

*Theory* & *Practice*  
of DNA strand displacement circuits

*October 8, 2018 @ DNA 24*

Chris Thachuk  
Winfree Lab, California Institute of Technology

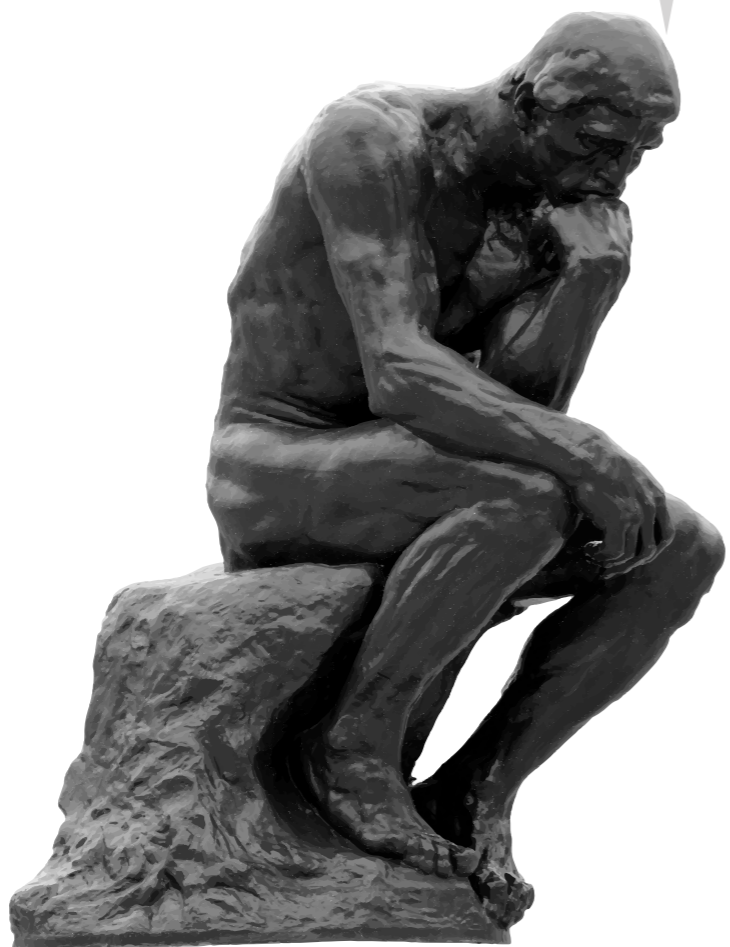
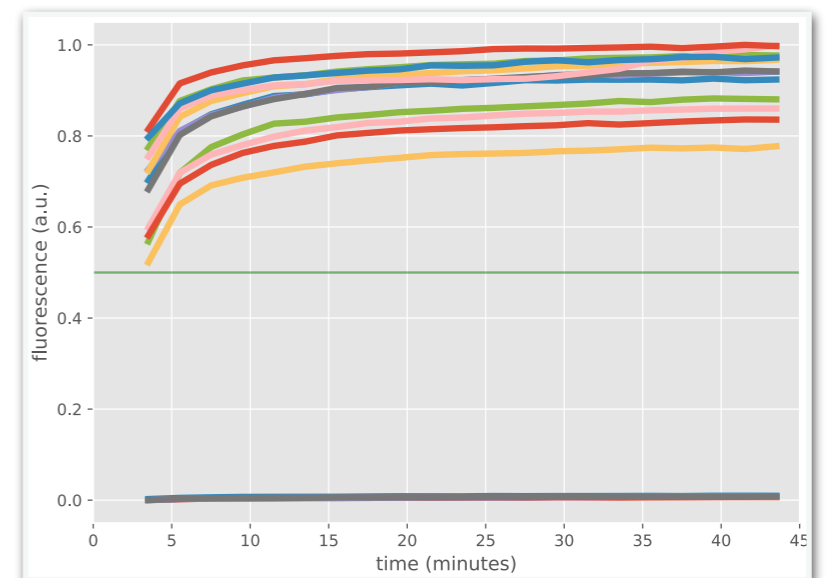
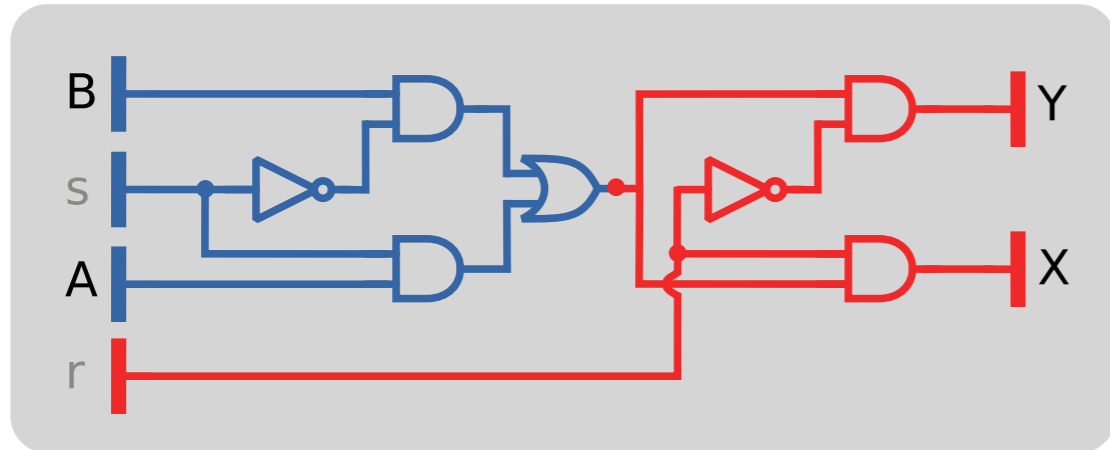


**Molecular Programming Coat of Arms**





# Today's tutorial in a nutshell



# Molecular Circuits

Built upon DNA strand displacement cascades

## Input

5'–ACCACGATCACATTAC–3'

5'–GCAACATACAT–3'

5'–CCCATACATCACCAG–3'

5'–TACCACATGAGCAGCA–3'

## Computation

DNA strand displacement cascades

## Output

5'–GAGCTACATCAC–3'

5'–TAAATCATGATCAG–3'

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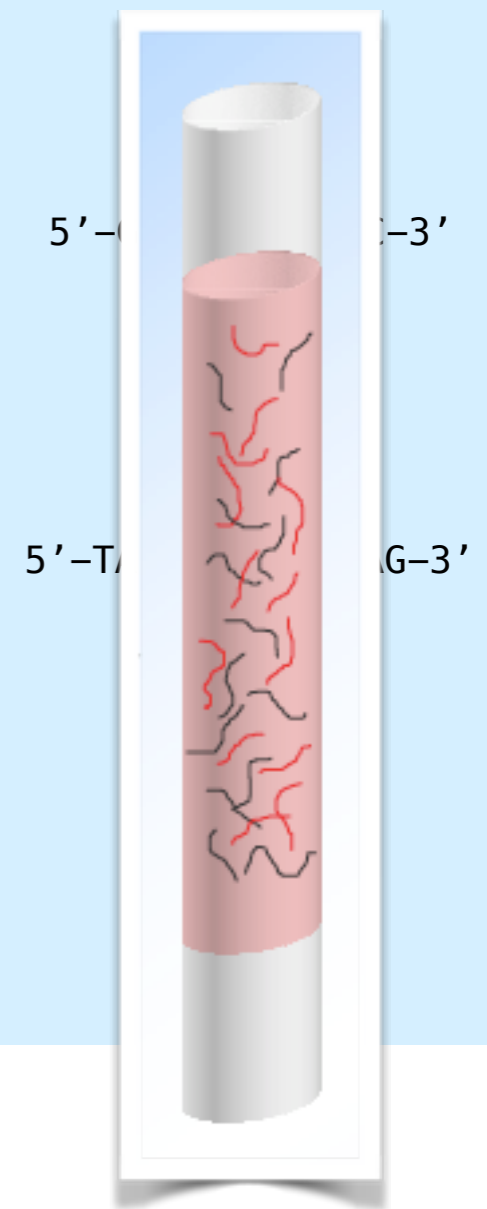
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DNA strand displacement cascades

## Output

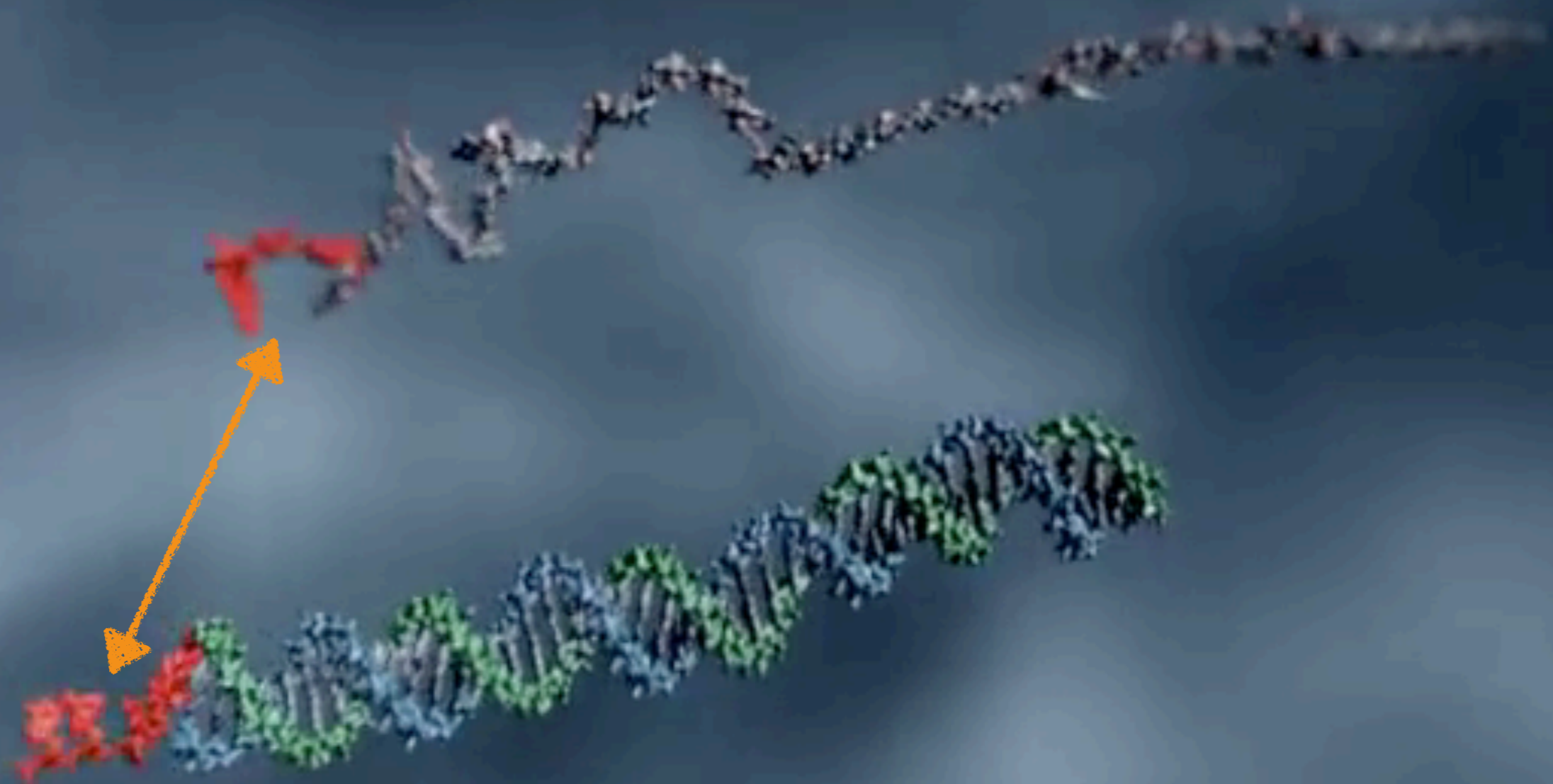




# Tutorial Outline

- ▶ **Review of strand displacement**
- ▶ Building and composing logic gates
- ▶ Tools for designing and verifying circuits
- ▶ Robustness of strand displacement

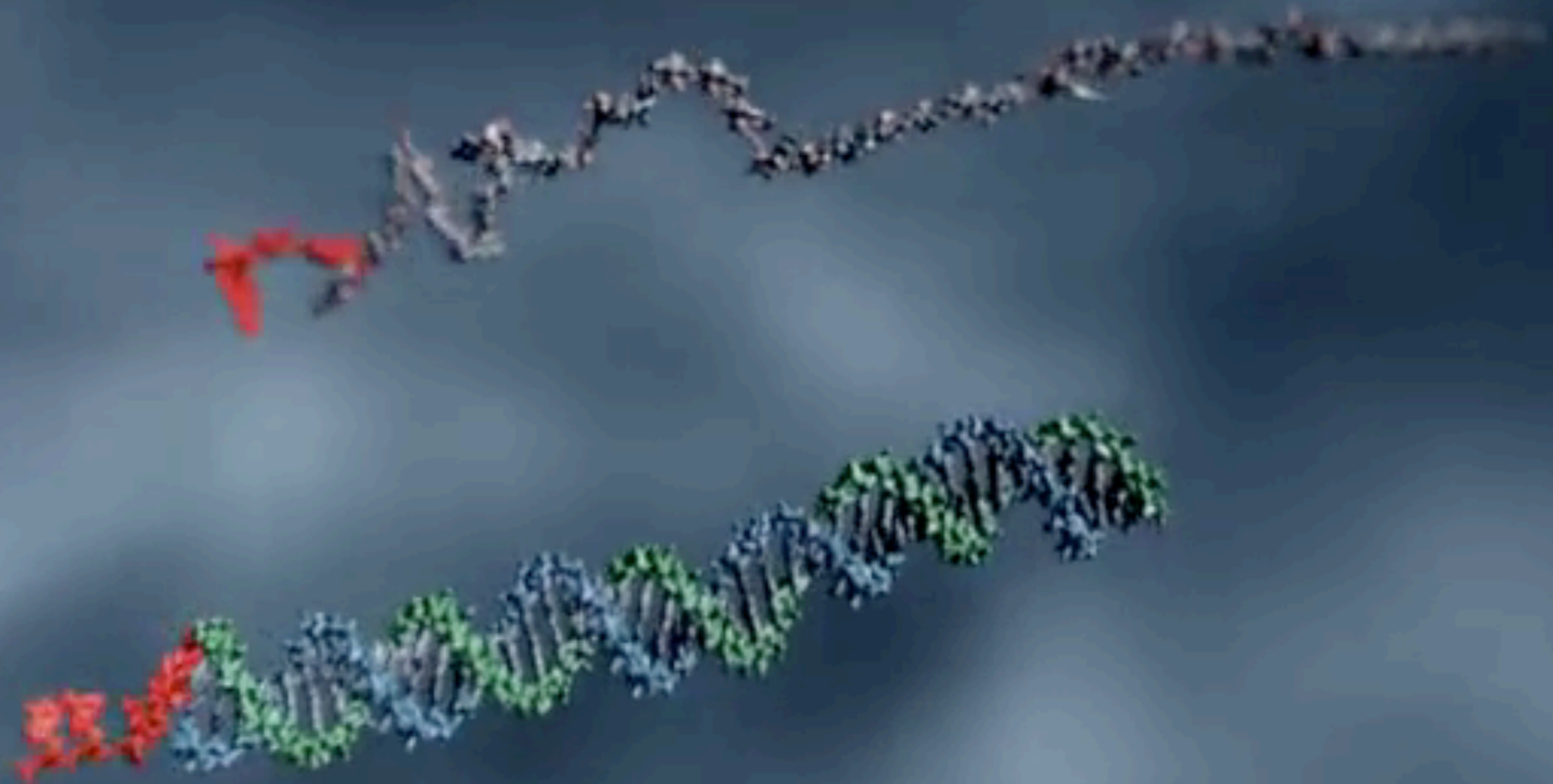
# Review of DNA Strand Displacement (DSD)



B. Yurke, A. J. Turberfield, A. P. Mills Jr., F. C. Simmel, J. L. Neumann, *Nature* 406, 605 (2000).

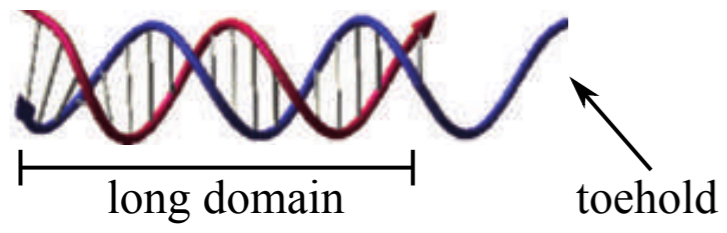
A. J. Turberfield et al., *Phys. Rev. Lett.* 90, 118102

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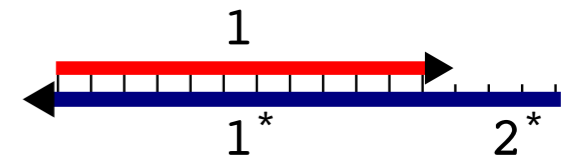


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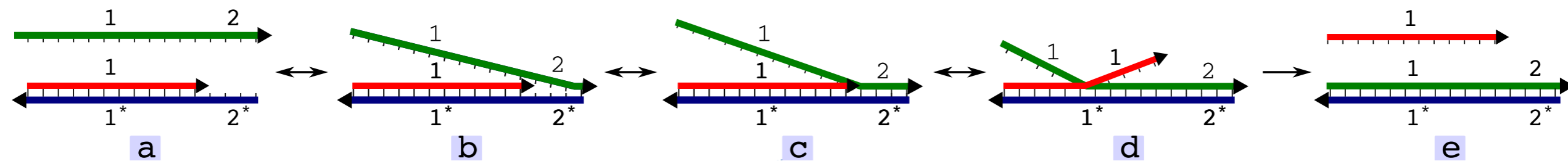


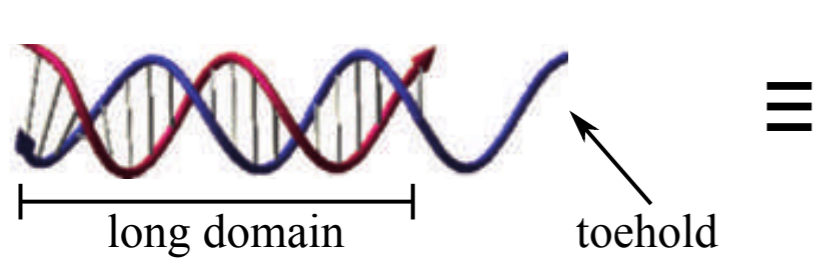
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Adapted from Zhang & Seelig 2011

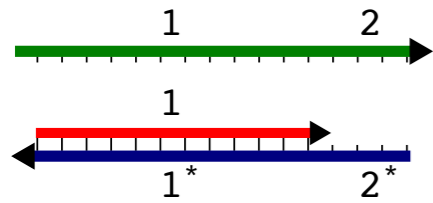
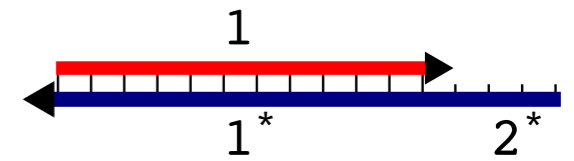


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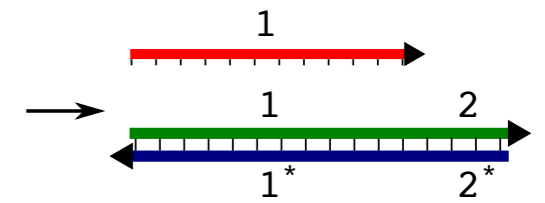




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a



e

# Strand Displacement Cascades

=

## Three Rules



# Domain level rules for DSD

## Rule 1: *Bind*

### Example

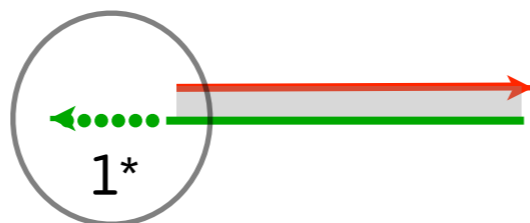
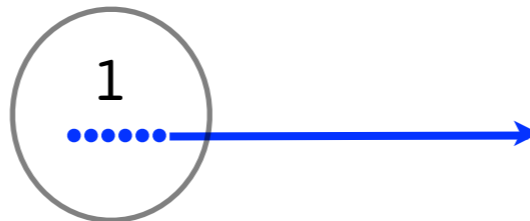




# Domain level rules for DSD

## Rule 1: *Bind*

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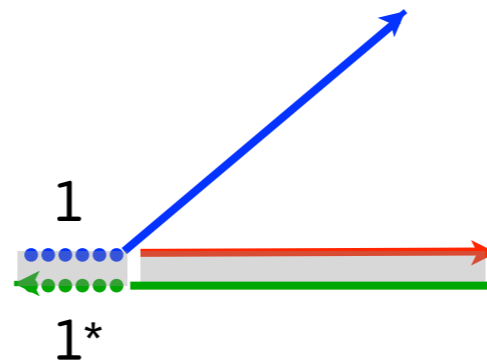


single-stranded  
complementary  
domains

# Domain level rules for DSD

## Rule 1: *Bind*

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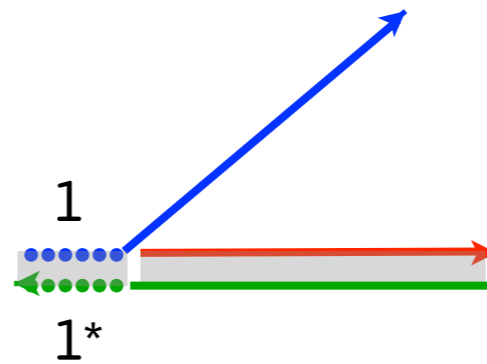


# Domain level rules for DSD

## Rule 1: *Bind*

Two single-stranded complementary domains can bind

Example



# Domain level rules for DSD

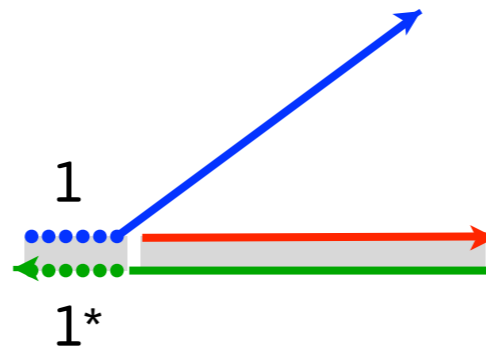
## Rule 2: *Release*

Example

# Domain level rules for DSD

## Rule 2: *Release*

### Example

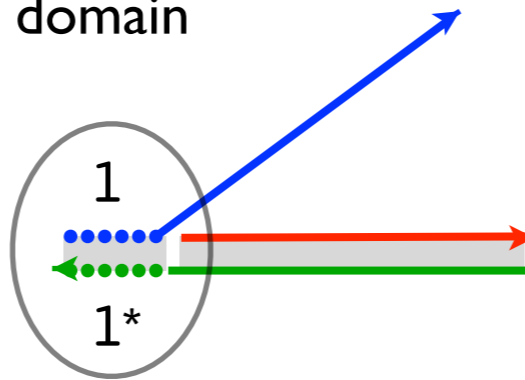


# Domain level rules for DSD

## Rule 2: *Release*

### Example

blue strand bound by only  
a short domain



# Domain level rules for DSD

## Rule 2: *Release*

### Example



# Domain level rules for DSD

## Rule 2: *Release*

Any strand bound by only a short domain can **release**

### Example

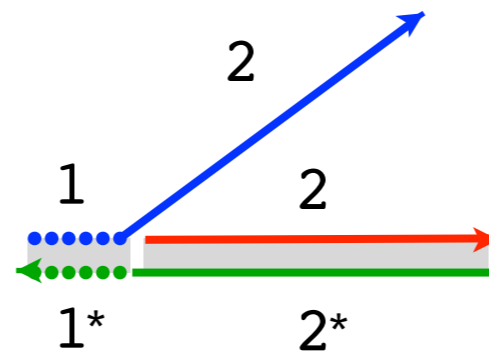




# Domain level rules for DSD

## Rule 3: *Displace*

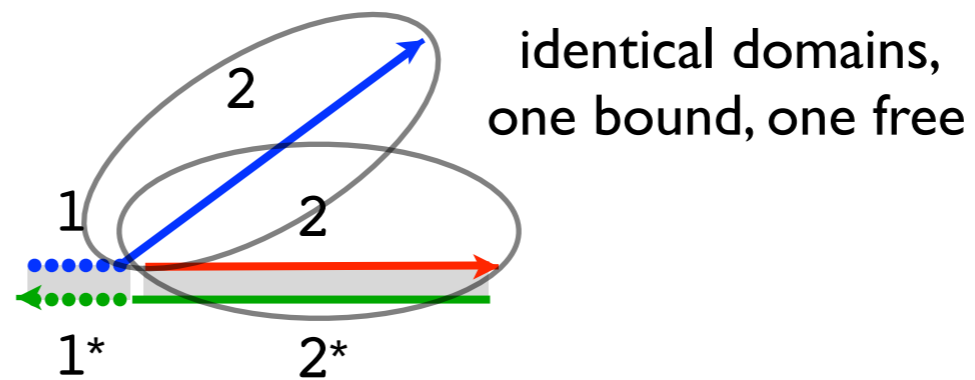
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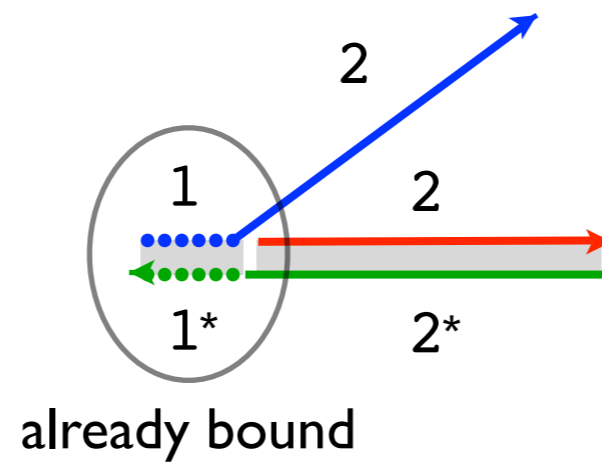
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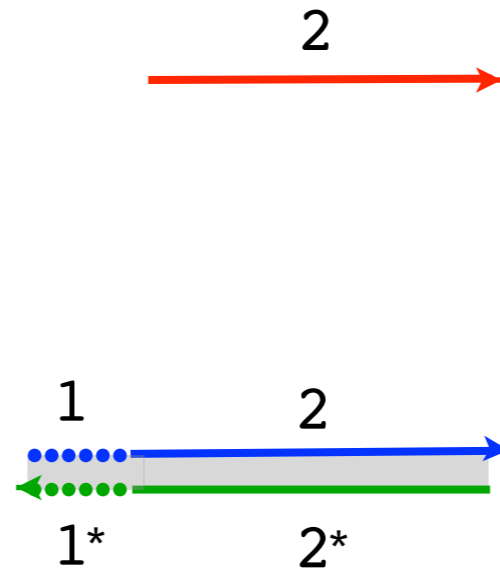
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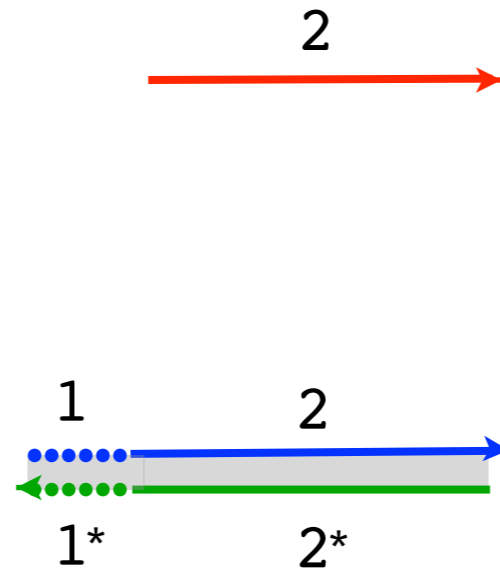


