand

Segment::=



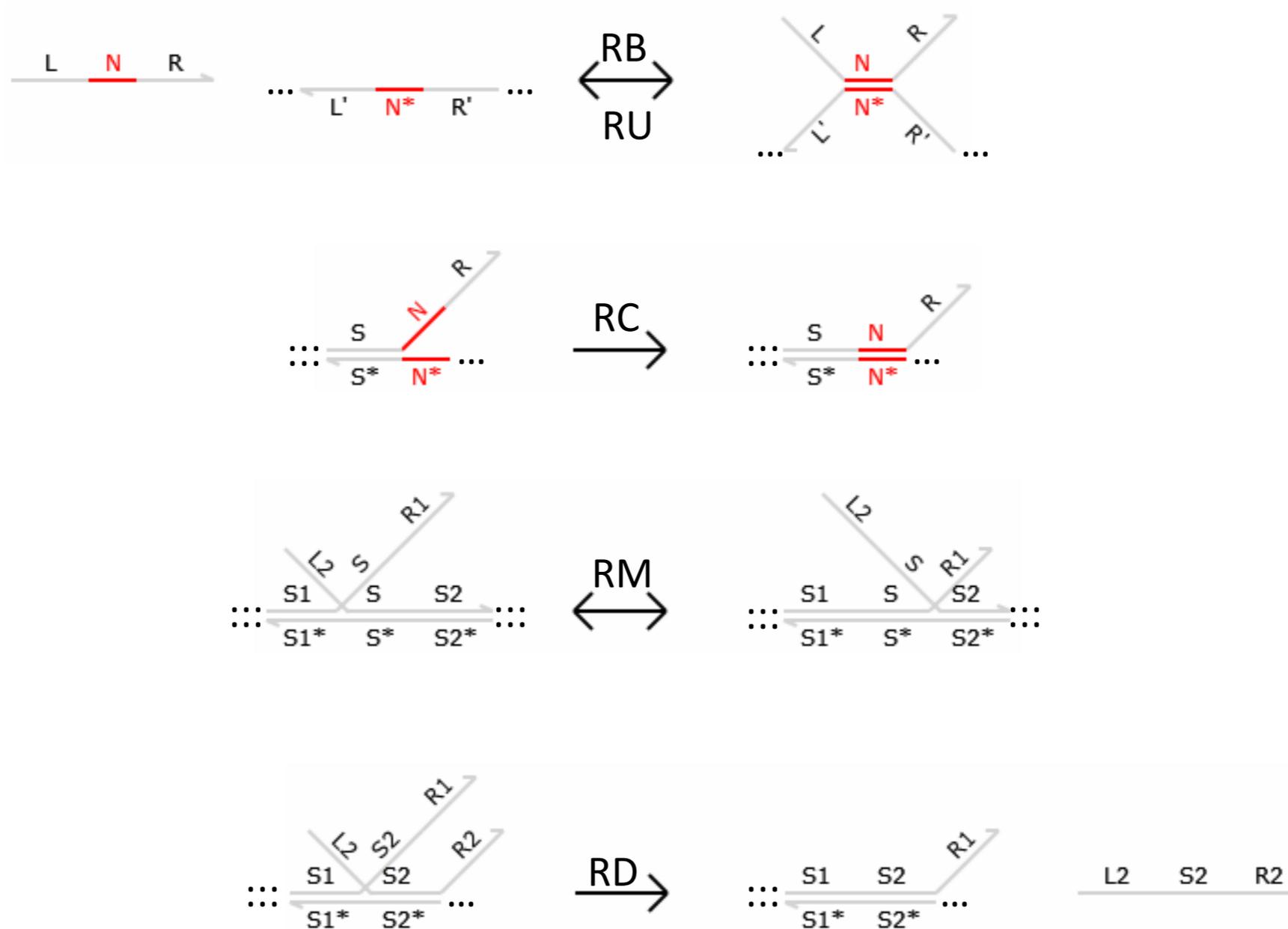
Double stranded complex with overhangs

Segment concatenation



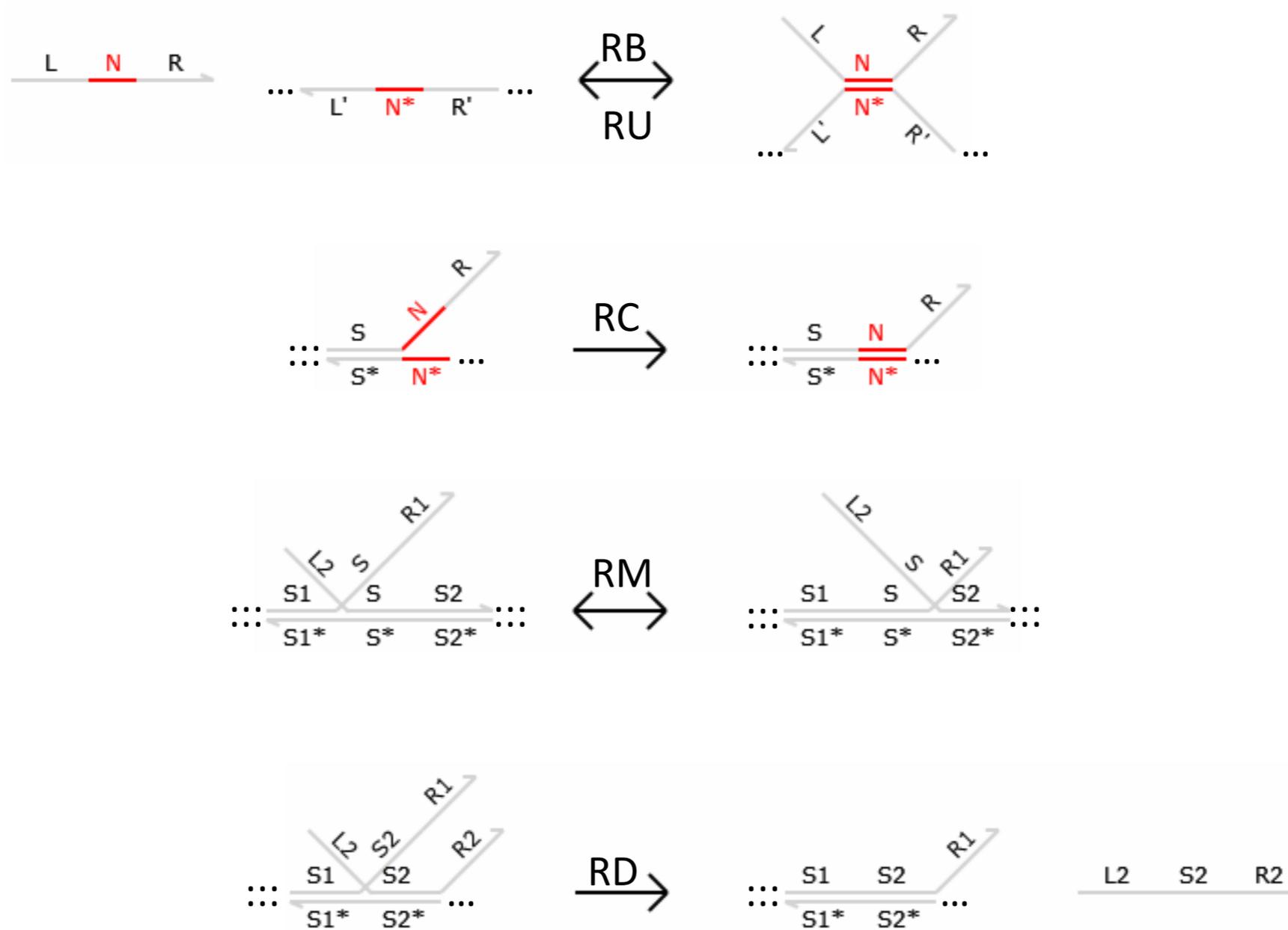
Slide credit: Andrew Phillips (MSR)

visual DSD: Syntax of strands and complexes



Slide credit: Andrew Phillips (MSR)

visual DSD: Reduction rules



Slide credit: Andrew Phillips (MSR)