# Domain level rules for DSD

## Rule 3: *Displace*

A domain can **displace** an identical domain of another strand, if neighboring domains are already bound

### Example



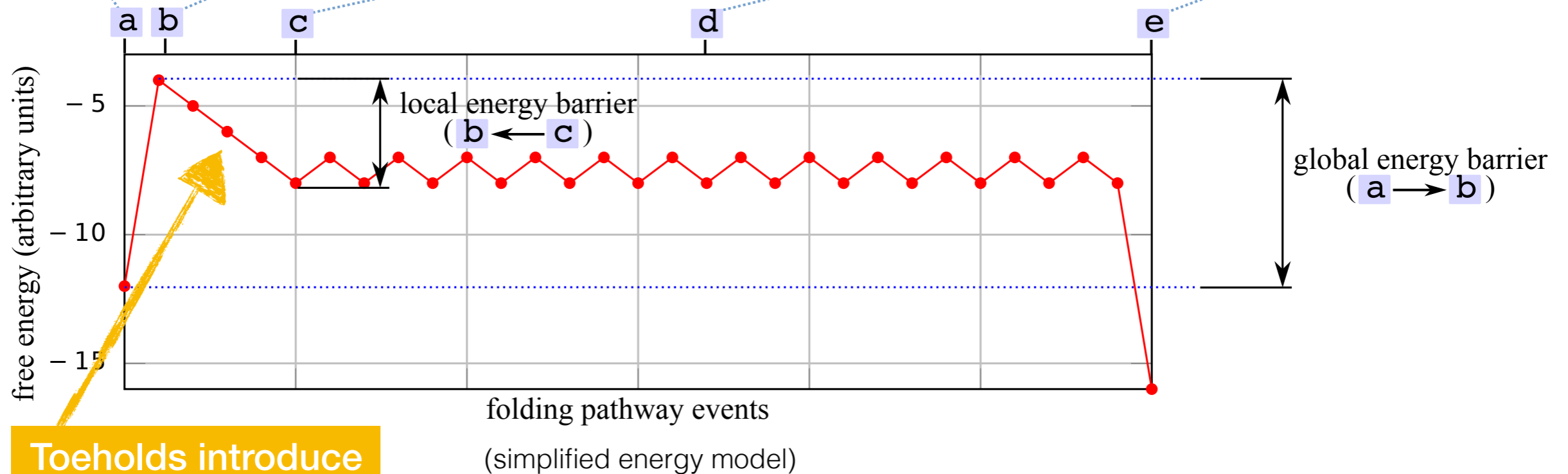
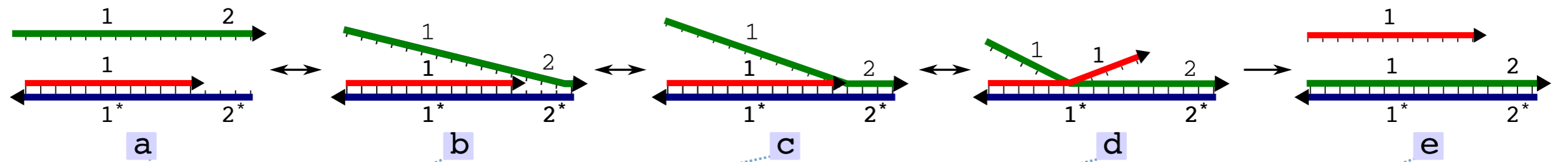
# Why do we use toeholds?



Adapted from Zhang & Seelig 2011

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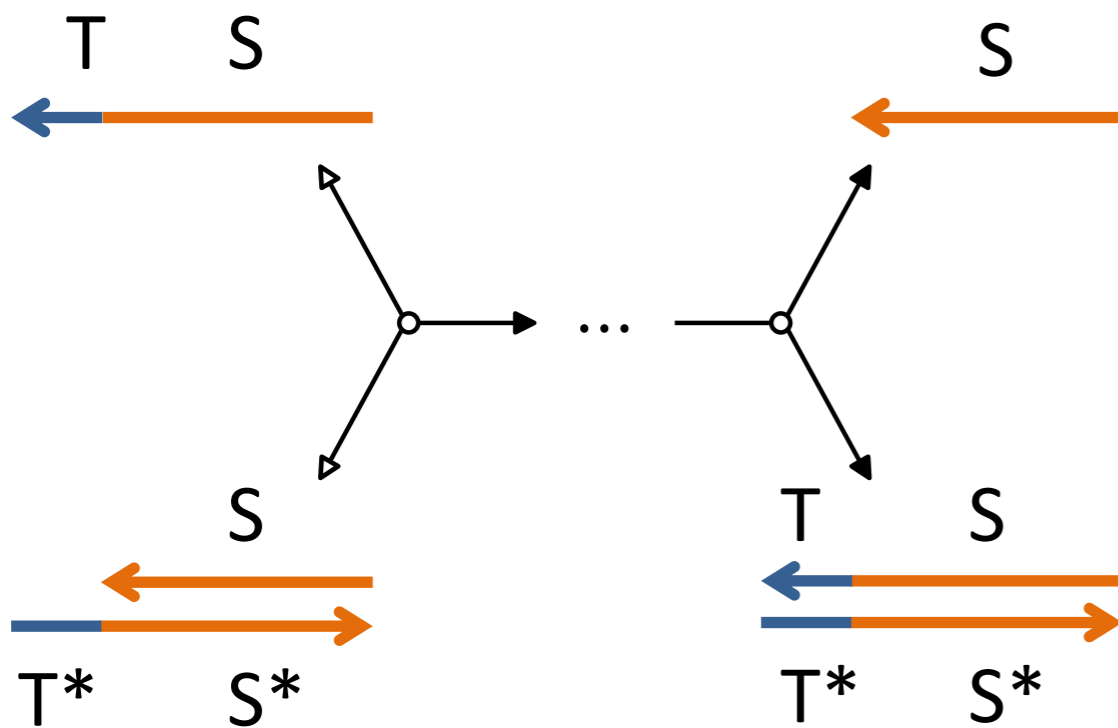
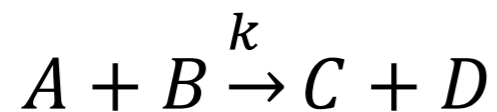


**Toeholds introduce energy barriers**

# Toehold-mediated DNA strand displacement

T: toehold domain (typically 3-7 nucleotides)

S: branch migration domain (typically 15-20 nucleotides)



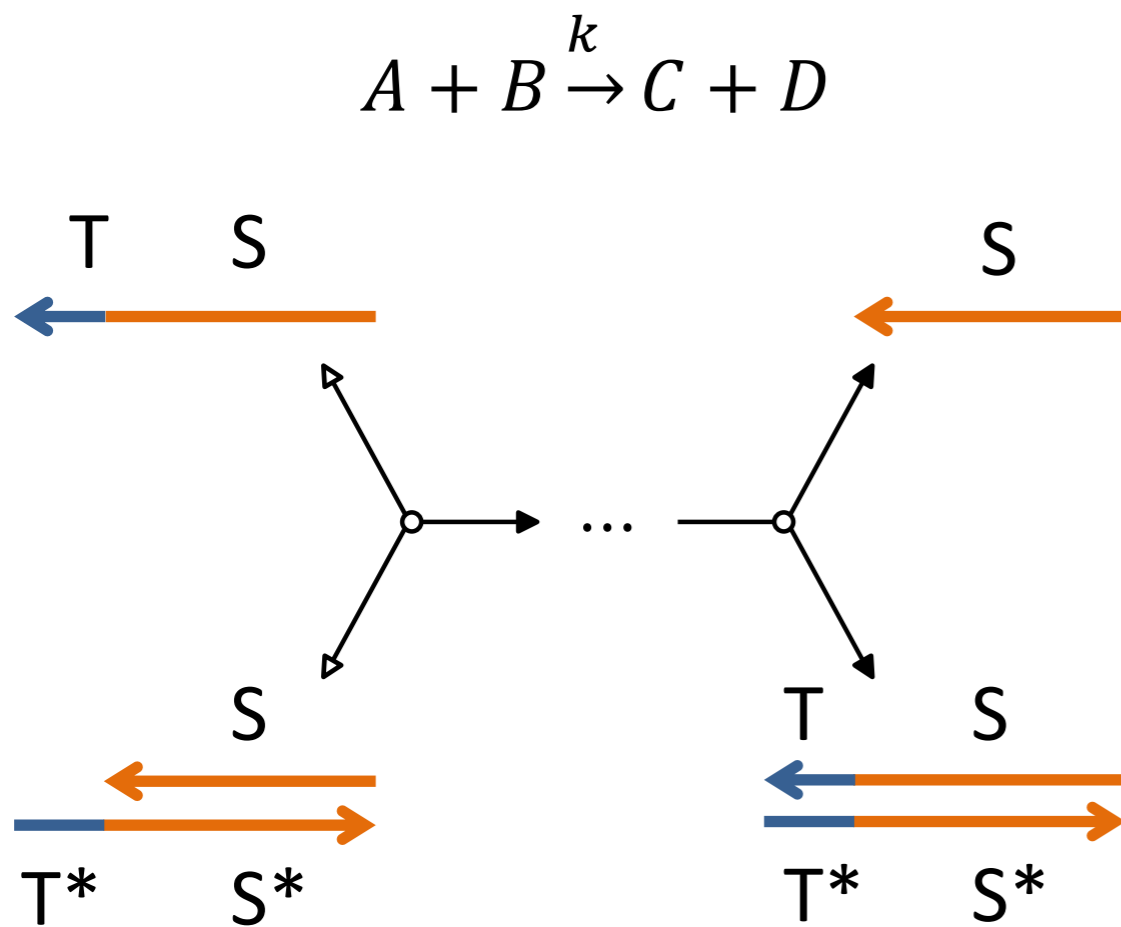
The rate of strand displacement grows exponentially with toehold length for short toeholds.



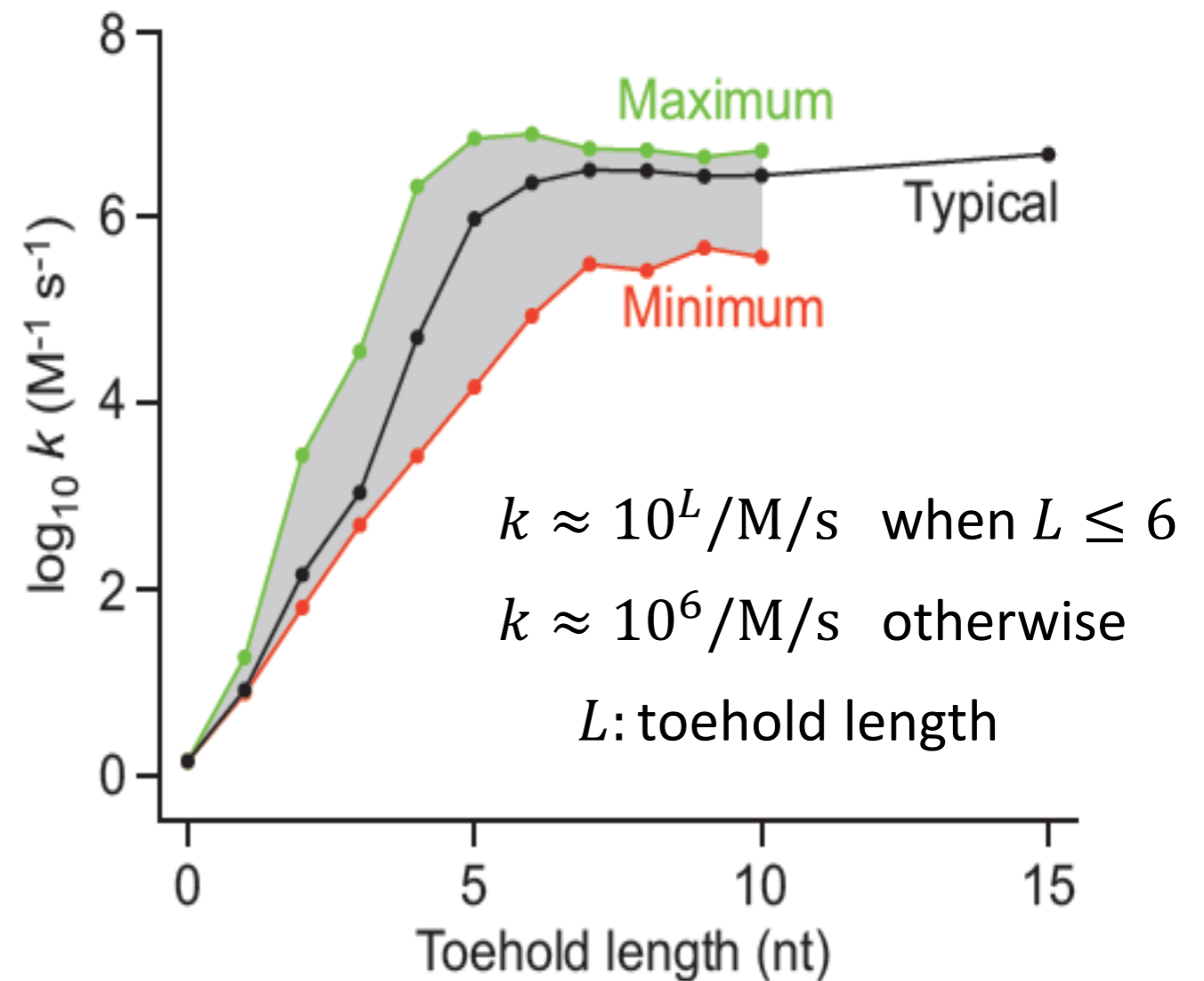
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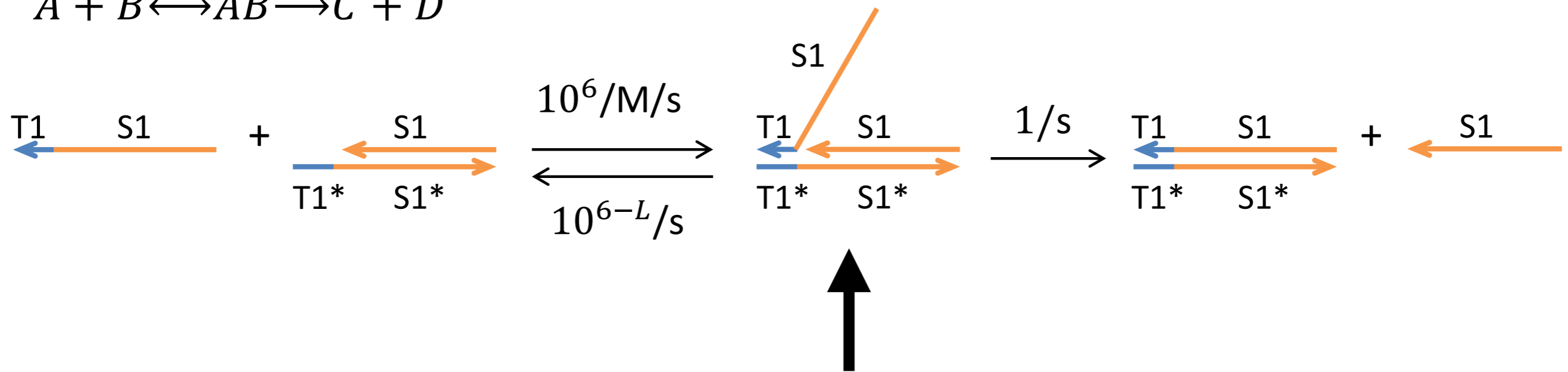


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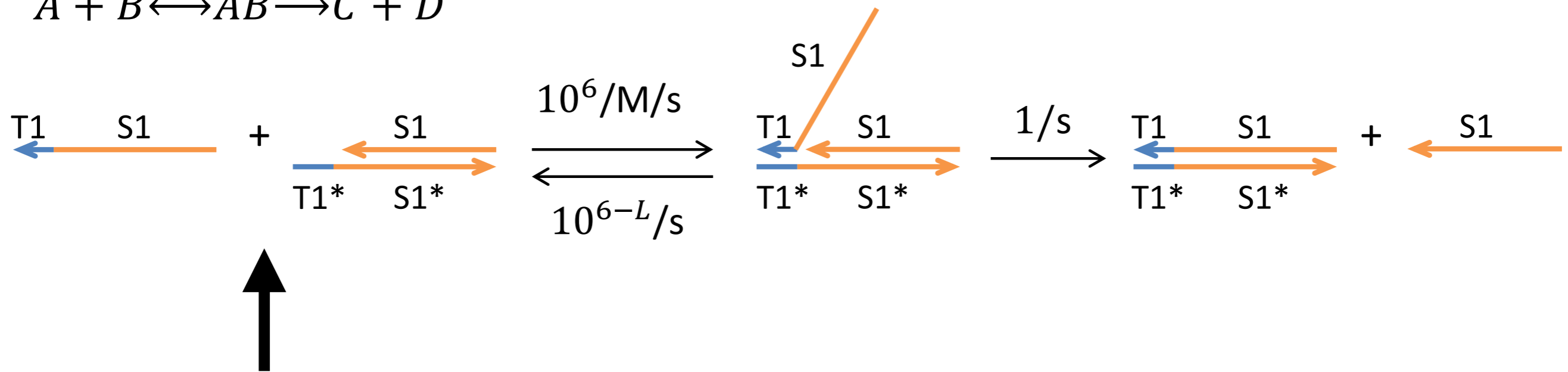


Zhang and Seelig, *Nature Chemistry* 2011

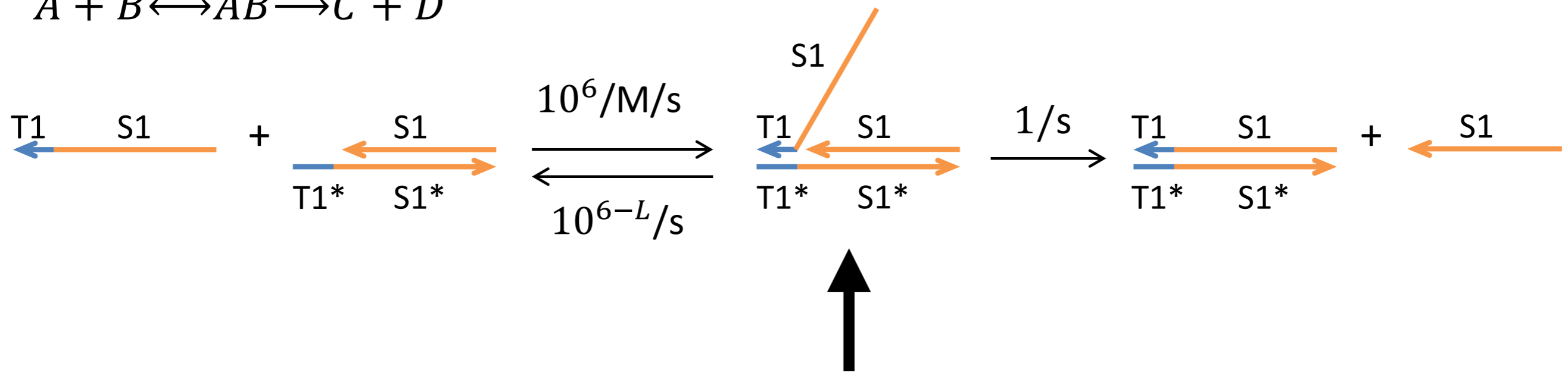
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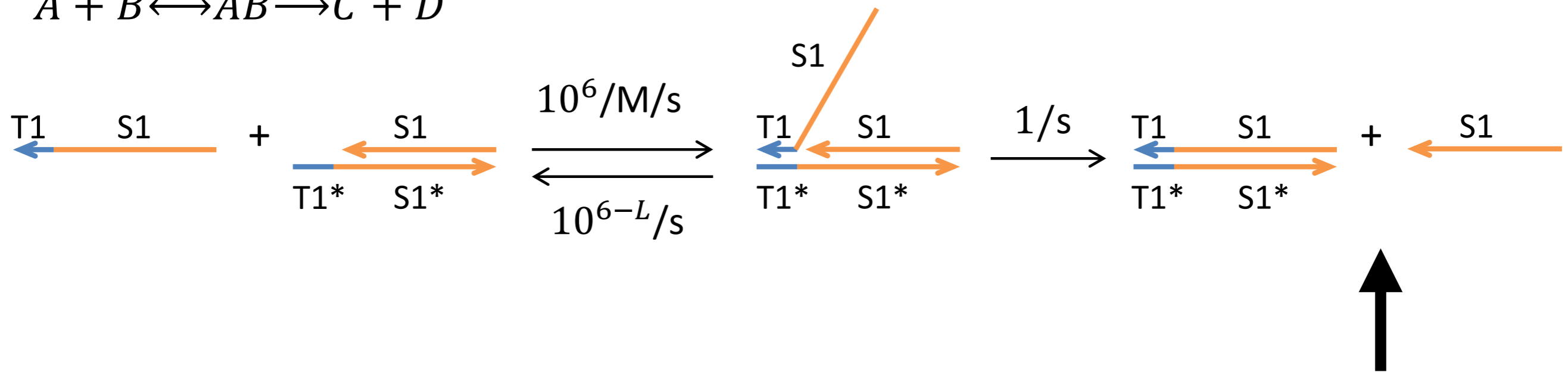
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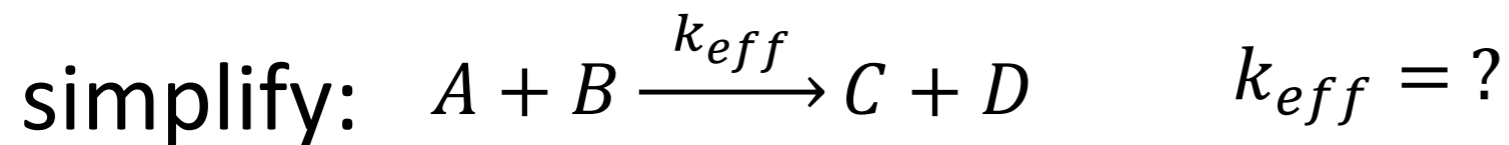
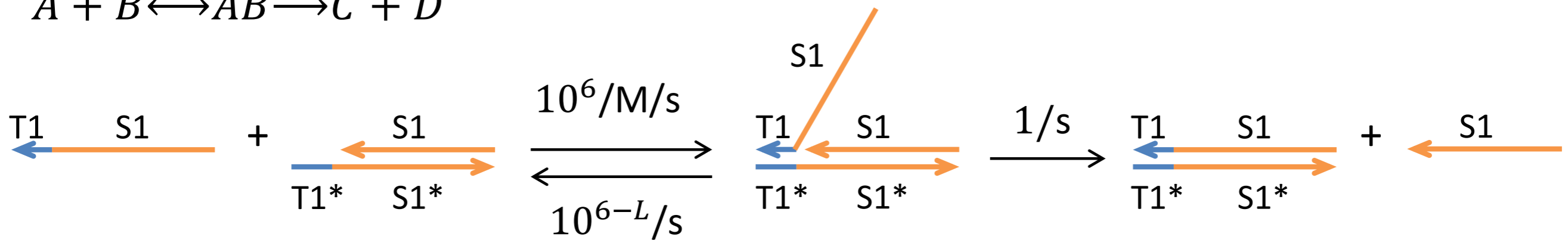
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collision rate:  $10^6[A][B]$

collision success probability:  $\frac{1/s}{1/s + 10^{6-L}/s}$

net rate of success:  $10^6 \cdot \frac{1}{1 + 10^{6-L}} [A][B]$   
 $k_{eff}$

$k_{eff} \approx 10^L/M/s$  when  $L \leq 6$   
 otherwise  $k_{eff} \approx 10^6/M/s$

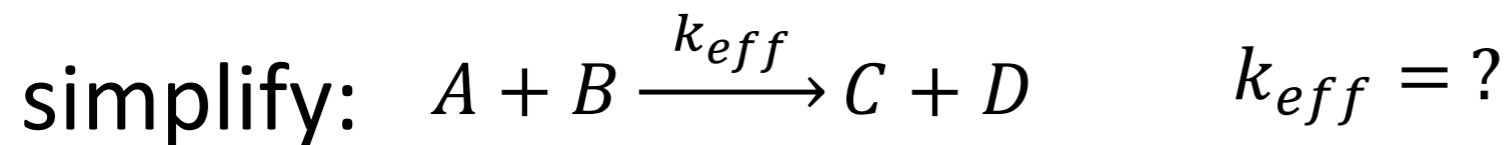
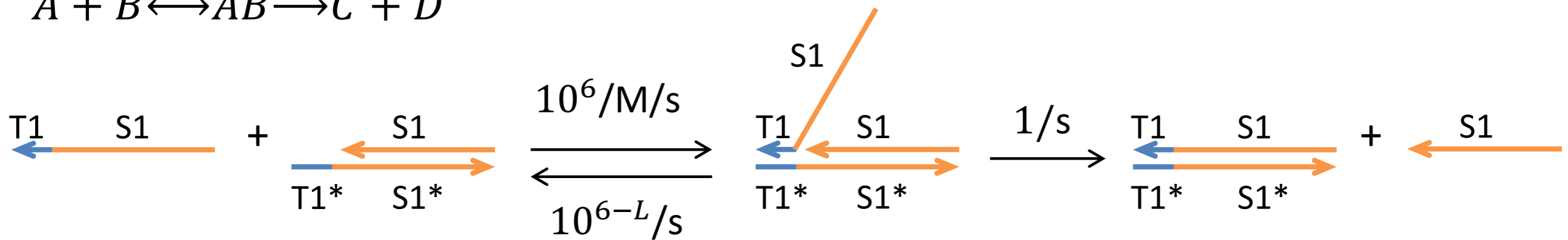
$L$ : toehold length  $|T1|$

Zhang et al, *JACS* 2009

Srinivas et al, *NAR* 2013

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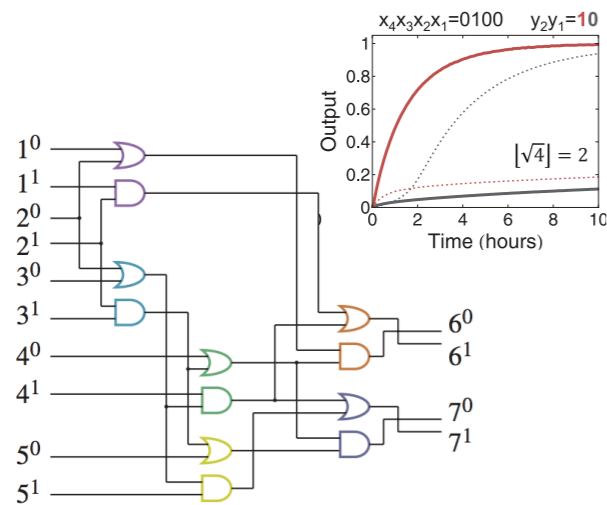
# Strand displacement in the lab





# Strand displacement in the lab

## molecular logic circuits



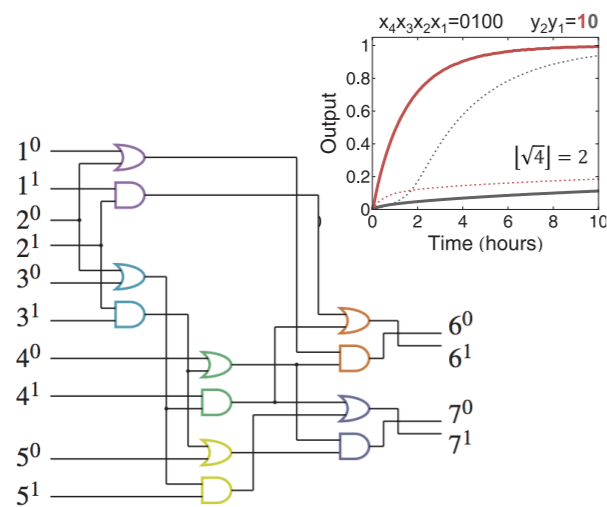
- Large autonomous biochemical networks built from scratch

Qian, Winfree, *Science* 2011



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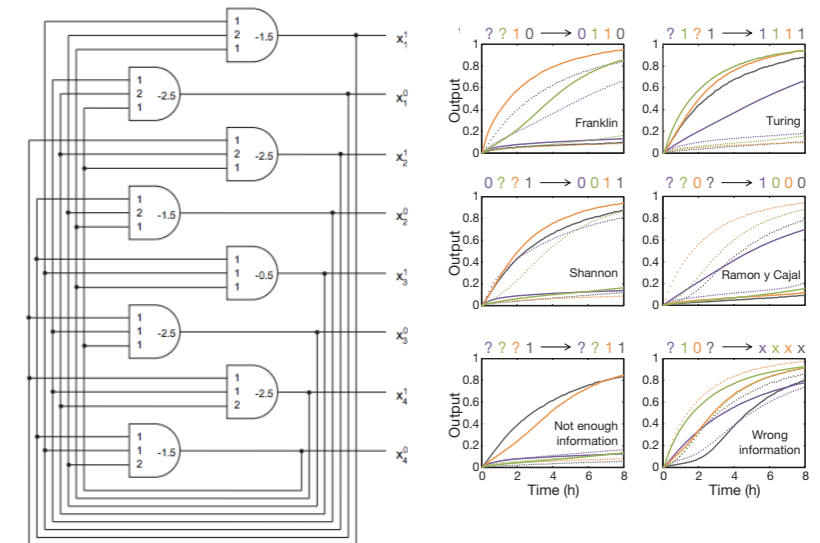


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## molecular artificial neural networks

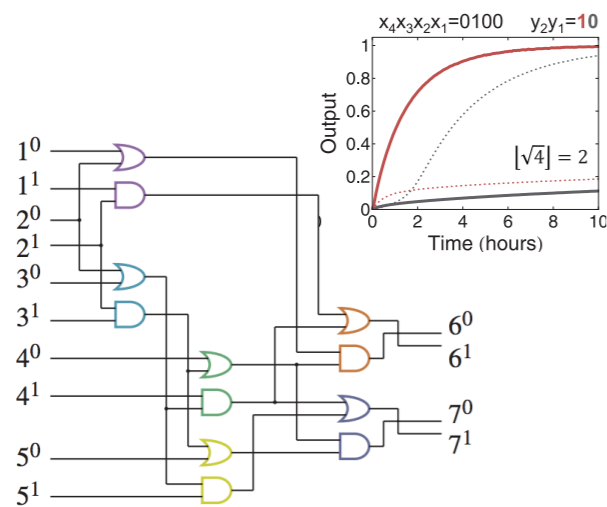


- Biochemical system doing inference

Qian, Winfree, Bruck *Nature* 2011

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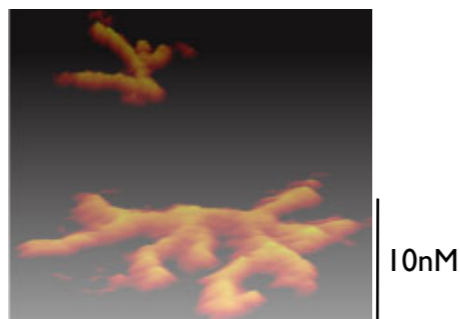
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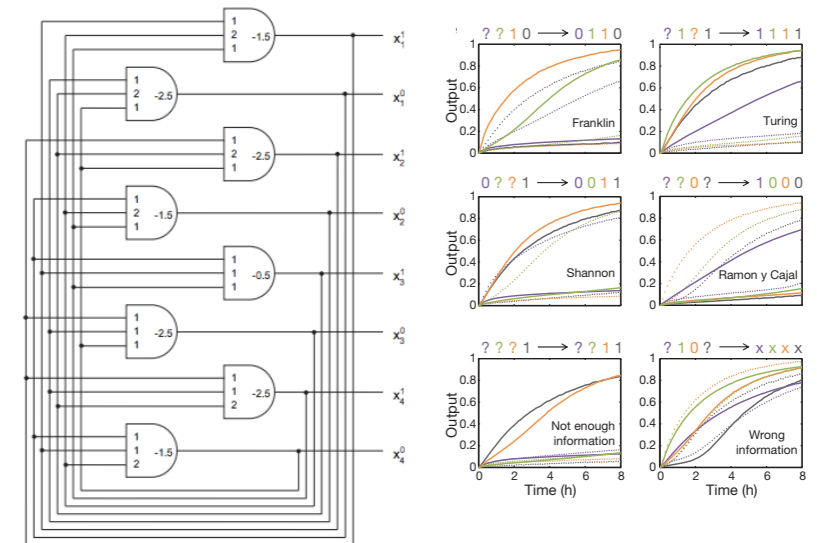
## controlling assembly of nanoscale structures



- Prescribed nanoscale structures seen under atomic force microscope

Yin, Choi, Calvert, Yurke, Pierce *Nature* 2008

## molecular artificial neural networks



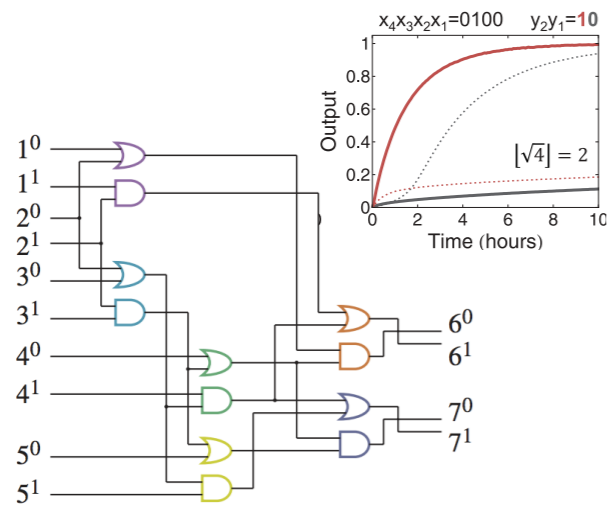
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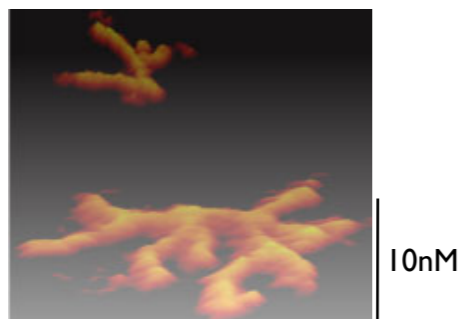
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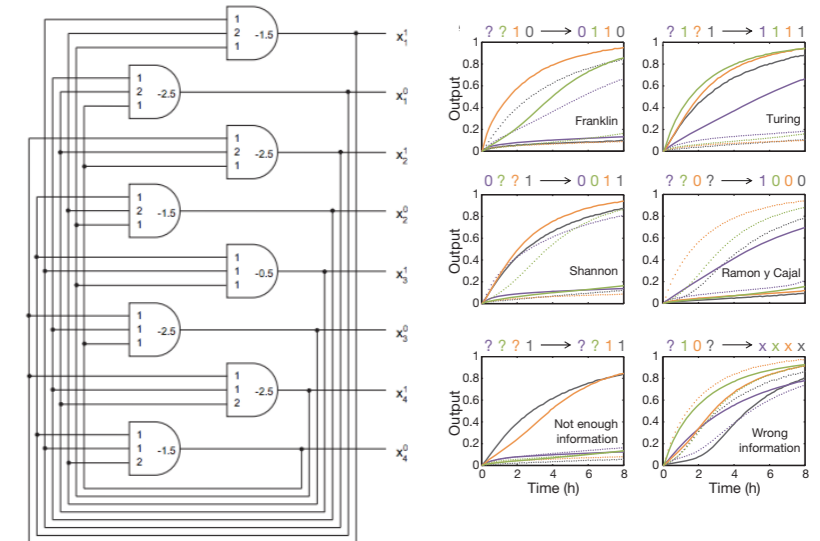


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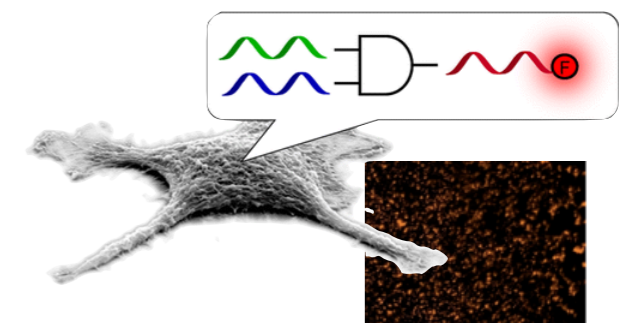
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## strand displacement in vivo

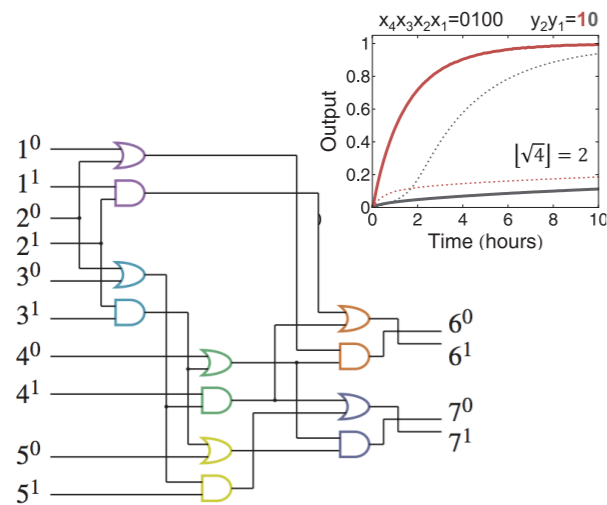


- Logic on biological signals

Hemphill, Deiters *J Am Chem Soc* 2013

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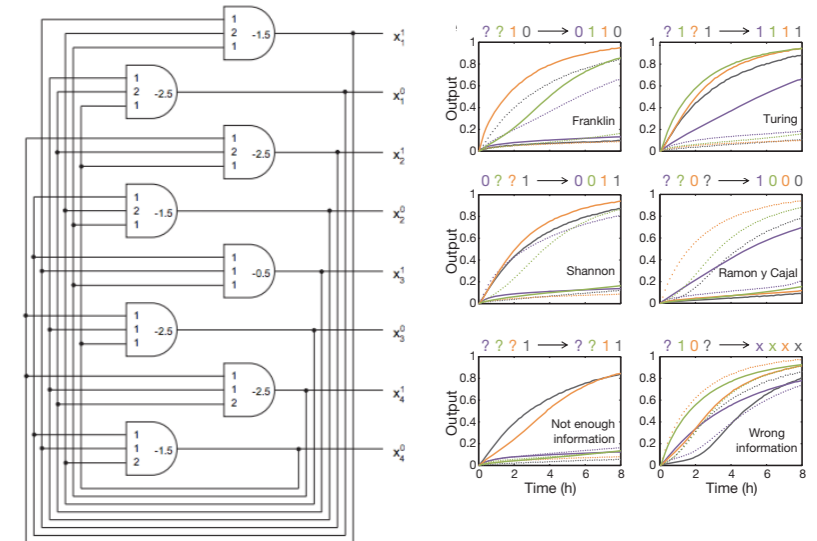
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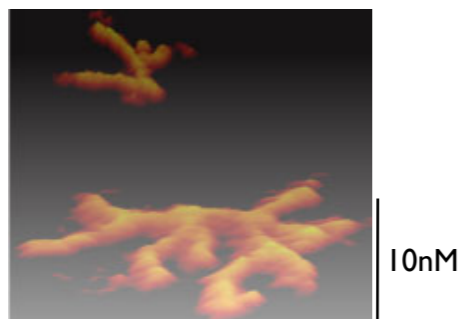
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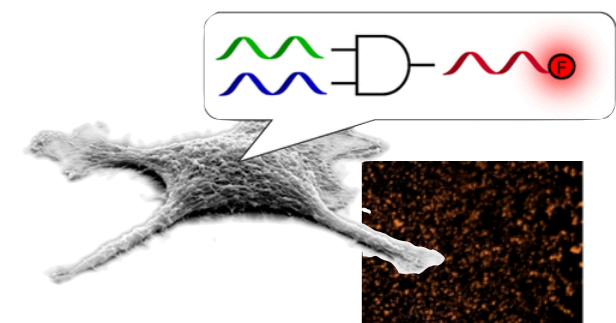
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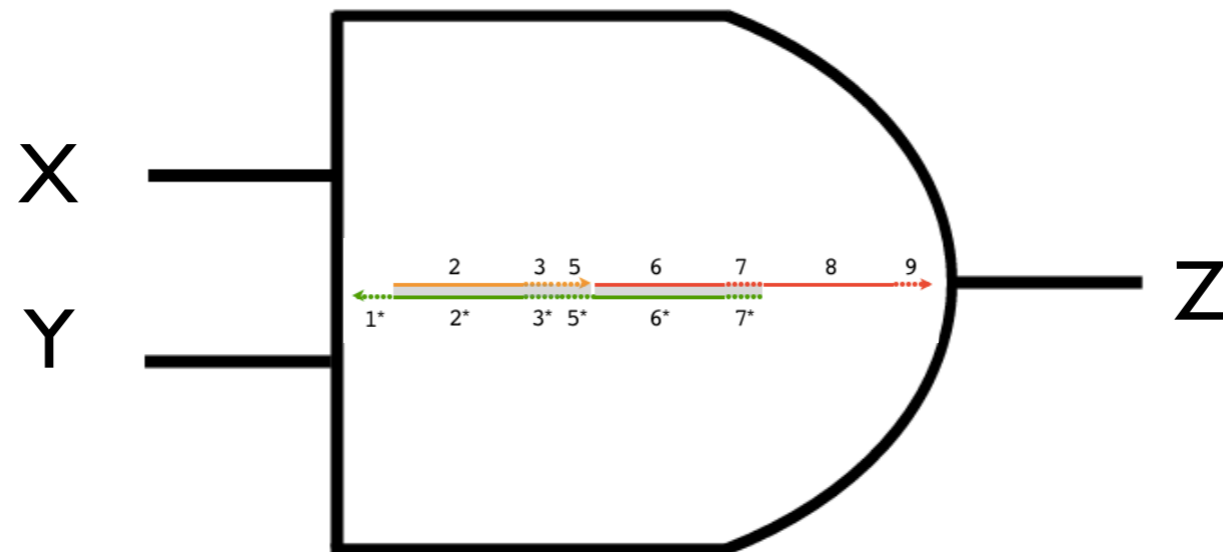
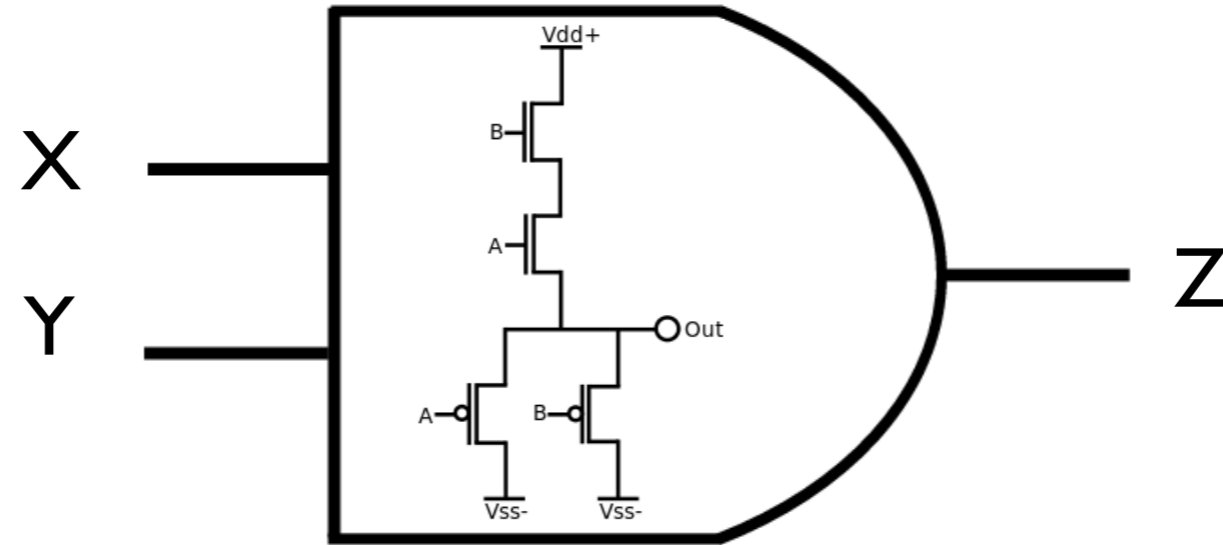


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# AND gate

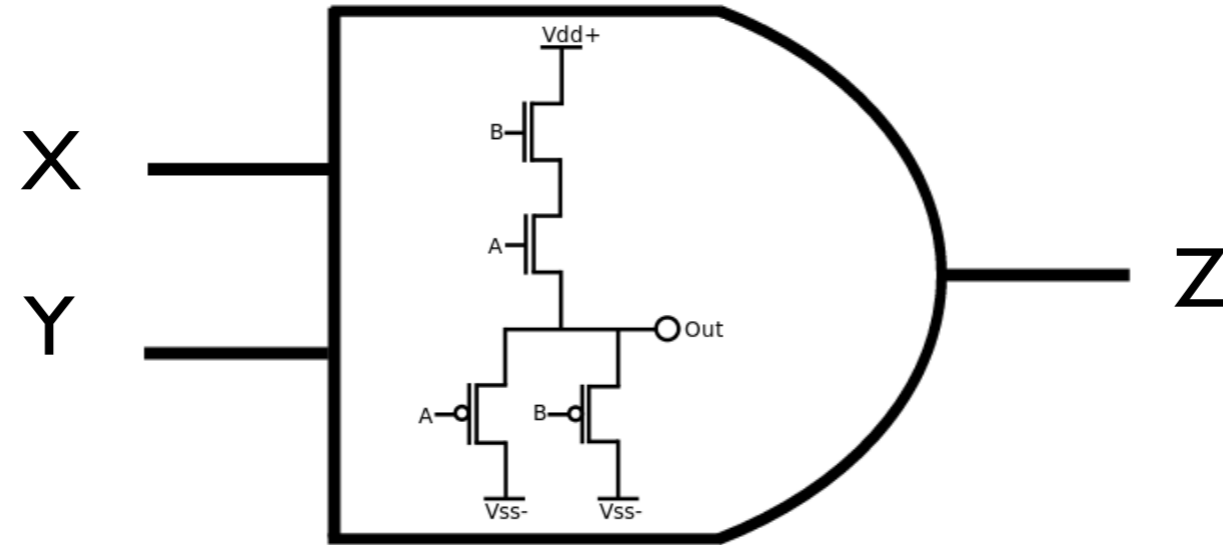
release Z if and only if X and Y are present



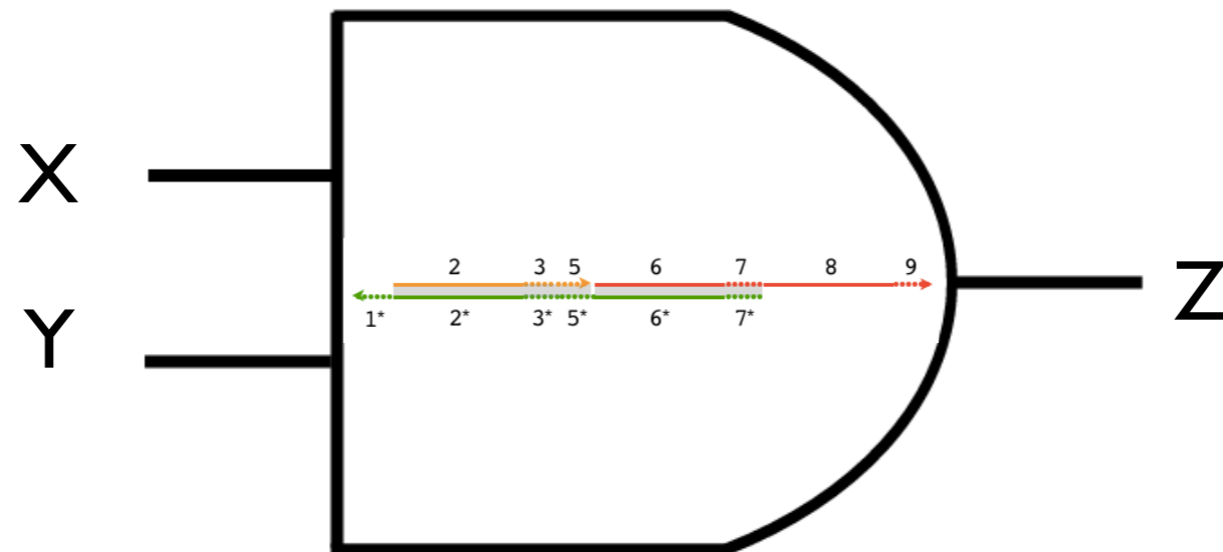
# AND gate

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voltages



strands



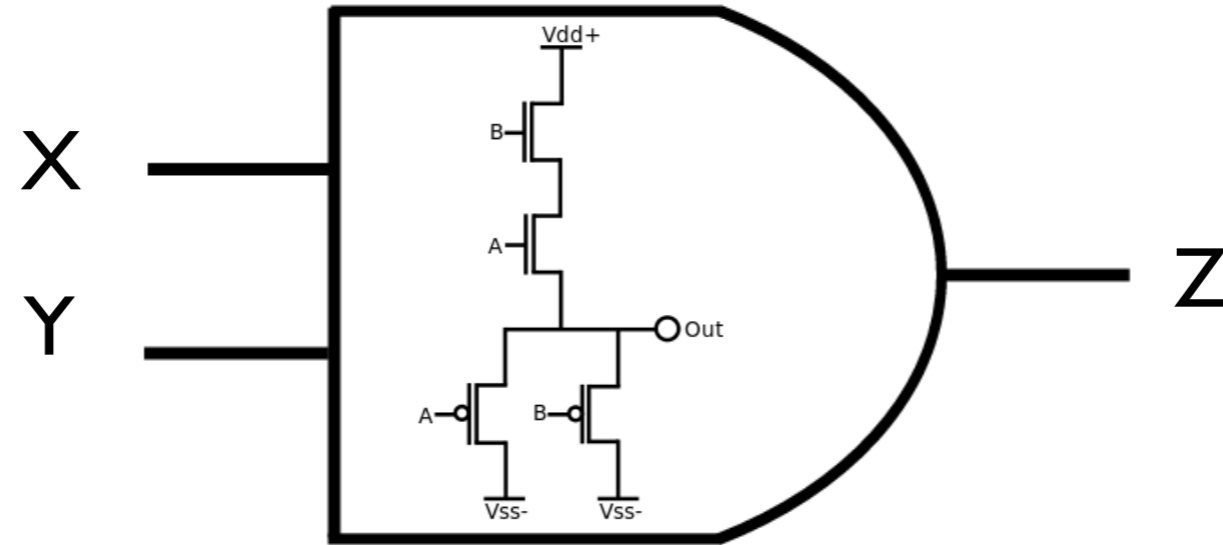
gate=complex



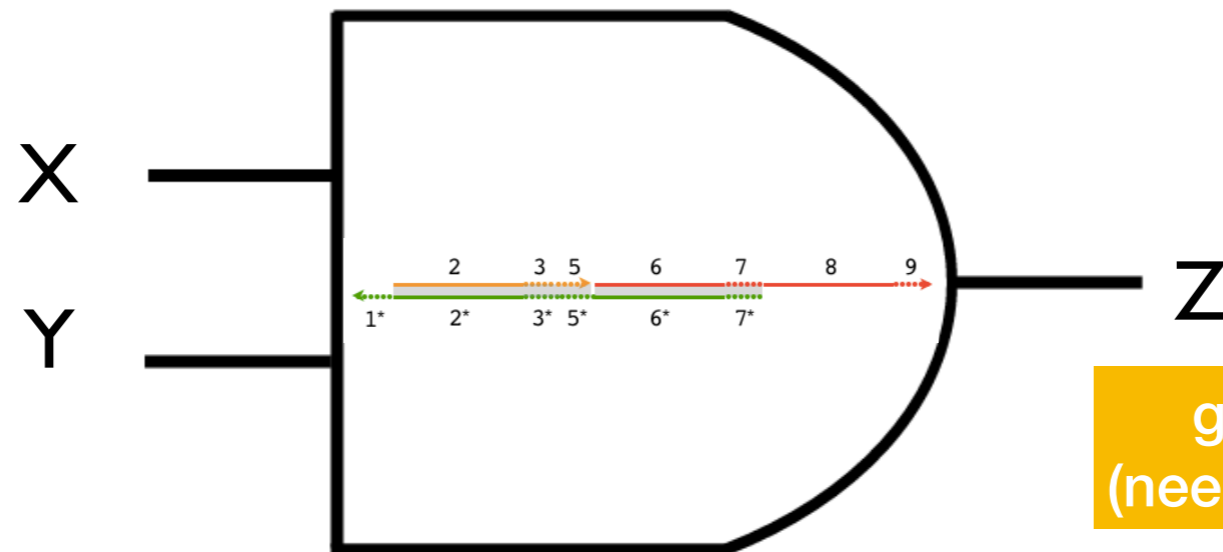
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strands

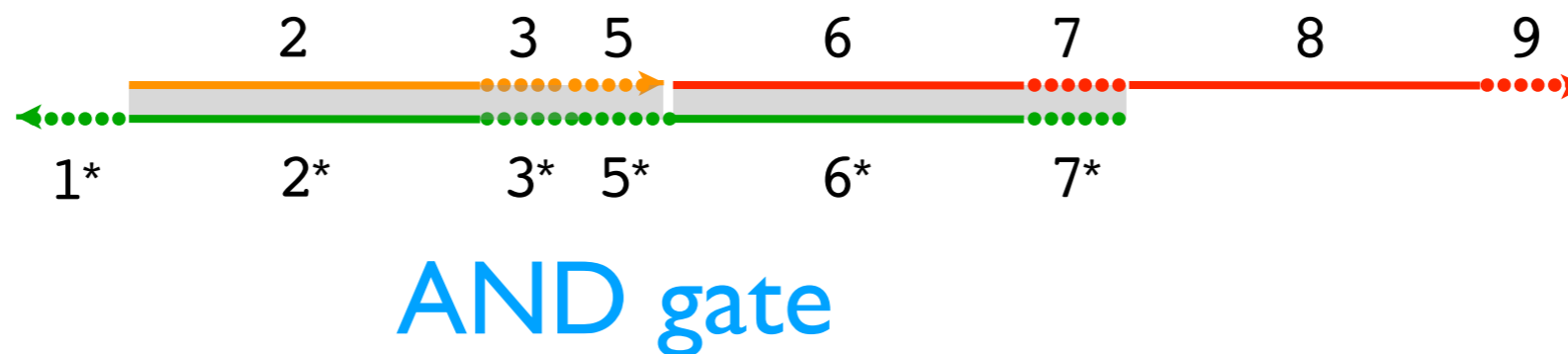
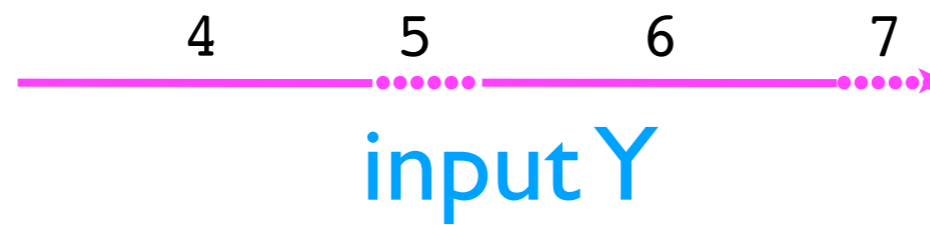
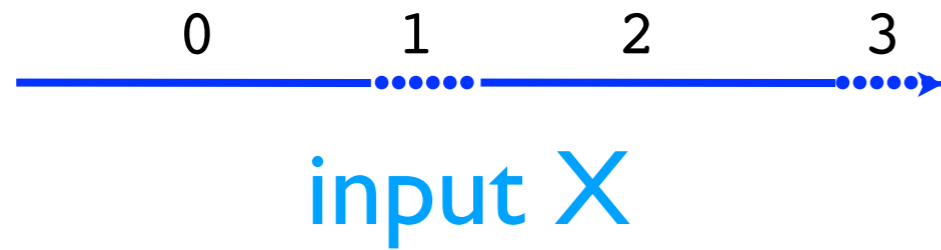


gates get consumed!  
(need to have many copies)

gate=complex

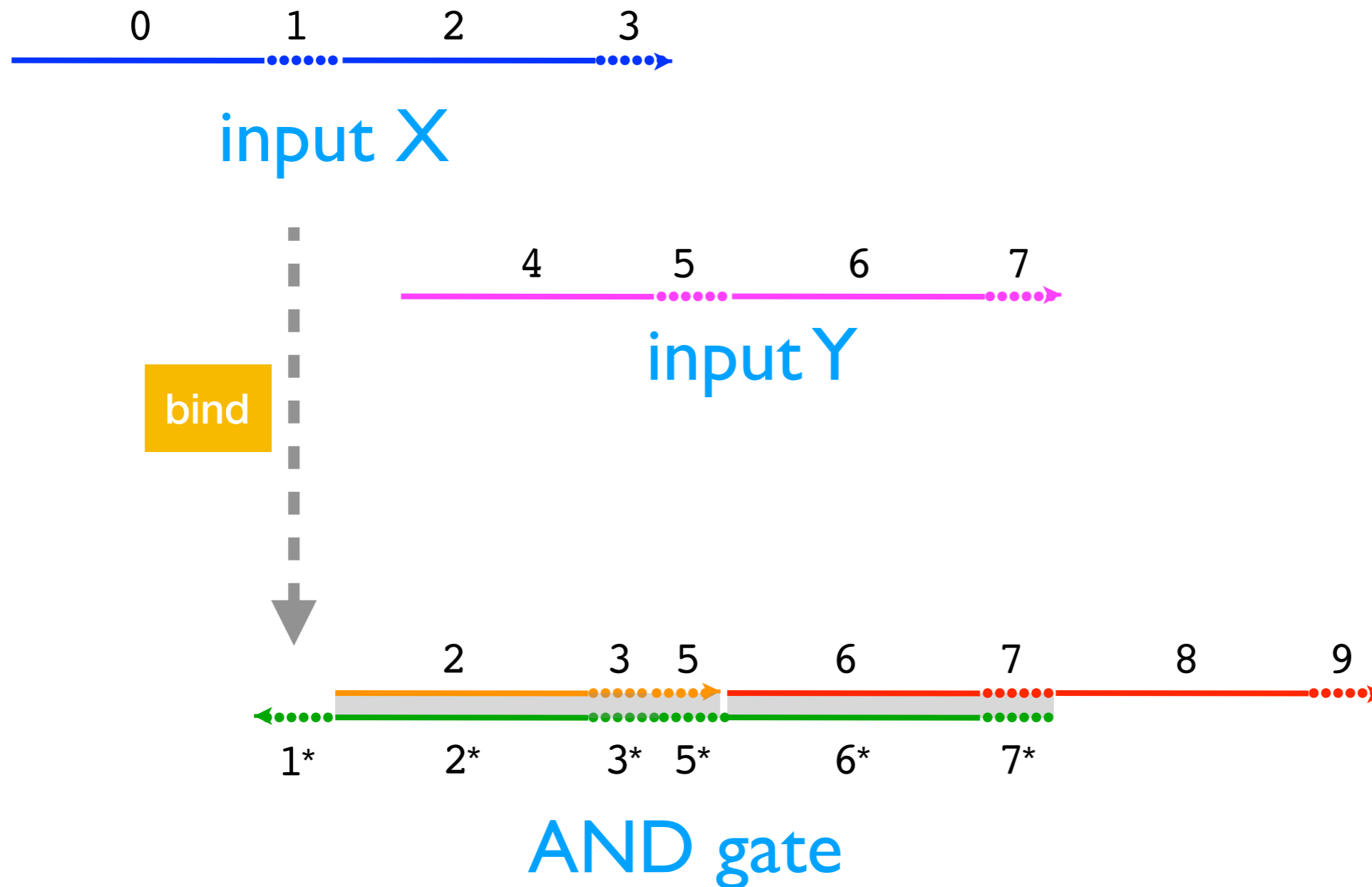
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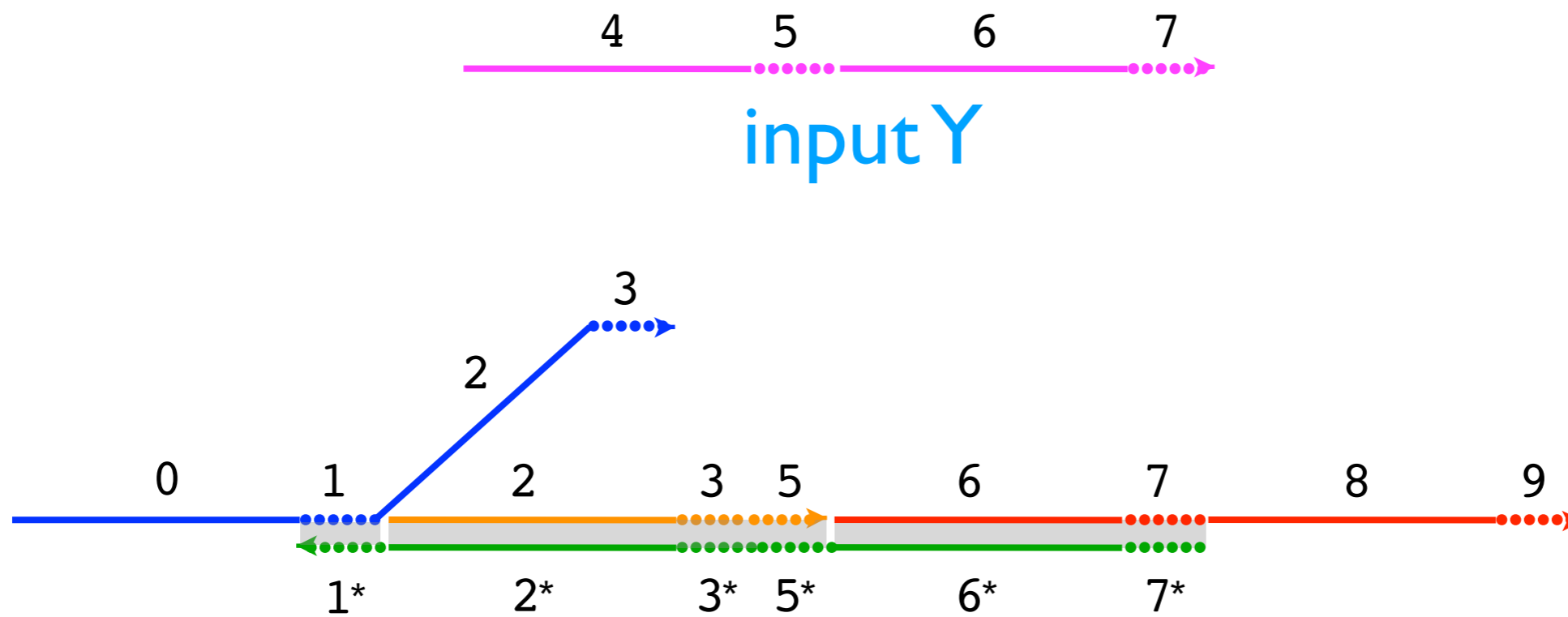
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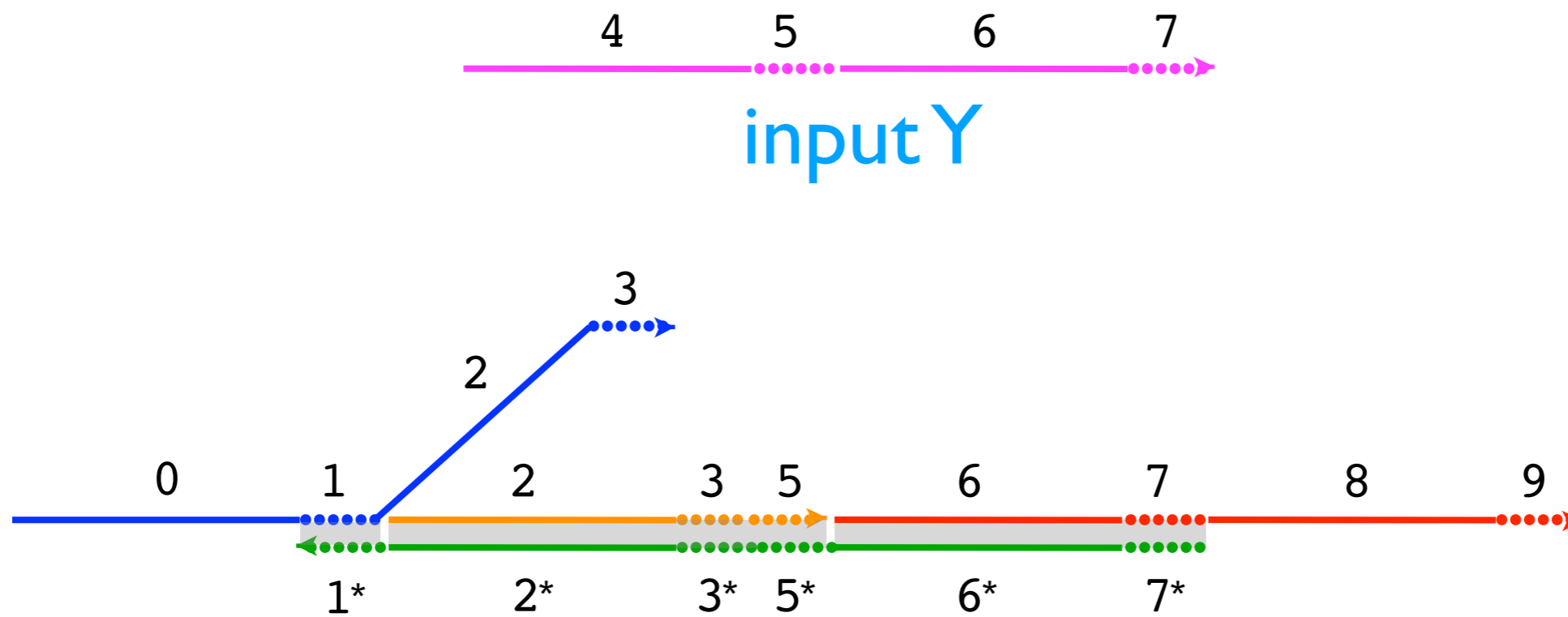
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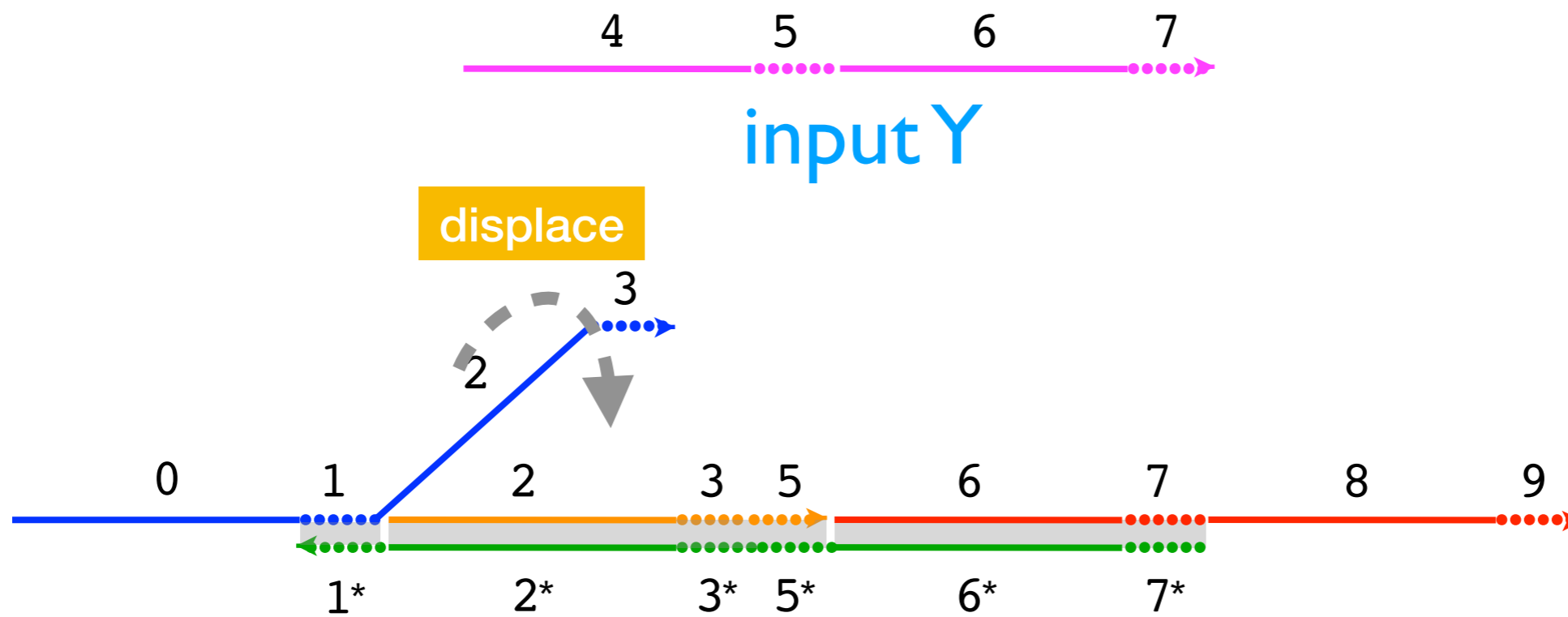
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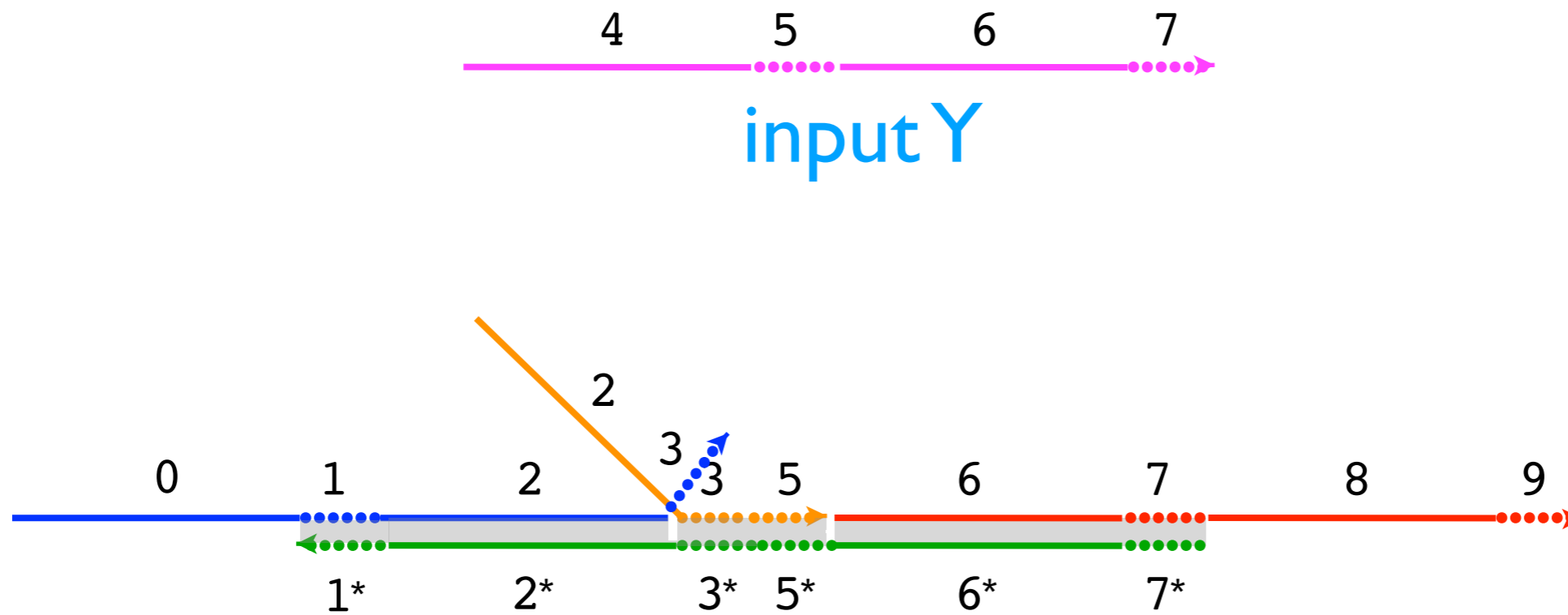
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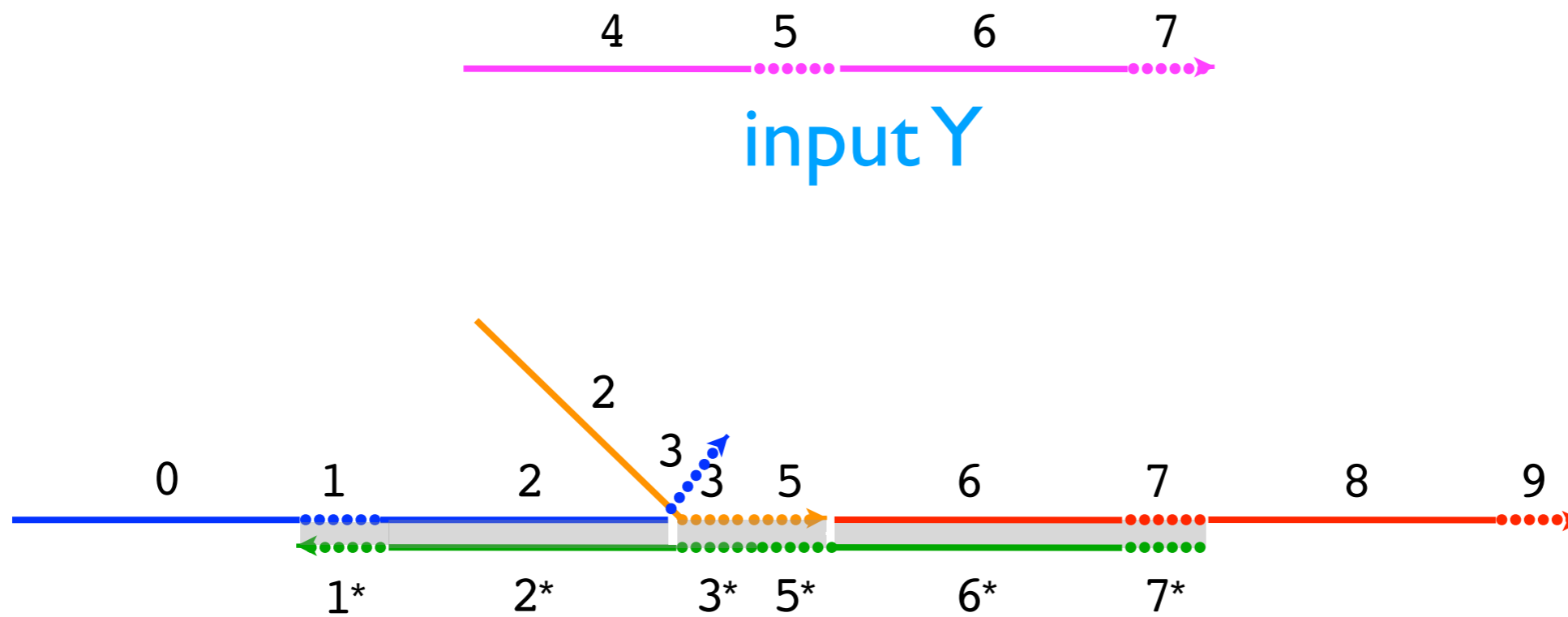
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release Z if and only if X and Y are present



# Strand Displacement Cascades Example: AND gate

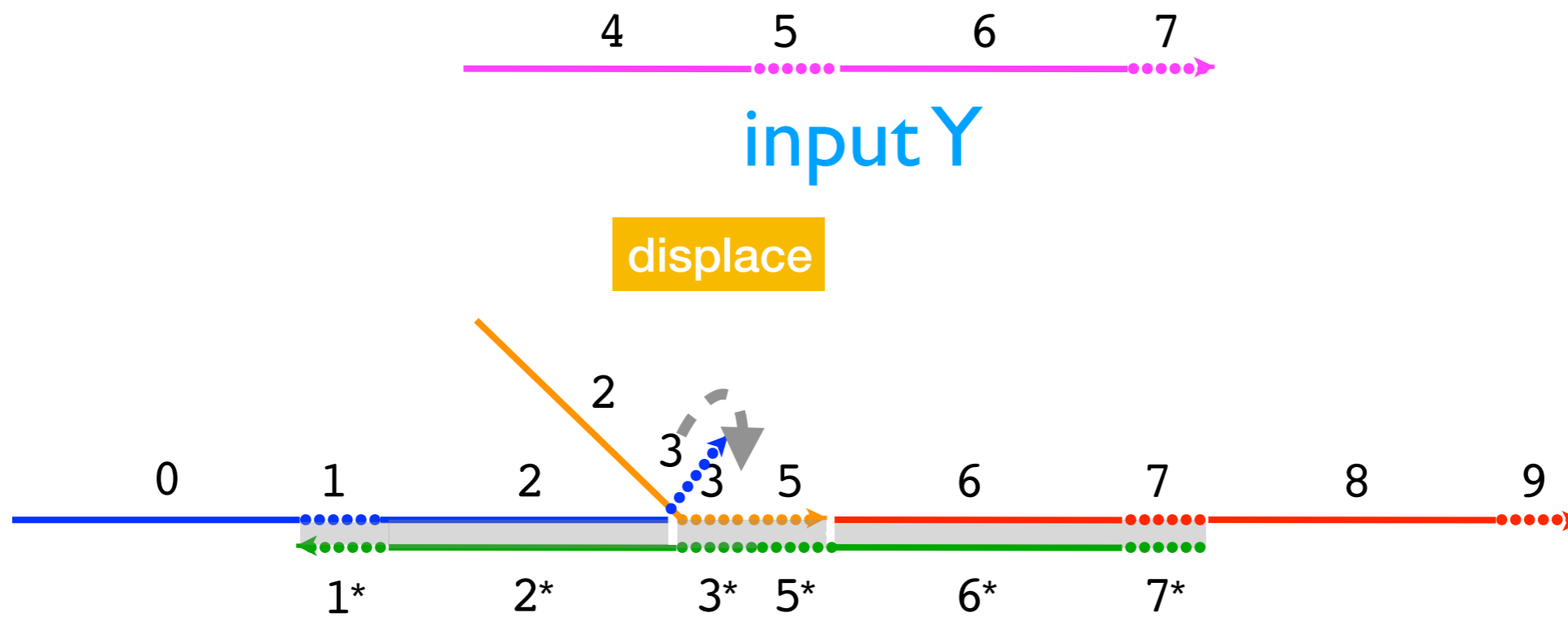
release Z if and only if X and Y are present





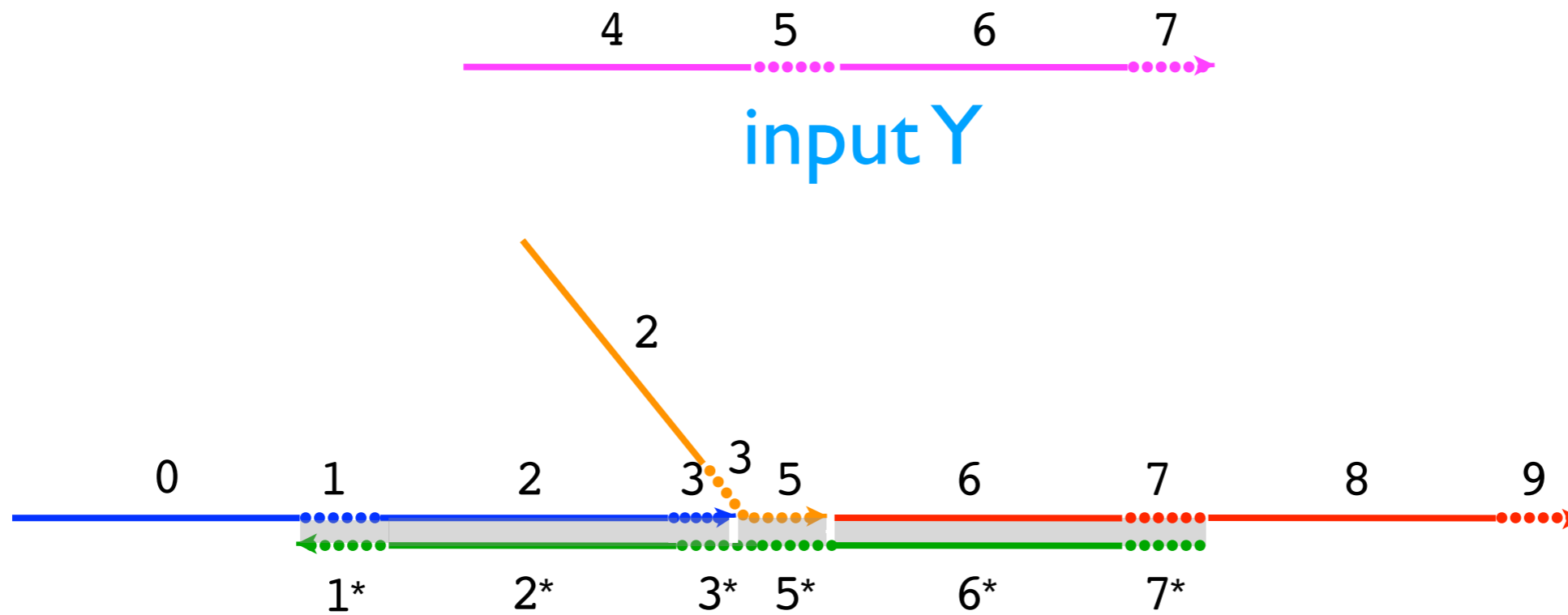
# Strand Displacement Cascades Example: AND gate

release Z if and only if X and Y are present



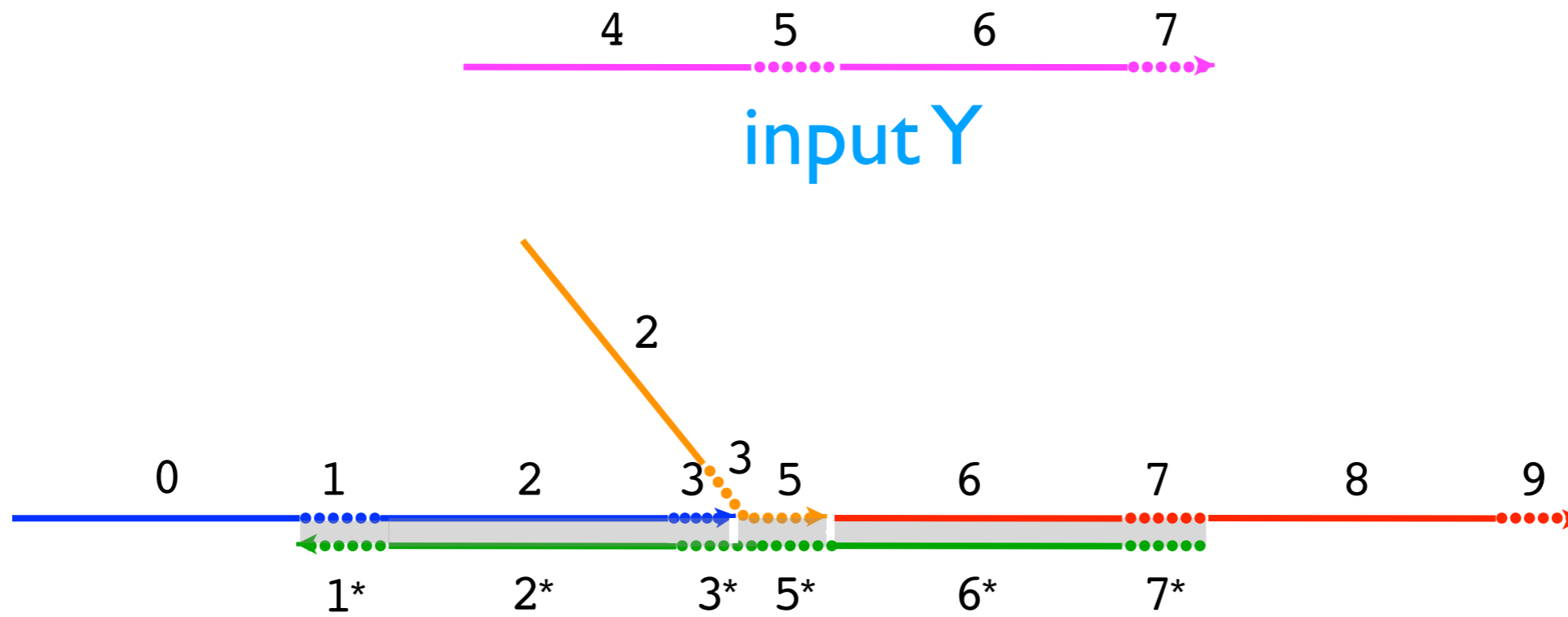
# Strand Displacement Cascades Example: AND gate

release Z if and only if X and Y are present



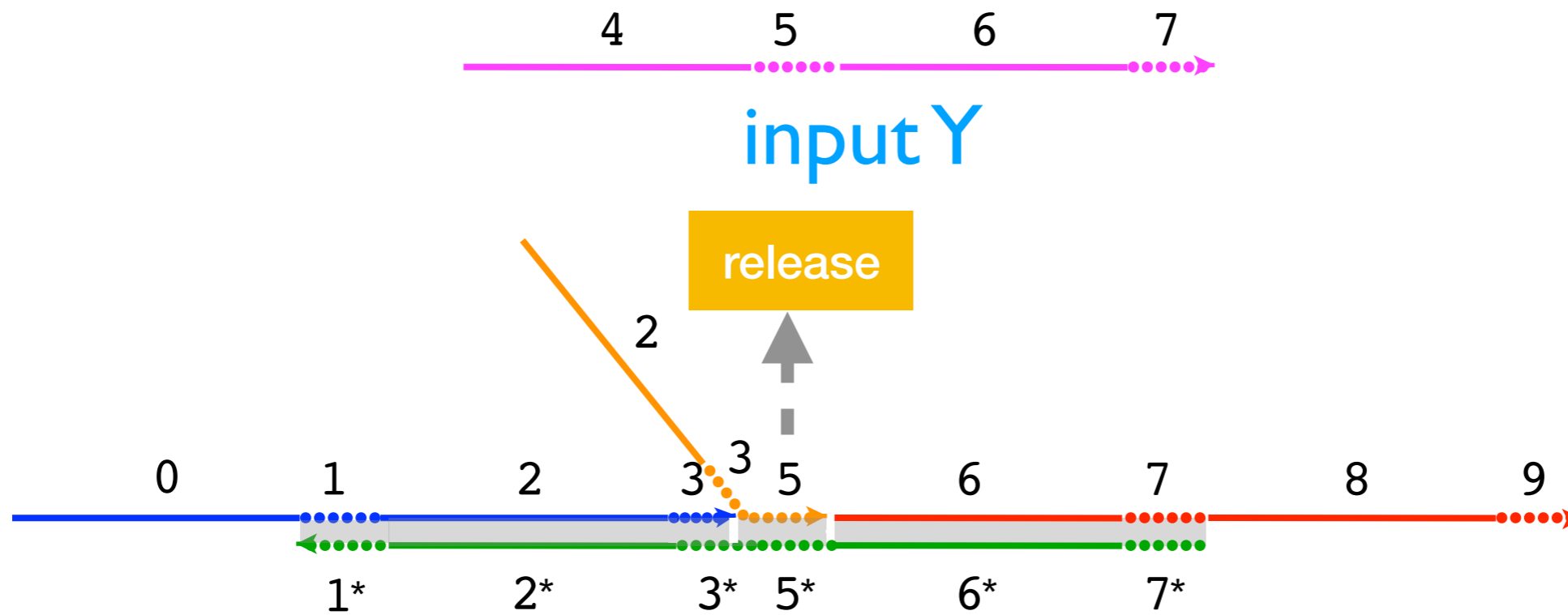
# Strand Displacement Cascades Example: AND gate

release Z if and only if X and Y are present



# Strand Displacement Cascades Example: AND gate

release Z if and only if X and Y are present



# Strand Displacement Cascades Example: AND gate

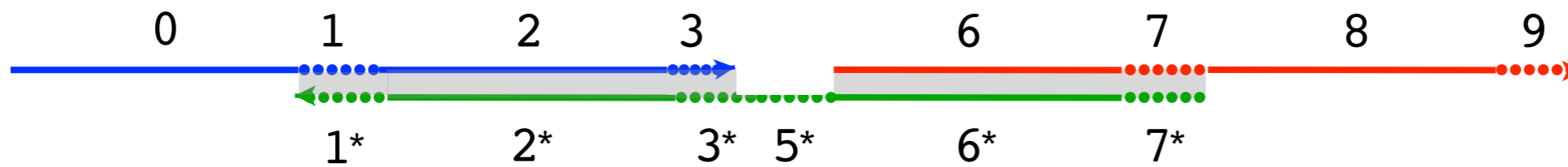
release Z if and only if X and Y are present



waste



input Y



# Strand Displacement Cascades Example: AND gate

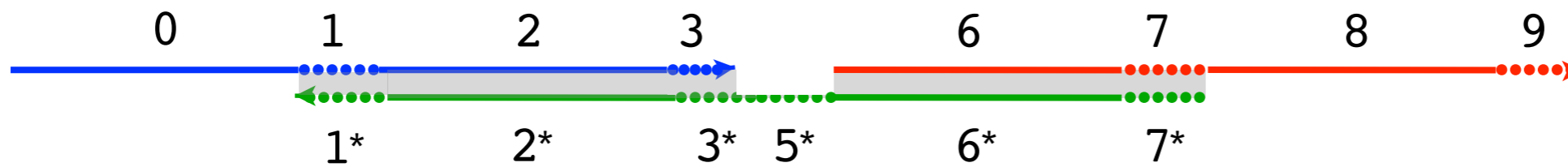
release Z if and only if X and Y are present



waste

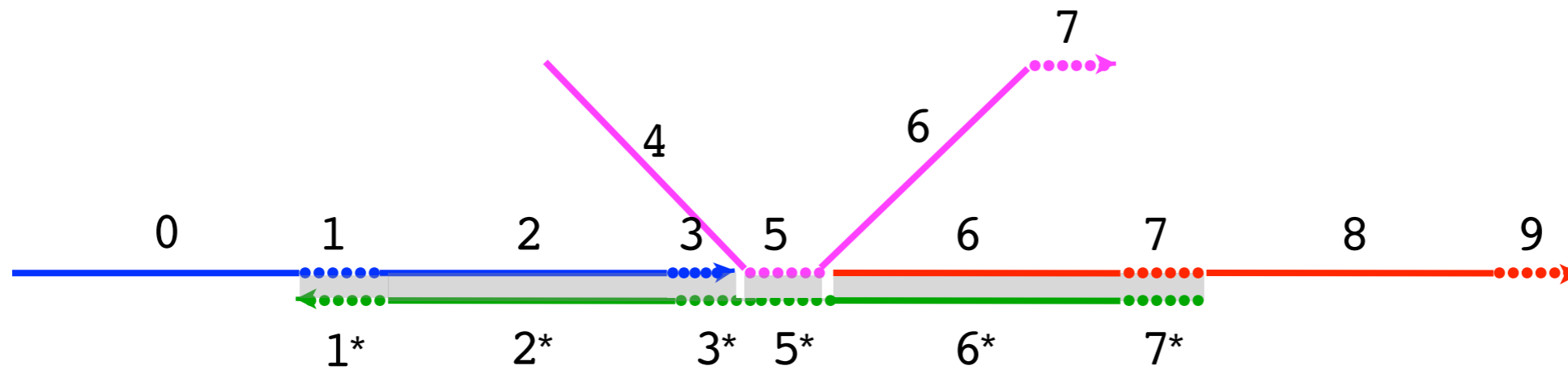


input Y



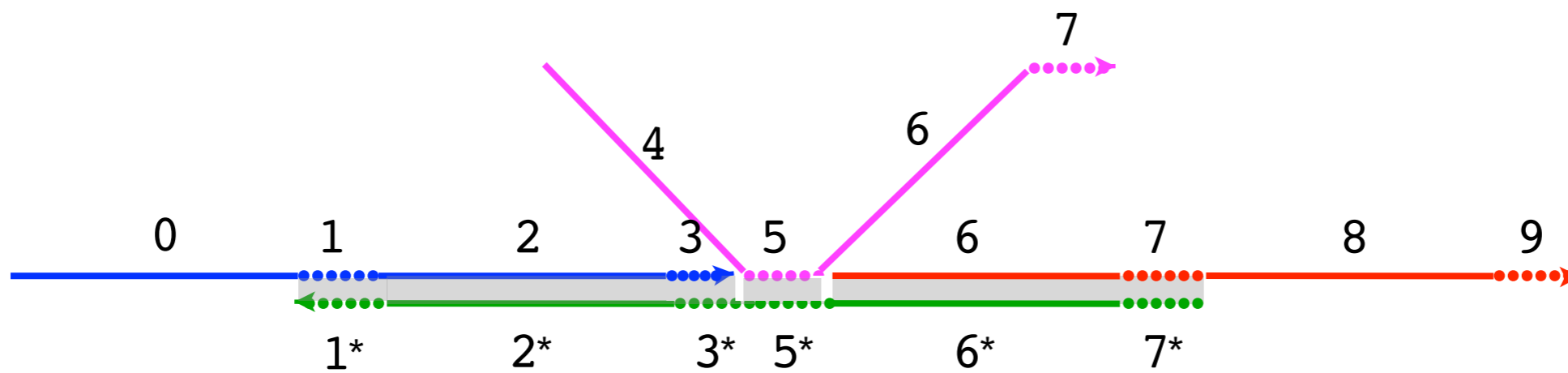
# Strand Displacement Cascades Example: AND gate

release Z if and only if X and Y are present



# Strand Displacement Cascades Example: AND gate

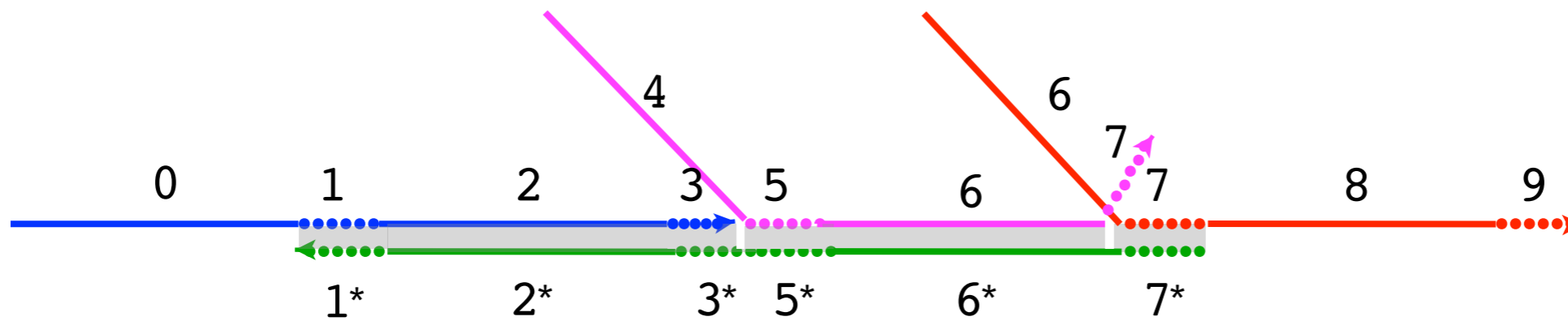
release Z if and only if X and Y are present





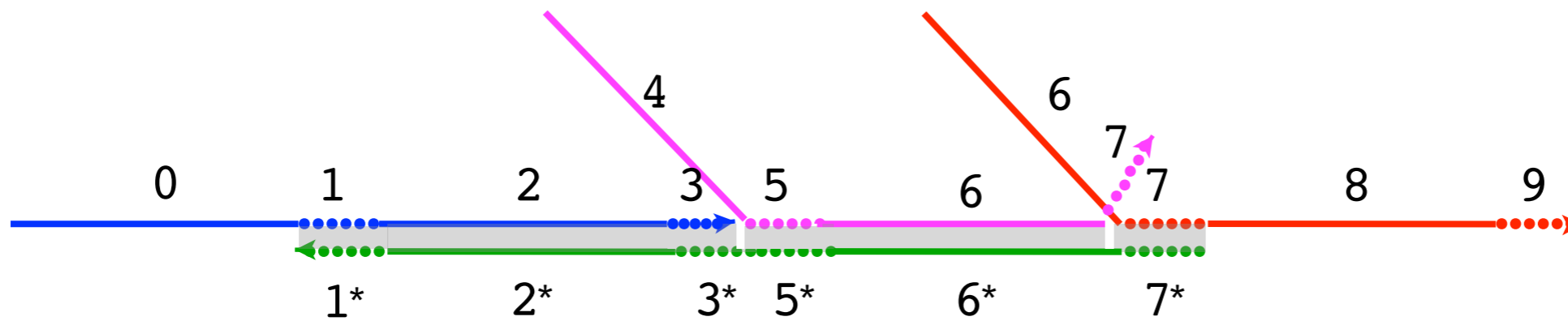
# Strand Displacement Cascades Example: AND gate

release Z if and only if X and Y are present



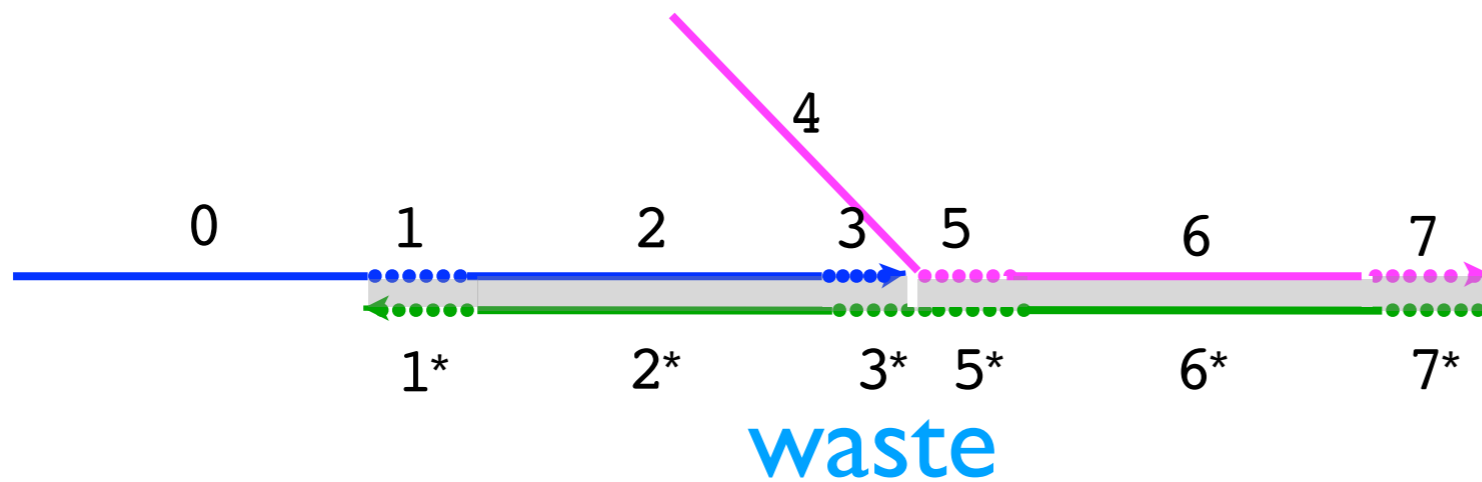
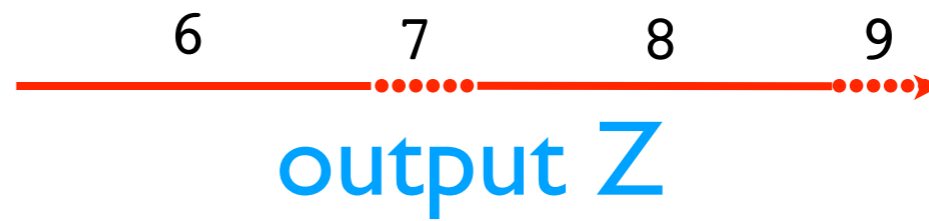
# Strand Displacement Cascades Example: AND gate

release Z if and only if X and Y are present



# Strand Displacement Cascades Example: AND gate

release Z if and only if X and Y are present



# Strand Displacement Cascades Example: AND gate

release Z if and only if X and Y are present

before



input X



input Y



AND gate



after



output Z



waste



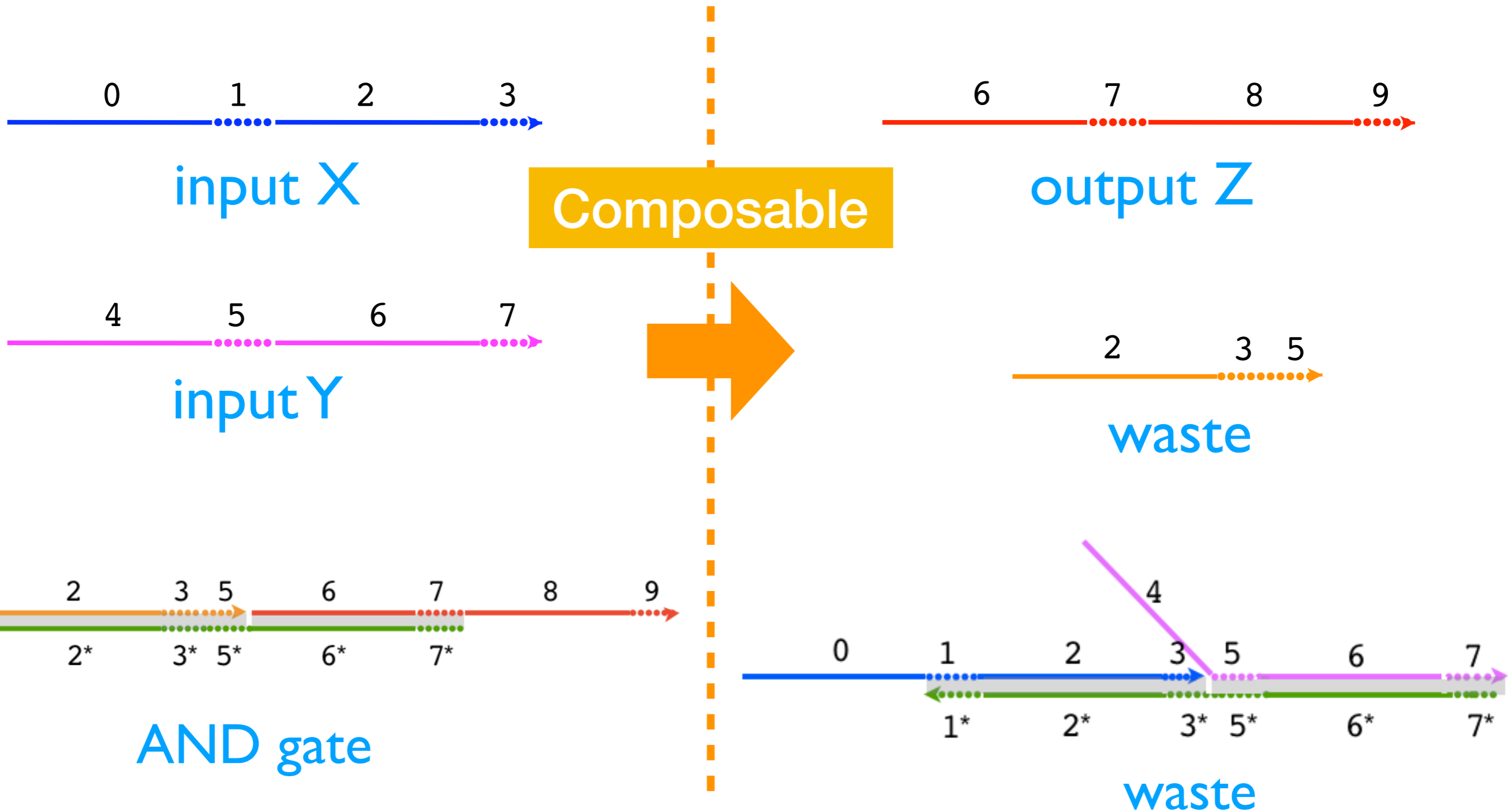
waste

# Strand Displacement Cascades Example: AND gate

release Z if and only if X and Y are present

before

after

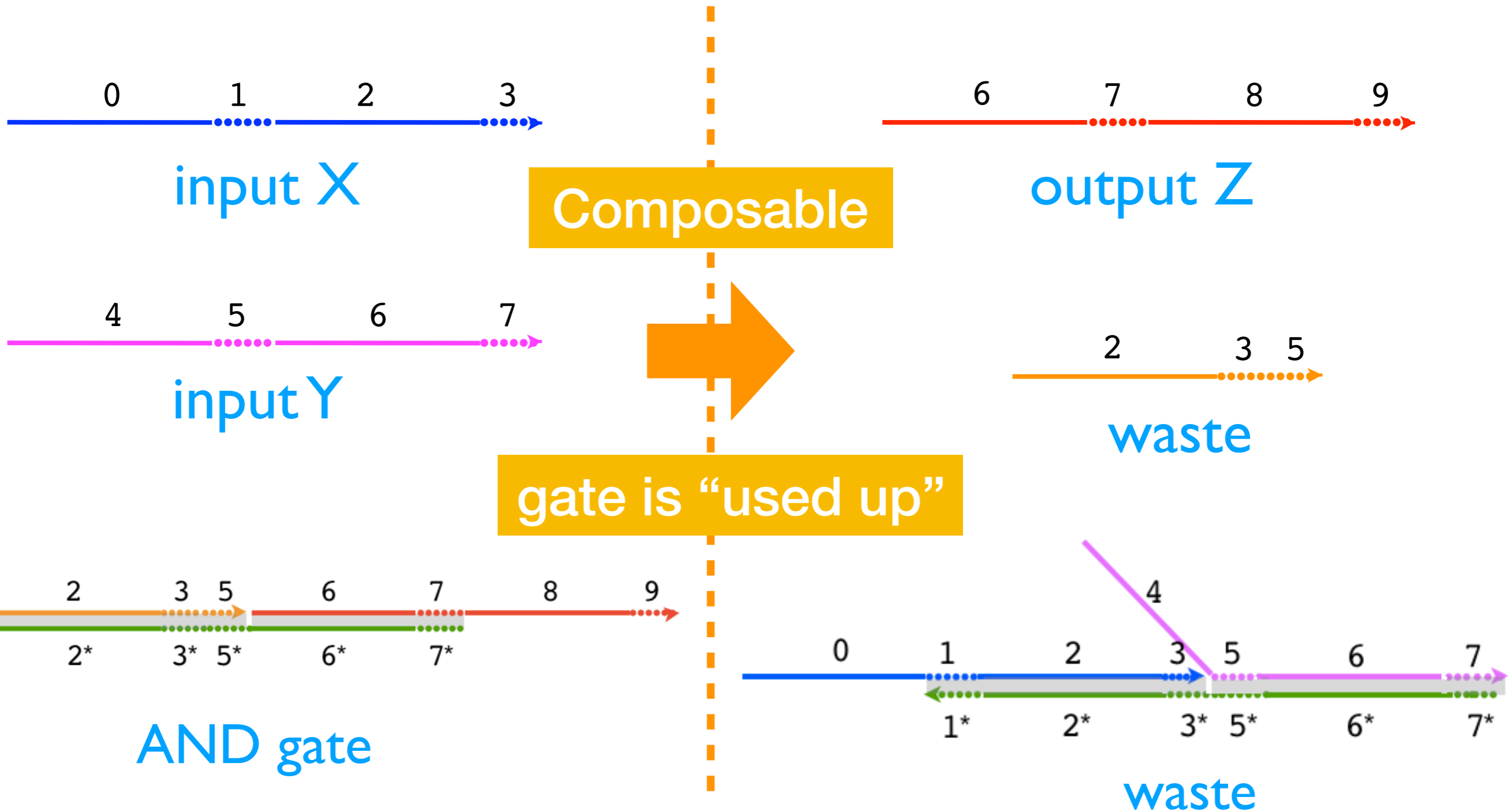


# Strand Displacement Cascades Example: AND gate

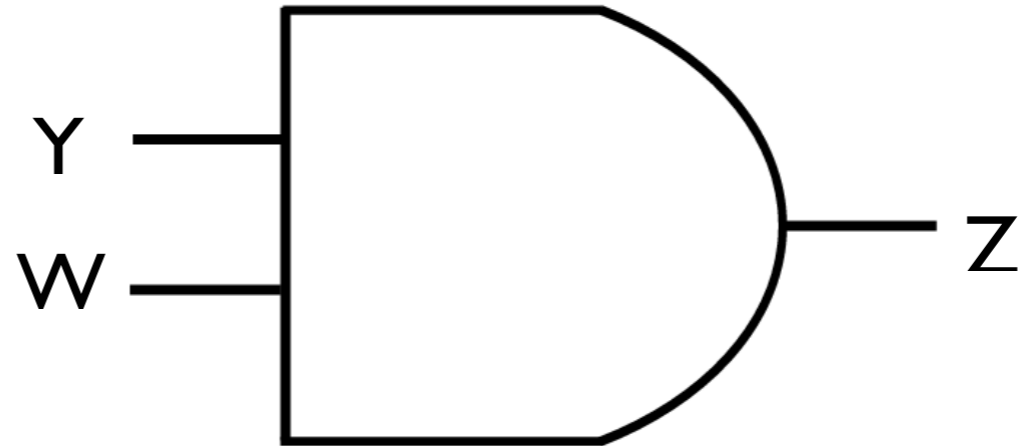
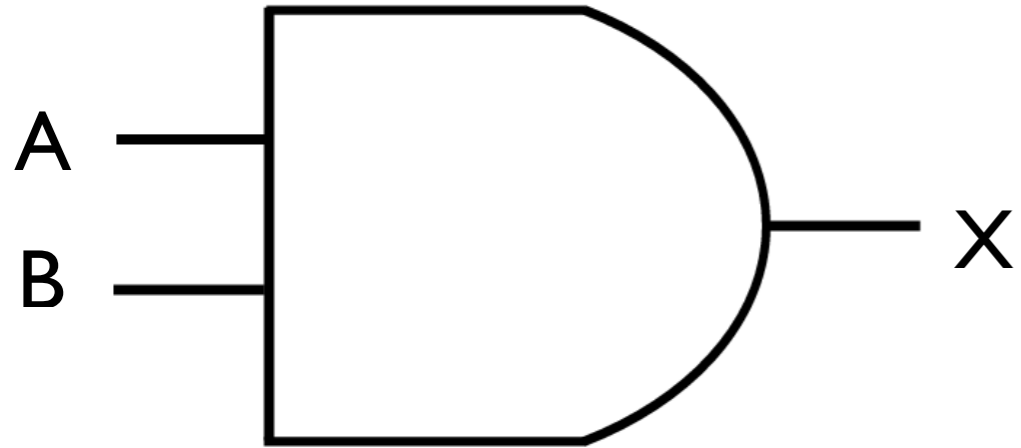
release Z if and only if X and Y are present

before

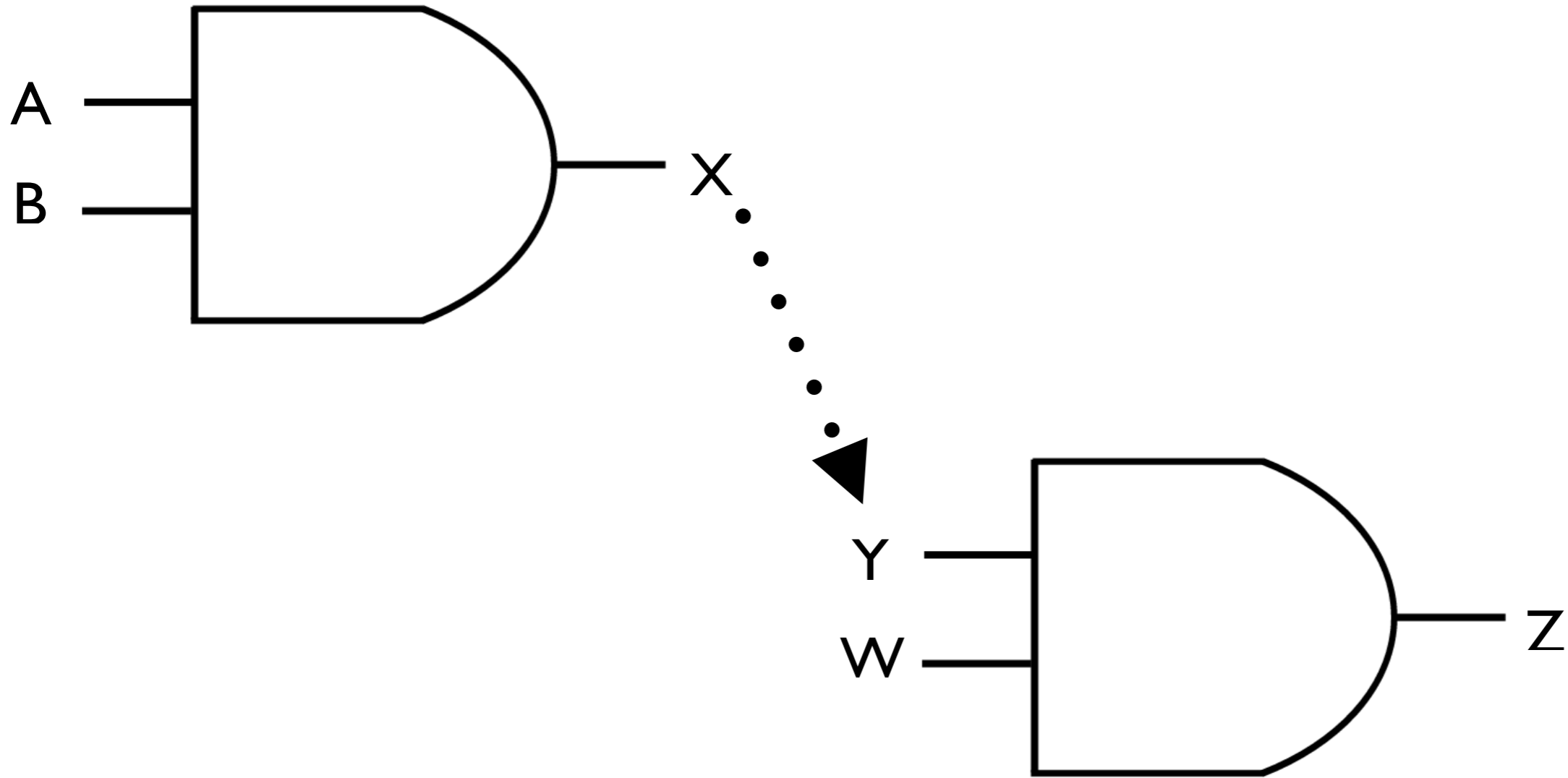
after



# Composing AND gates



# Composing AND gates





We need a “wire”

# Sequence Independence

Translator (a “wire”):  $X \rightarrow Y$

input  $X$



output  $Y$



Different coloring scheme to emphasize sequence (in)dependence!

# Sequence Independence

Translator (a “wire”):  $X \rightarrow Y$

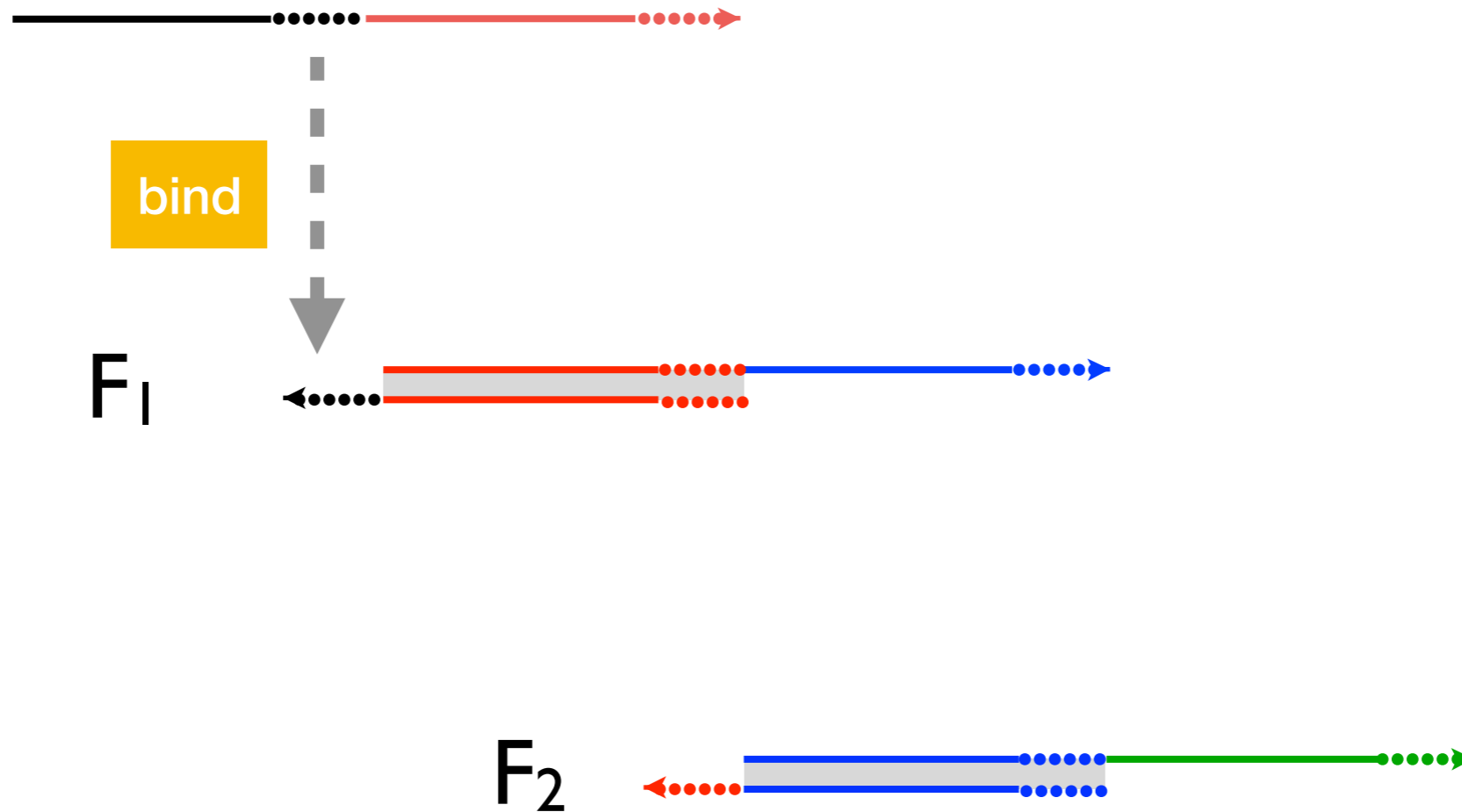
input  $X$



# Sequence Independence

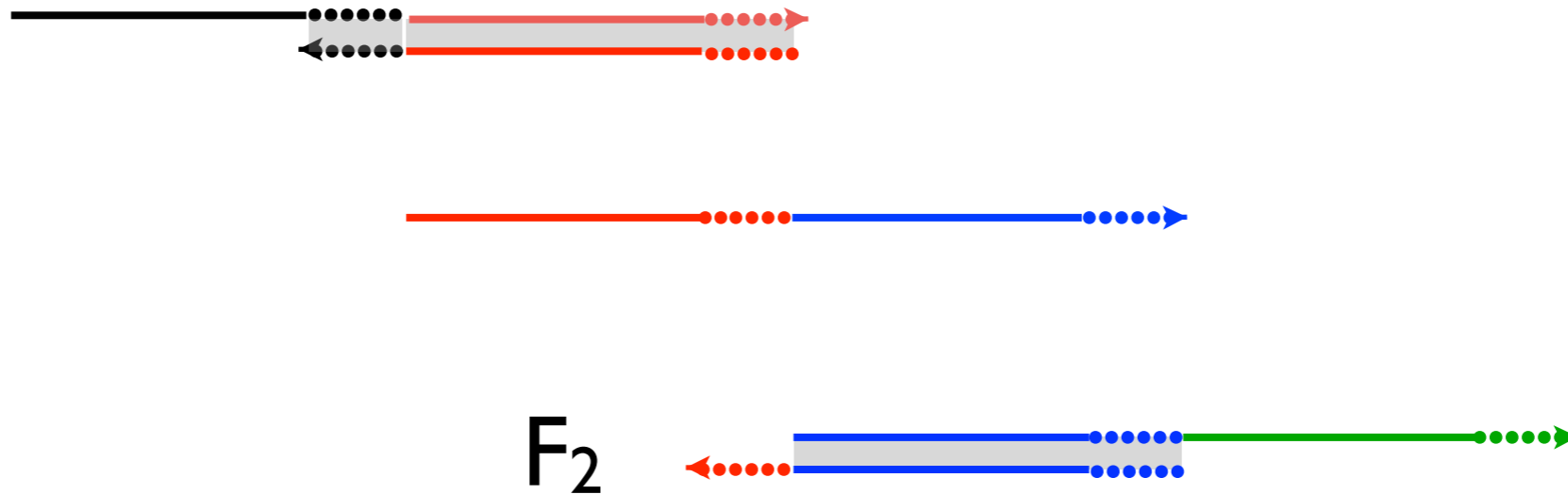
Translator (a “wire”):  $X \rightarrow Y$

input  $X$



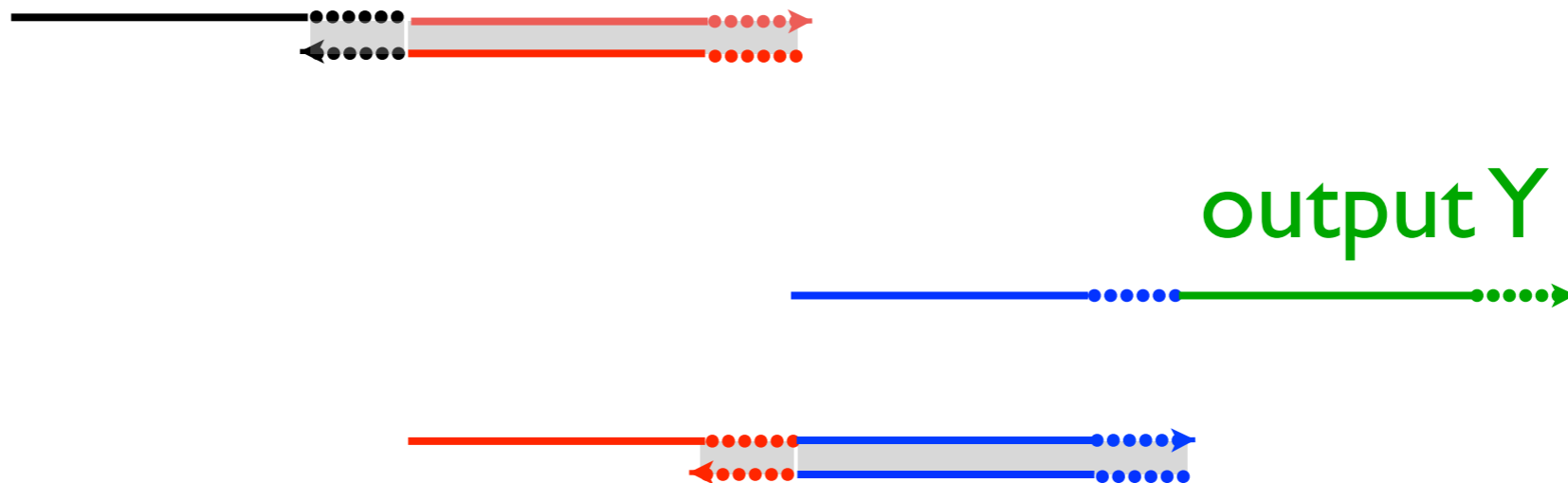
# Sequence Independence

Translator (a “wire”):  $X \rightarrow Y$

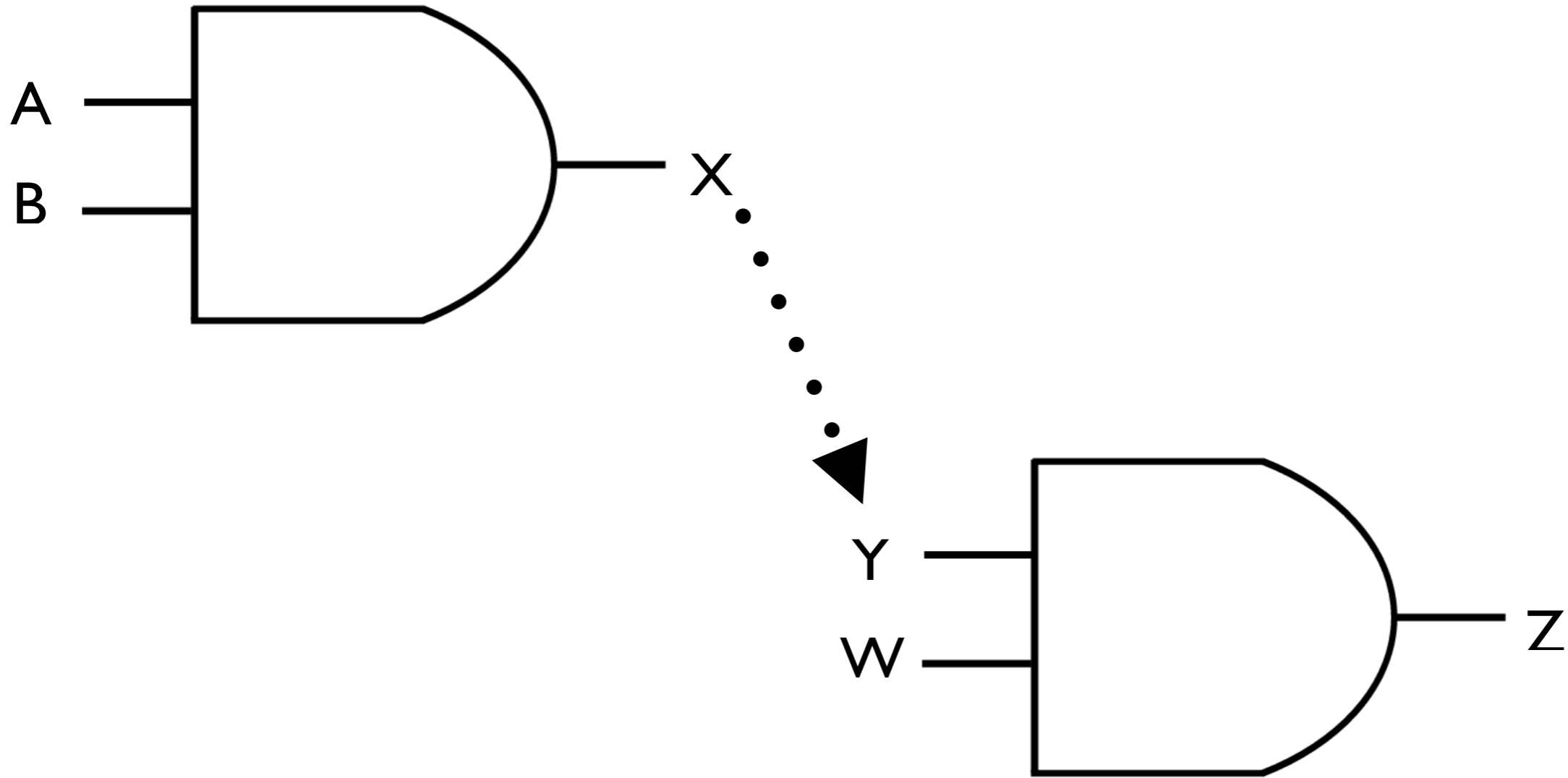


# Sequence Independence

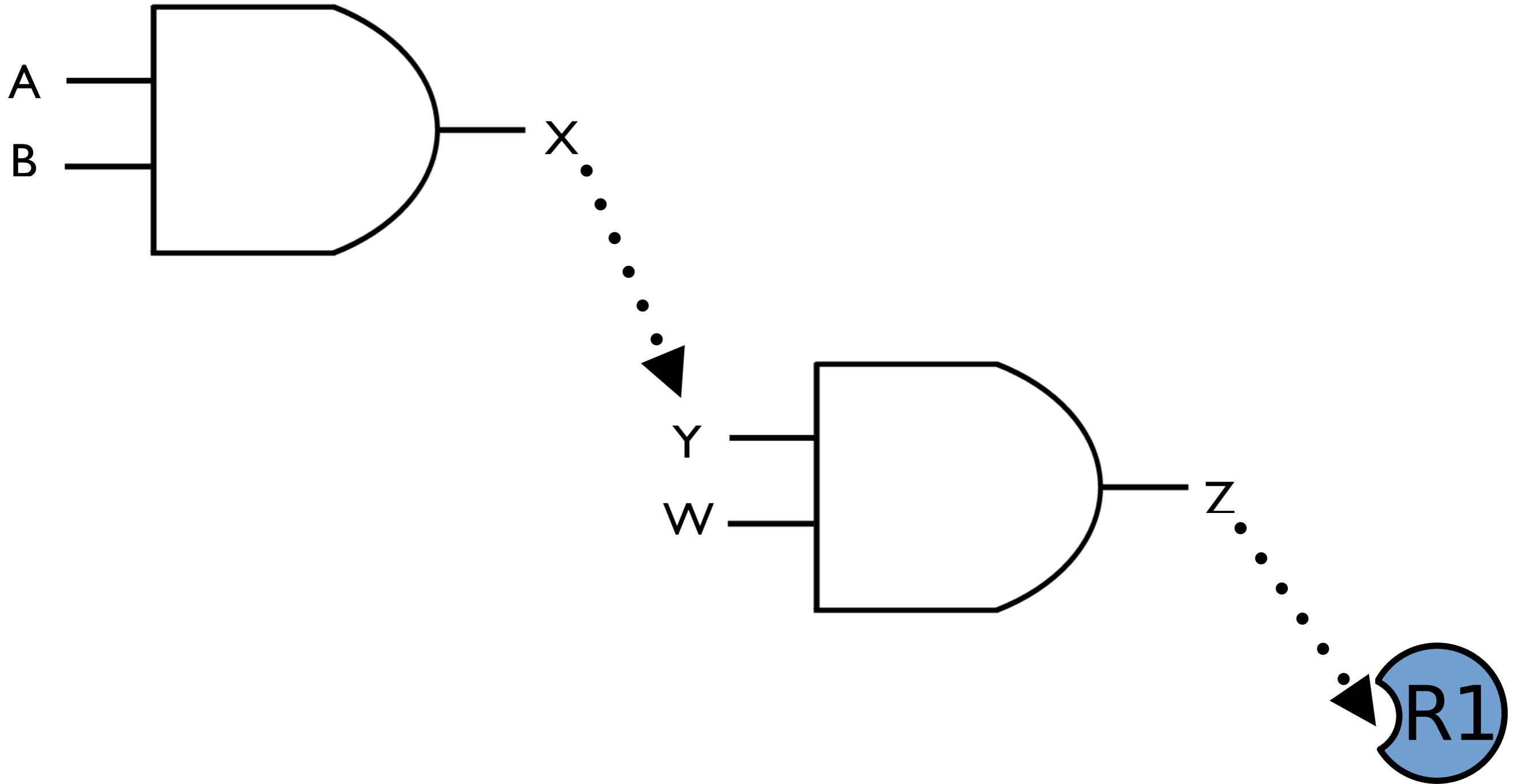
Translator (a “wire”):  $X \rightarrow Y$



# Reading Output

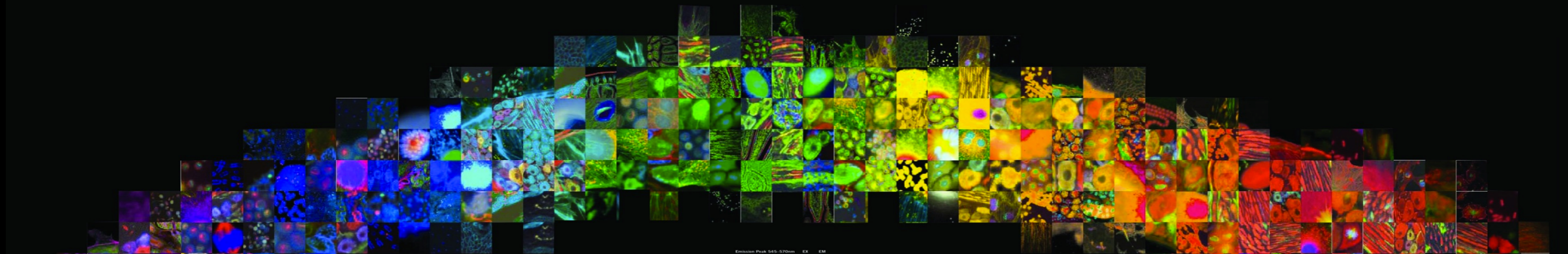


# Reading Output

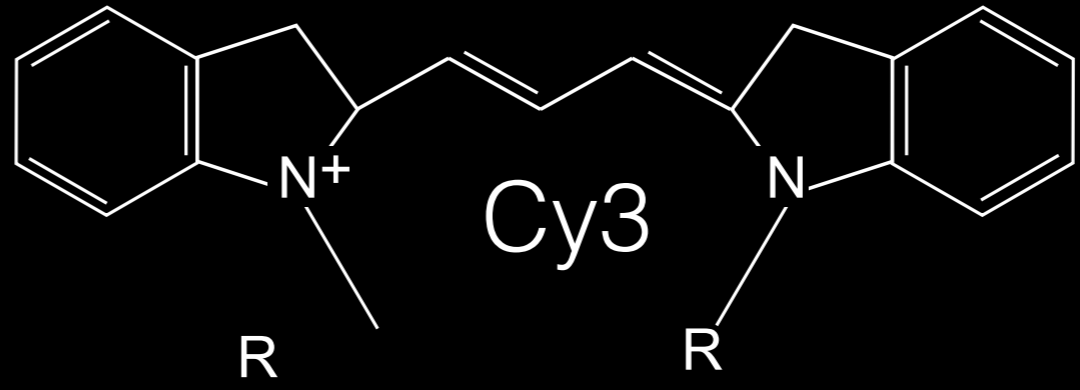




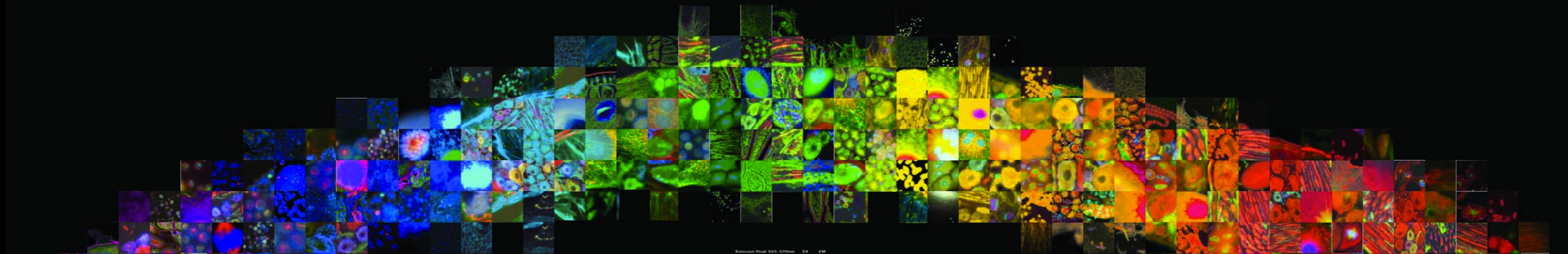
# F L U O R O E S S E N C E



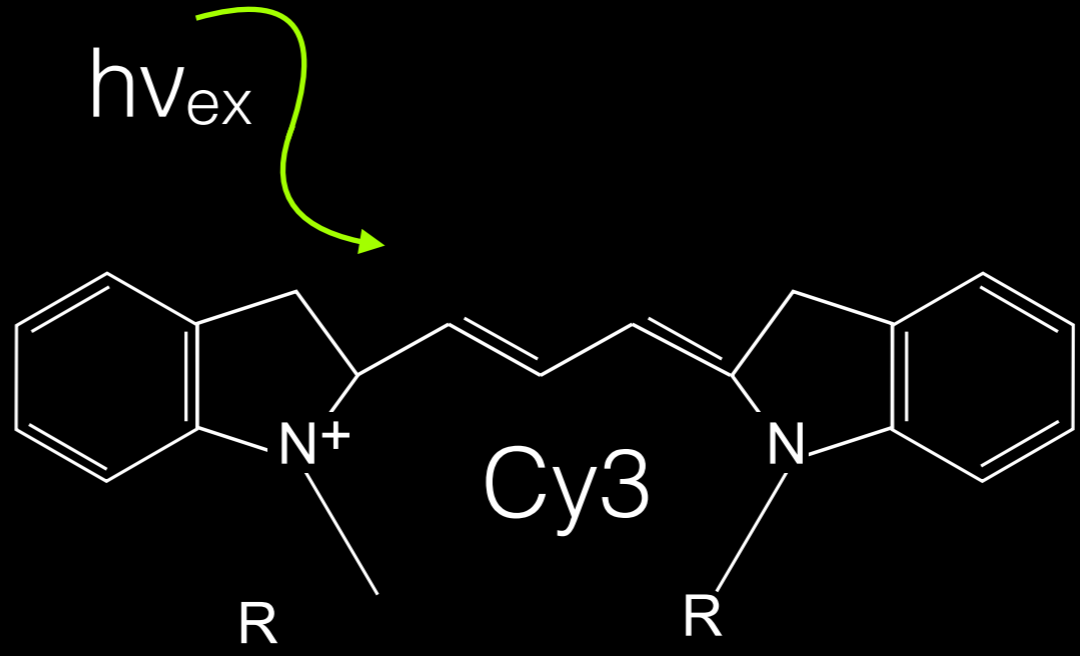
Emission Peak 375-425nm	EX	EM	Emission Peak 510-545nm	EX	EM	Emission Peak 545-570nm	EX	EM	Emission Peak 570-585nm	EX	EM	Emission Peak 585-595nm	EX	EM	Emission Peak 595-605nm	EX	EM	Emission Peak 605-625nm	EX	EM	Emission Peak 655-800nm	EX	EM			
Calcium Blue	375	420	Acridine orange (+DNA)	492	518	Rhodamine GG	525	555	Allexa Fluor® 545	558	573	ATTO TAG™ FG	486	591	Acridine orange (+RNA)	460	650	5-Carboxyaphthofluorescein	508	668	Allexa Fluor® 647	663	669	Alphacyanine (APC)	650	660
Calcium Blue™	400	420	Allexa Fluor® 480	488	505	Rhodamine 6G	525	568	Rhodamine 6G	568	570	ATTO TAG™ FG	486	591	Alphacyanine (APC)	650	660	5-Carboxyaphthofluorescein	508	668	Allexa Fluor® 647	663	669	Alphacyanine (APC)	650	660
DIDS	341	414	Allexa Fluor® 488	488	519	Rhodamine 101	568	568	Rhodamine 101	568	570	ATTO TAG™ FG	486	591	Alphacyanine (APC)	650	660	5-Carboxyaphthofluorescein	508	668	Allexa Fluor® 647	663	669	Alphacyanine (APC)	650	660
Fast Blue	365	420	Allexa Fluor® 500	500	506	Rhodamine 123	507	529	Rhodamine 123	507	529	ATTO TAG™ FG	486	591	Alphacyanine (APC)	650	660	5-Carboxyaphthofluorescein	508	668	Allexa Fluor® 647	663	669	Alphacyanine (APC)	650	660
Fluoro-Jade® (low pH)	323	408	Allexa Fluor® 513	513	513	Rhodamine 123	507	529	Rhodamine 123	507	529	ATTO TAG™ FG	486	591	Alphacyanine (APC)	650	660	5-Carboxyaphthofluorescein	508	668	Allexa Fluor® 647	663	669	Alphacyanine (APC)	650	660
Indo-1 (high calcium)	330	401	Allexa Fluor® 530	530	530	Rhodamine 123	507	529	Rhodamine 123	507	529	ATTO TAG™ FG	486	591	Alphacyanine (APC)	650	660	5-Carboxyaphthofluorescein	508	668	Allexa Fluor® 647	663	669	Alphacyanine (APC)	650	660
LysoTracker® Blue (pH 5)	374	424	Allexa Fluor® 555	555	555	Rhodamine 123	507	529	Rhodamine 123	507	529	ATTO TAG™ FG	486	591	Alphacyanine (APC)	650	660	5-Carboxyaphthofluorescein	508	668	Allexa Fluor® 647	663	669	Alphacyanine (APC)	650	660
Mag Indo-1	350	417	Allexa Fluor® 568	568	568	Rhodamine 123	507	529	Rhodamine 123	507	529	ATTO TAG™ FG	486	591	Alphacyanine (APC)	650	660	5-Carboxyaphthofluorescein	508	668	Allexa Fluor® 647	663	669	Alphacyanine (APC)	650	660
Pyrene	345	378	Allexa Fluor® 590	590	590	Rhodamine 123	507	529	Rhodamine 123	507	529	ATTO TAG™ FG	486	591	Alphacyanine (APC)	650	660	5-Carboxyaphthofluorescein	508	668	Allexa Fluor® 647	663	669	Alphacyanine (APC)	650	660



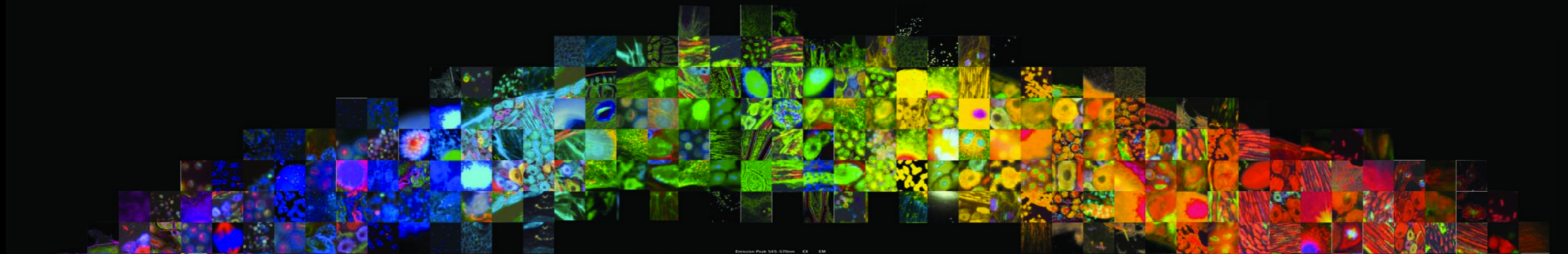
# F L U O R O E S S E N C E



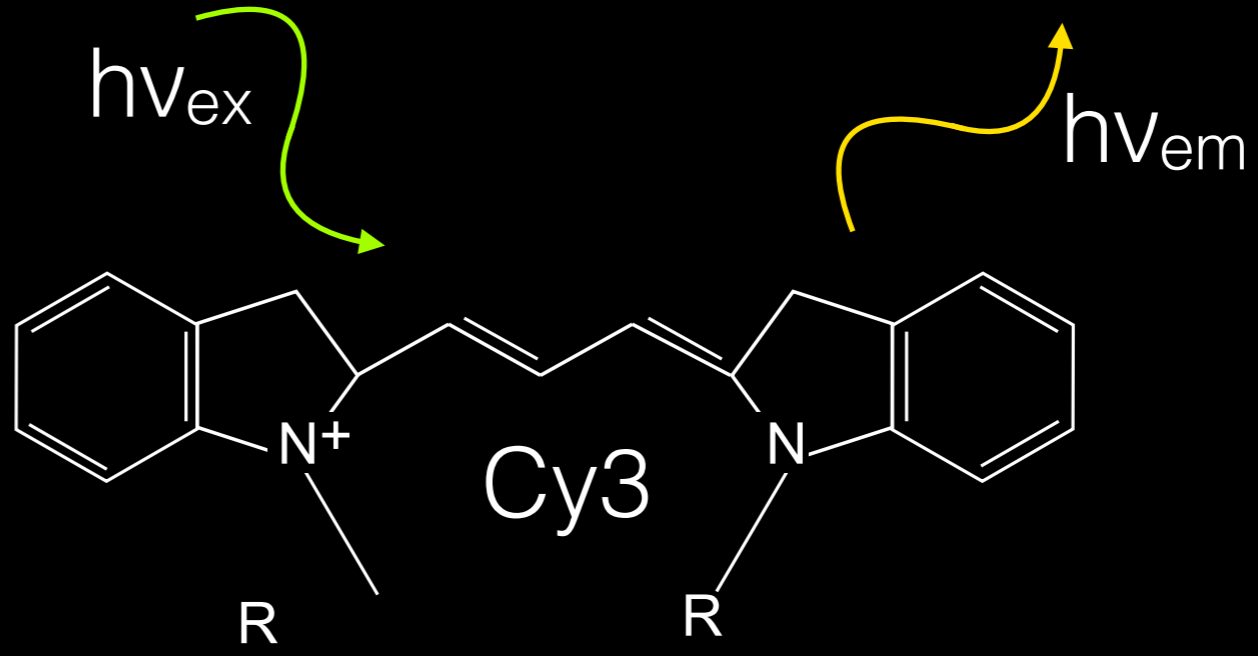
Emission Peak 375-425nm	EX	EM	Emission Peak 510-545nm	EX	EM	Emission Peak 545-570nm	EX	EM	Emission Peak 570-585nm	EX	EM	Emission Peak 585-595nm	EX	EM	Emission Peak 595-605nm	EX	EM	Emission Peak 605-650nm	EX	EM	Emission Peak 655-800nm	EX	EM			
Calcium Blue	375	420	Acridine orange (AFAM)	492	518	rhodamine GG	525	555	Allox Fluor <sup>®</sup> 545	558	573	ATTO TAG <sup>®</sup> FG	486	591	Acridine orange (+HNA)	460	650	5-Carboxyaphthofluorescein	598	668	Allox Fluor <sup>®</sup> 647	663	669	Allox Fluor <sup>®</sup> 640	679	702
Calcium Blue <sup>™</sup>	400	420	Acridine orange (+DNA)	500	526	K-23E	525	555	Allox Fluor <sup>®</sup> 545	558	573	ATTO TAG <sup>®</sup> FG	486	591	Allox Fluor <sup>®</sup> 647	663	669	5-Carboxyaphthofluorescein	598	668	Allox Fluor <sup>®</sup> 647	663	669	Allox Fluor <sup>®</sup> 640	679	702
DIDS	341	414	Allox Fluor <sup>®</sup> 480	434	540	Allox Fluor <sup>®</sup> 532	531	554	Allox Fluor <sup>®</sup> 555	553	568	Allox Fluor <sup>®</sup> 555	553	568	Allox Fluor <sup>®</sup> 568	579	604	Allox Fluor <sup>®</sup> 568	579	604	Allox Fluor <sup>®</sup> 568	579	604	Allox Fluor <sup>®</sup> 660	663	690
Fast Blue	365	420	Allox Fluor <sup>®</sup> 488	495	519	Allox Fluor <sup>®</sup> 555	553	568	Allox Fluor <sup>®</sup> 555	553	568	Allox Fluor <sup>®</sup> 555	553	568	Allox Fluor <sup>®</sup> 568	579	604	Allox Fluor <sup>®</sup> 568	579	604	Allox Fluor <sup>®</sup> 568	579	604	Allox Fluor <sup>®</sup> 660	663	690
Fluoro-Jade <sup>®</sup> (low pH)	323	408	Allox Fluor <sup>®</sup> 490	503	506	ATTO TAG <sup>®</sup> CBGA	460	560	Allox Fluor <sup>®</sup> 555	553	568	Allox Fluor <sup>®</sup> 555	553	568	Allox Fluor <sup>®</sup> 568	579	604	Allox Fluor <sup>®</sup> 568	579	604	Allox Fluor <sup>®</sup> 568	579	604	Allox Fluor <sup>®</sup> 660	663	690
Indo-1 (high calcium)	330	401	Allox Fluor <sup>®</sup> 500	505	513	Allox Fluor <sup>®</sup> 555	553	568	Allox Fluor <sup>®</sup> 555	553	568	Allox Fluor <sup>®</sup> 555	553	568	Allox Fluor <sup>®</sup> 568	579	604	Allox Fluor <sup>®</sup> 568	579	604	Allox Fluor <sup>®</sup> 568	579	604	Allox Fluor <sup>®</sup> 660	663	690
LysoTracker <sup>®</sup> Blue (pH 5)	374	424	Allox Fluor <sup>®</sup> 510	515	523	Allox Fluor <sup>®</sup> 555	553	568	Allox Fluor <sup>®</sup> 555	553	568	Allox Fluor <sup>®</sup> 555	553	568	Allox Fluor <sup>®</sup> 568	579	604	Allox Fluor <sup>®</sup> 568	579	604	Allox Fluor <sup>®</sup> 568	579	604	Allox Fluor <sup>®</sup> 660	663	690
Mag Indo-1	330	417	Allox Fluor <sup>®</sup> 520	525	533	Allox Fluor <sup>®</sup> 555	553	568	Allox Fluor <sup>®</sup> 555	553	568	Allox Fluor <sup>®</sup> 555	553	568	Allox Fluor <sup>®</sup> 568	579	604	Allox Fluor <sup>®</sup> 568	579	604	Allox Fluor <sup>®</sup> 568	579	604	Allox Fluor <sup>®</sup> 660	663	690
Pyrene	345	378	Allox Fluor <sup>®</sup> 530	535	543	Allox Fluor <sup>®</sup> 555	553	568	Allox Fluor <sup>®</sup> 555	553	568	Allox Fluor <sup>®</sup> 555	553	568	Allox Fluor <sup>®</sup> 568	579	604	Allox Fluor <sup>®</sup> 568	579	604	Allox Fluor <sup>®</sup> 568	579	604	Allox Fluor <sup>®</sup> 660	663	690

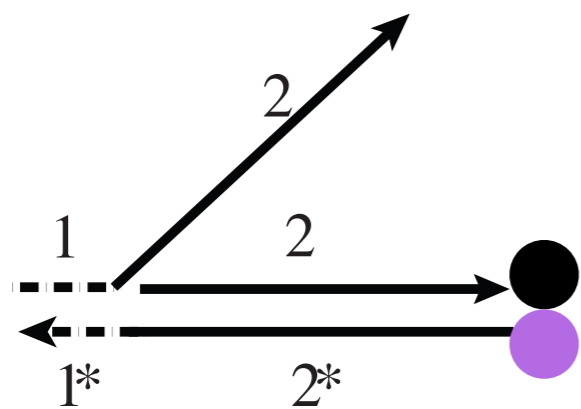


# F L U O R O S E S E N C E

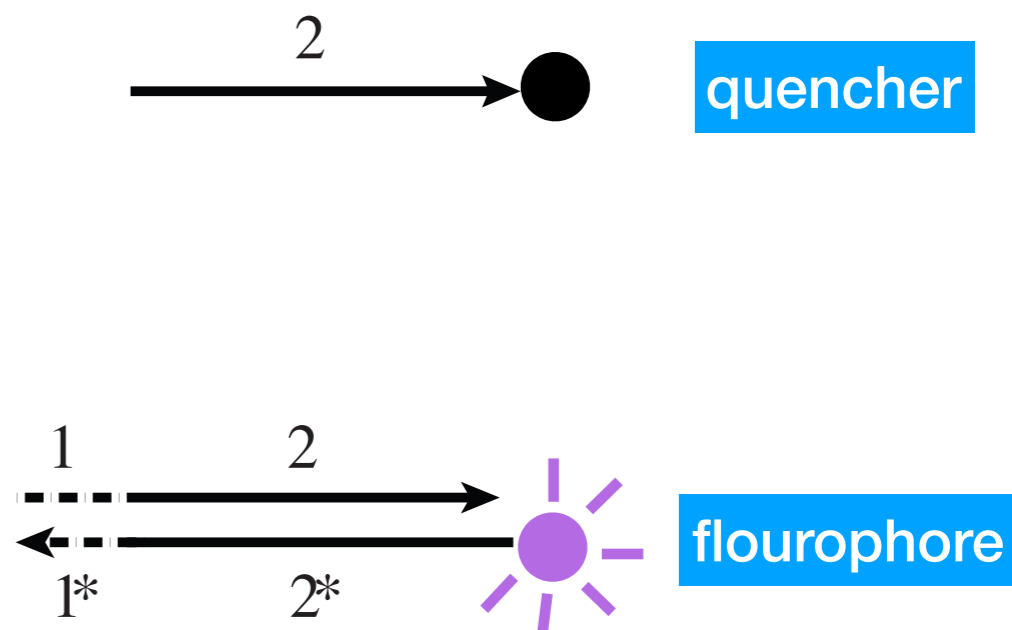


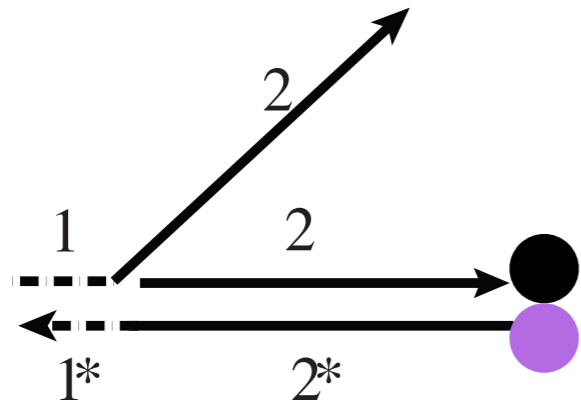
Emission Peak 375-425nm	EX	EM	Emission Peak 490-510nm	EX	EM	Emission Peak 510-545nm	EX	EM	Emission Peak 545-570nm	EX	EM	Emission Peak 570-585nm	EX	EM	Emission Peak 585-595nm	EX	EM	Emission Peak 595-605nm	EX	EM	Emission Peak 605-625nm	EX	EM	Emission Peak 625-650nm	EX	EM	Emission Peak 655-800nm	EX	EM			
Calcium Blue	375	420	Acridine orange (+DNA)	492	518	5-Carboxyfluorescein (CFAM)	492	518	Rhodamine GG	542	568	Di-4-ANEPPS	570	585	ATTO-TAG™ FG	486	591	2-Amino-6-methoxy-10,7,2'-diiodo-5',6'-dihydroxyfluorene (DAM)	605	625	Acridine orange (+RNA)	460	650	5-Carboxyaphthofluorescein	598	668	5-Carboxyaphthofluorescein	598	668			
Calcium Blue™	400	420	Alexa Fluor® 480	488	505	Alexa Fluor® 488	485	519	K262	525	555	Alexa Fluor® 546	565	573	Alexa Fluor® 546	565	573	Alexa Fluor® 594	591	618	5-Carboxyaphthofluorescein	598	668	Alexa Fluor® 647	653	669	Alexa Fluor® 647	653	669			
DIDS	341	414	BOXPYR™	462	483	BOXPYR™ 488	462	483	ATTO-TAG™ CBGCA	460	560	ATTO-TAG™ CBGCA	460	560	BOXPYR™ 568	562	574	Alexa Fluor® 600	603	620	Alexa Fluor® 600	603	620	Alexa Fluor® 600	603	620	Alexa Fluor® 600	603	620	Alexa Fluor® 600	603	620
Fura Blue	365	420	Cy2™	489	505	BOXPYR™ 505	503	506	Alexa Fluor® 555	553	568	BOXPYR™ 555	549	576	BOXPYR™ 555	549	576	Alexa Fluor® 630	633	650	Alexa Fluor® 630	633	650	Alexa Fluor® 630	633	650	Alexa Fluor® 630	633	650	Alexa Fluor® 630	633	650
Fura-2 (high calcium)	323	408	DID (DiI(18) 18)	484	501	BOXPYR™ FL	505	513	ATTO-TAG™ CF-3™	445	576	BOXPYR™ 510/510	505	560	ATTO-TAG™ CF-4™	445	560	Alexa Fluor® 640	639	656	Alexa Fluor® 640	639	656	Alexa Fluor® 640	639	656	Alexa Fluor® 640	639	656	Alexa Fluor® 640	639	656
Indo-1 (high calcium)	330	401	Fura-2 (high calcium)	335	505	BTC	401/464	529	BOXPYR™ 530/530	533	550	BOXPYR™ 530/530	533	550	BOXPYR™ 530/530	533	550	Alexa Fluor® 680	679	696	Alexa Fluor® 680	679	696	Alexa Fluor® 680	679	696	Alexa Fluor® 680	679	696	Alexa Fluor® 680	679	696
LysoTracker™ Blue (pH 5)	374	424	GFP (enhanced)	488	508	Calccein	494	517	BOXPYR™ 540/540	538	568	BOXPYR™ 540/540	538	568	BOXPYR™ 540/540	538	568	Alexa Fluor® 700	702	723	Alexa Fluor® 700	702	723	Alexa Fluor® 700	702	723	Alexa Fluor® 700	702	723	Alexa Fluor® 700	702	723
Mag Indo-1	350	417	GFP (tagged)	488	508	Calccein Green™	506	531	Di (DiI(18) 18)	449	546	Calccein Green™	506	531	Calccein Green™	506	531	Alexa Fluor® 750	749	775	Alexa Fluor® 750	749	775	Alexa Fluor® 750	749	775	Alexa Fluor® 750	749	775	Alexa Fluor® 750	749	775
Pyrene	345	378	1,6-DIAMCyan	336	480	CFP (enhanced)	435	505	Erythrosin	529	554	CFP (enhanced)	435	505	Erythrosin	529	554	Alexa Fluor® 780	779	805	Alexa Fluor® 780	779	805	Alexa Fluor® 780	779	805	Alexa Fluor® 780	779	805	Alexa Fluor® 780	779	805



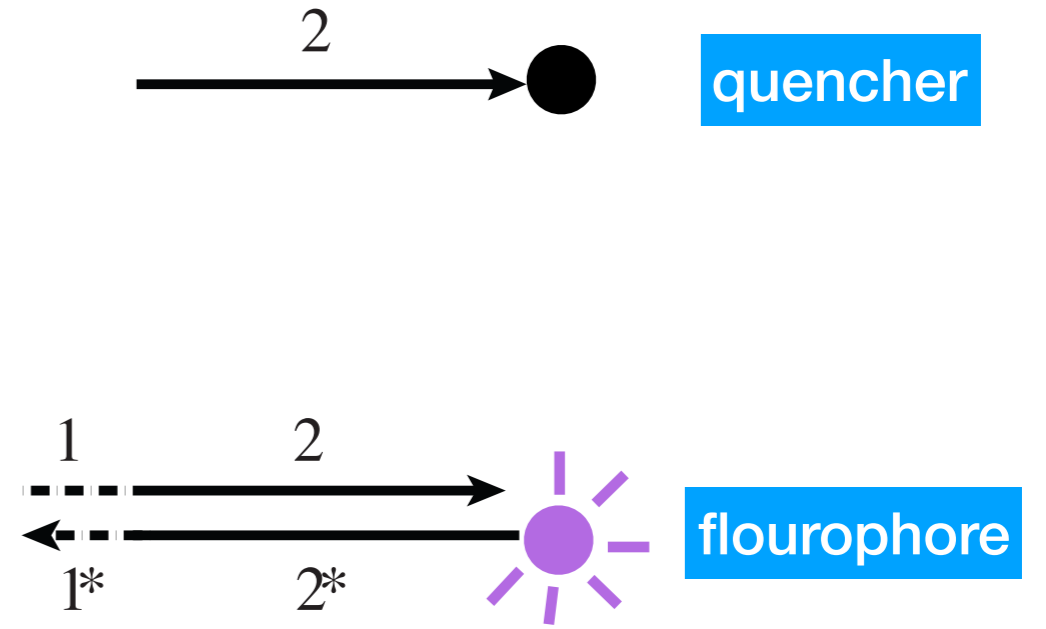


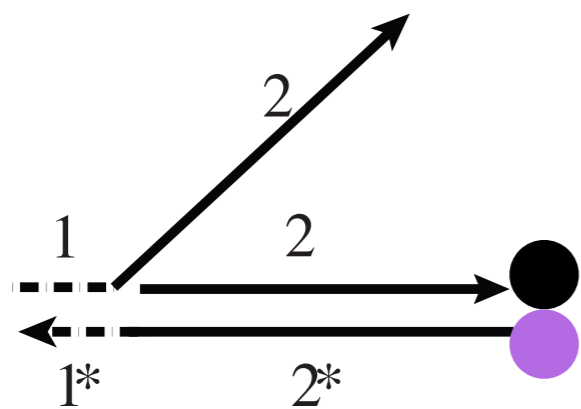
**displace**



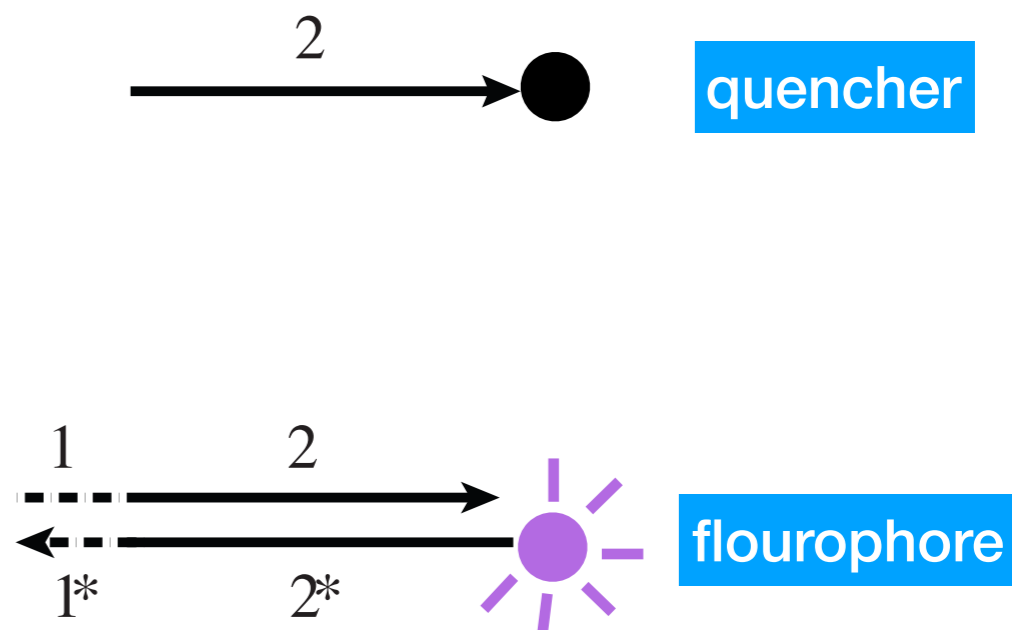


**displace**

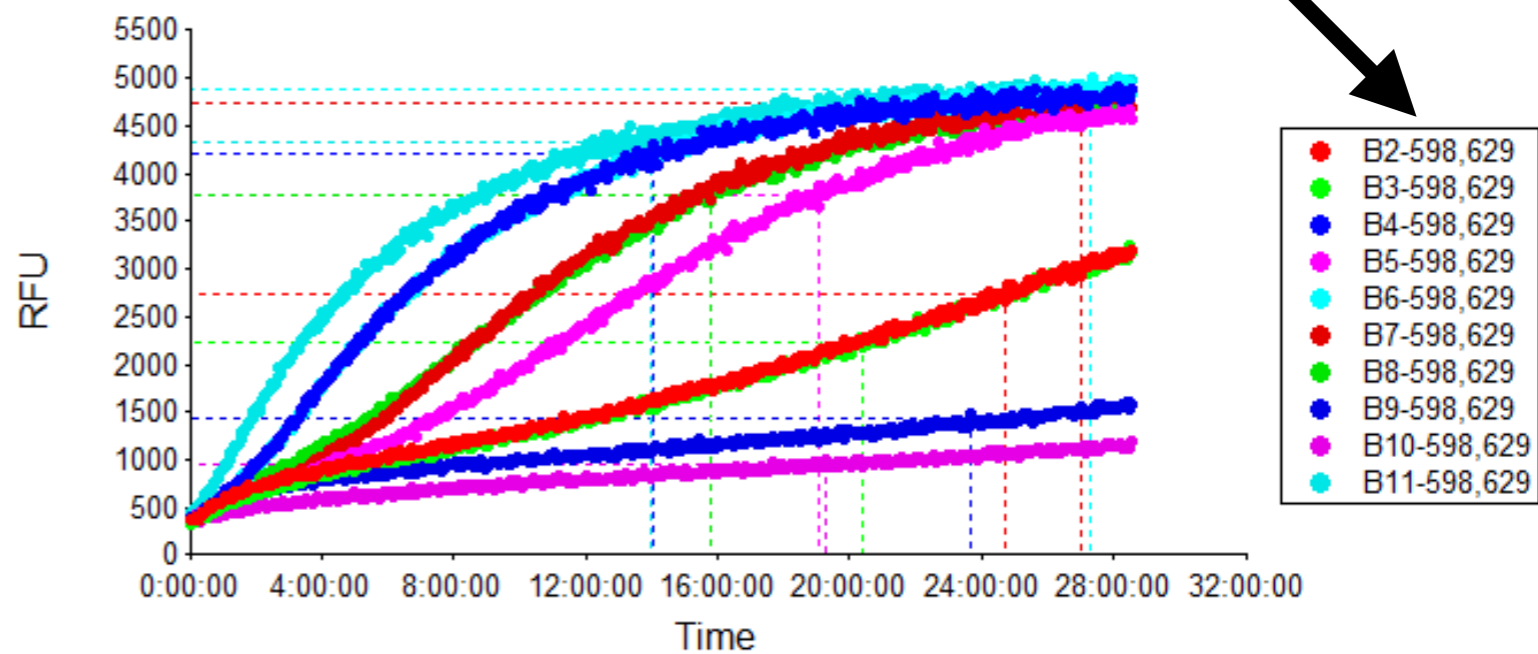




**displace**



**read many different samples**

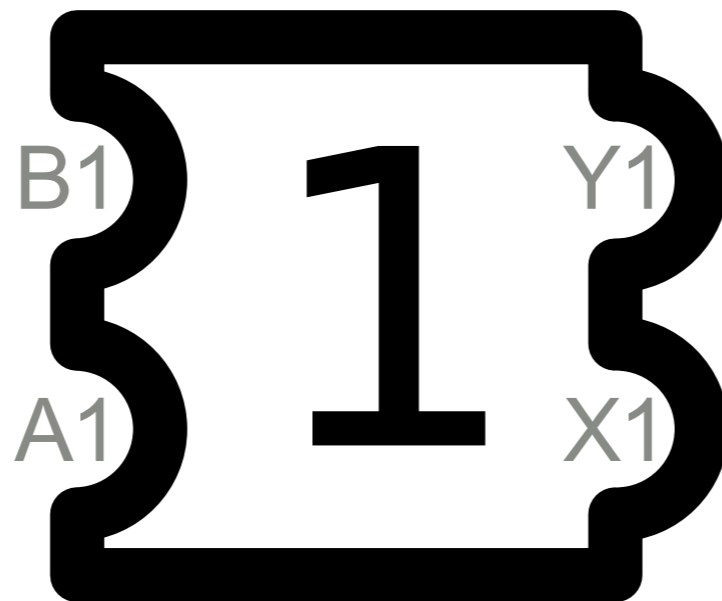


# A reaction gate



This *universal component*  
can realize a number of logic gates

# A reaction gate



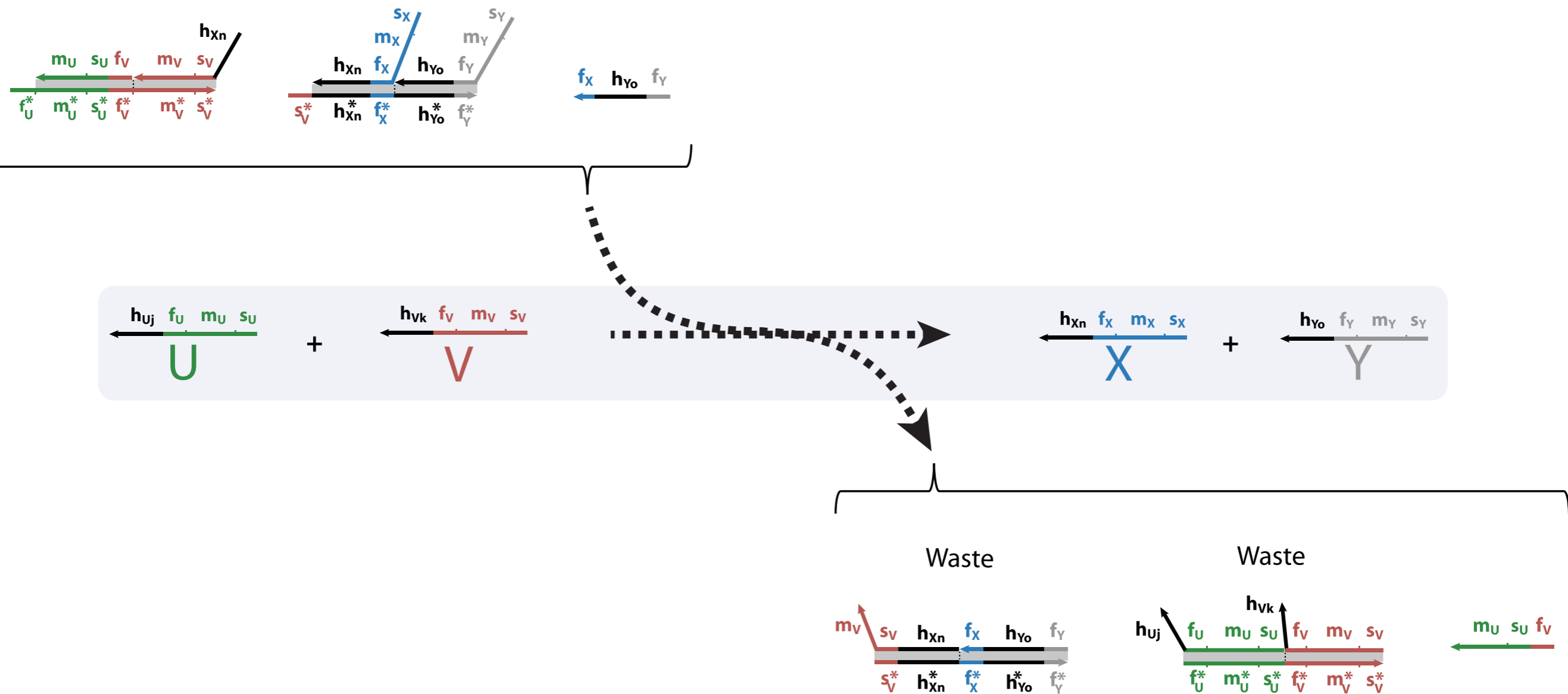
This *universal component* can realize a number of logic gates



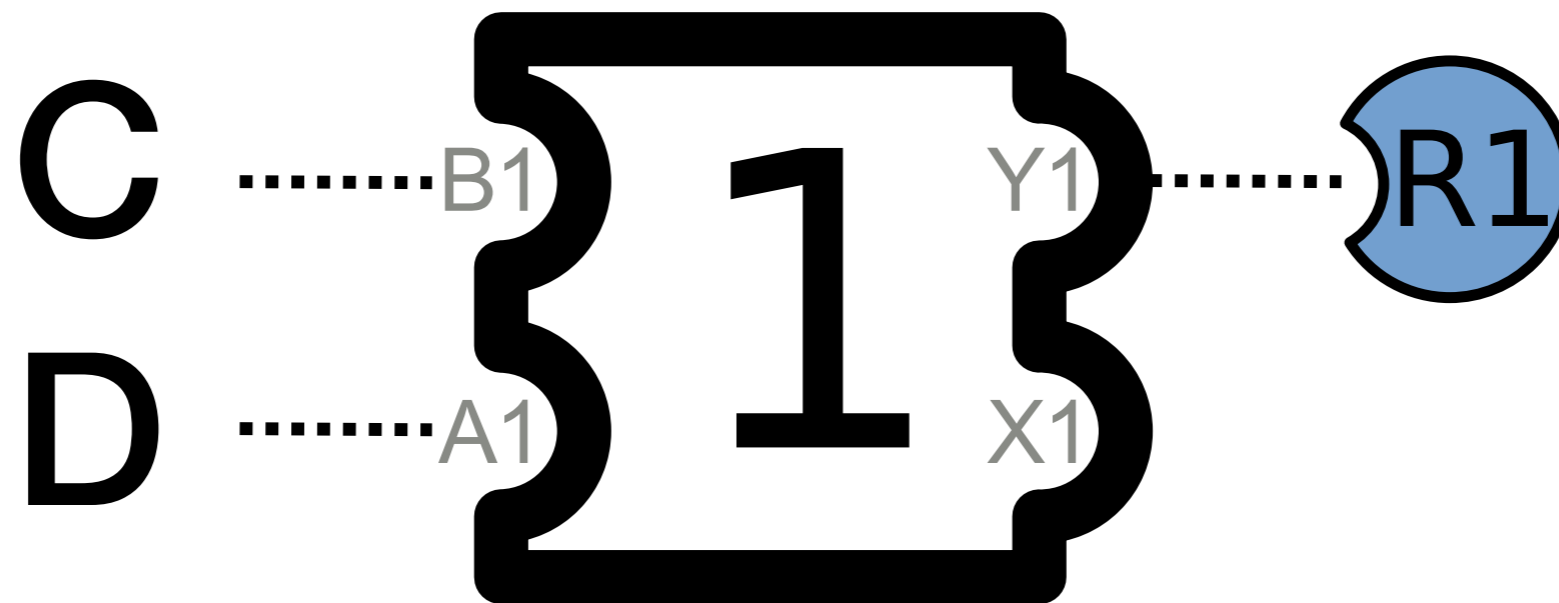
To implement this:



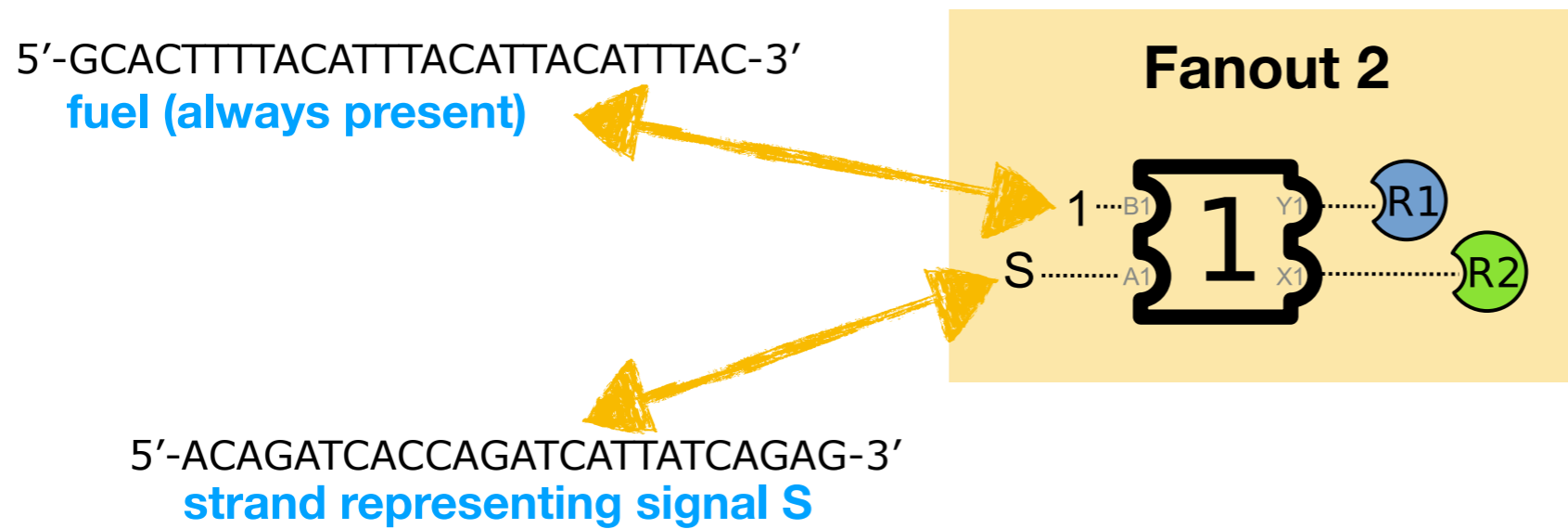
We start with large excess of DNA complexes (fuels) that mediate the reaction:



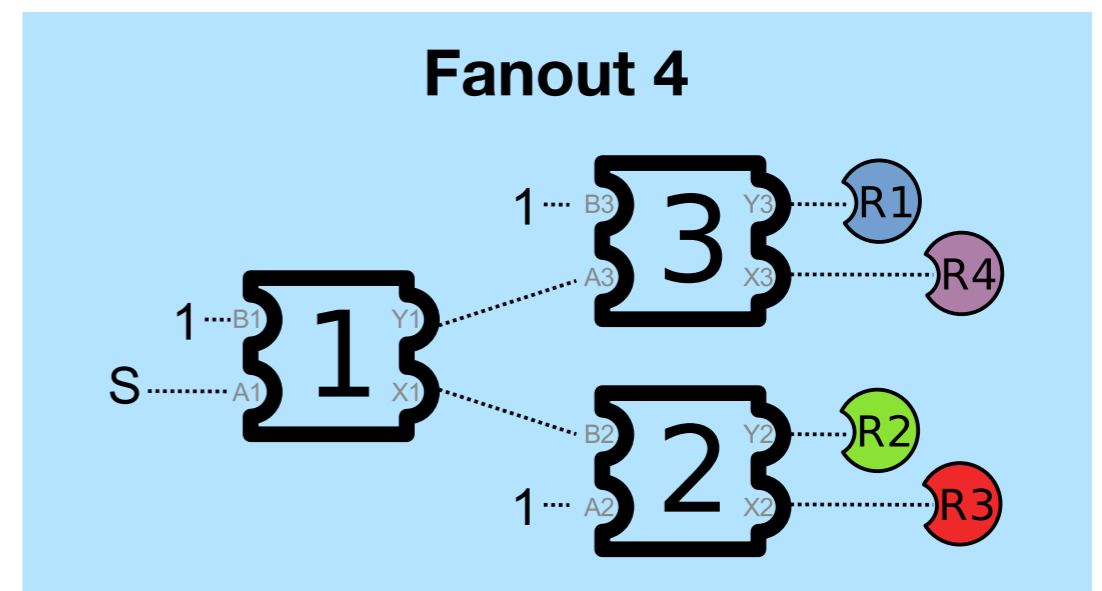
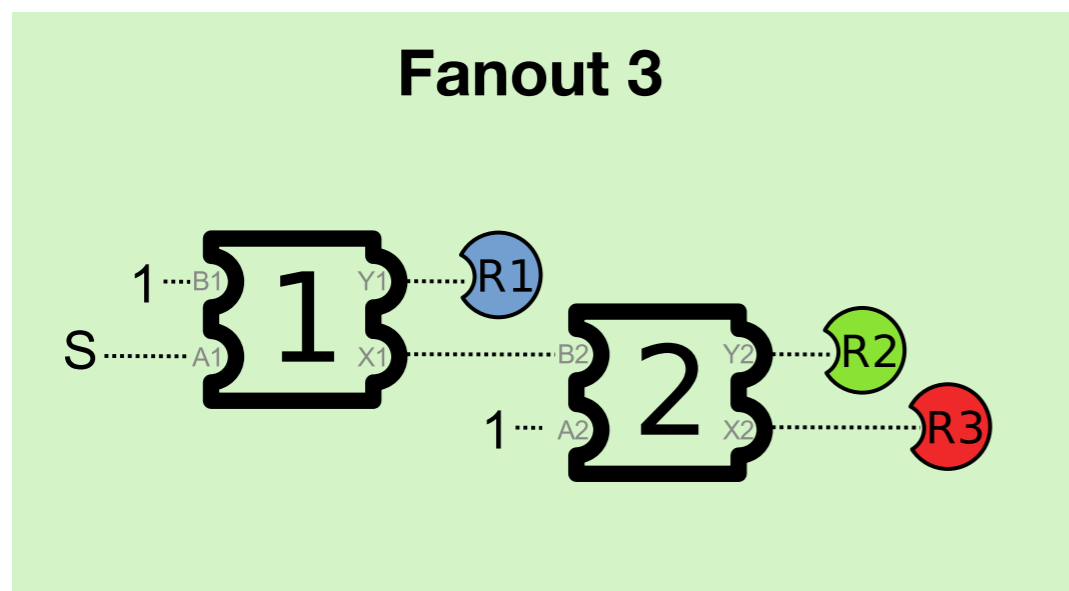
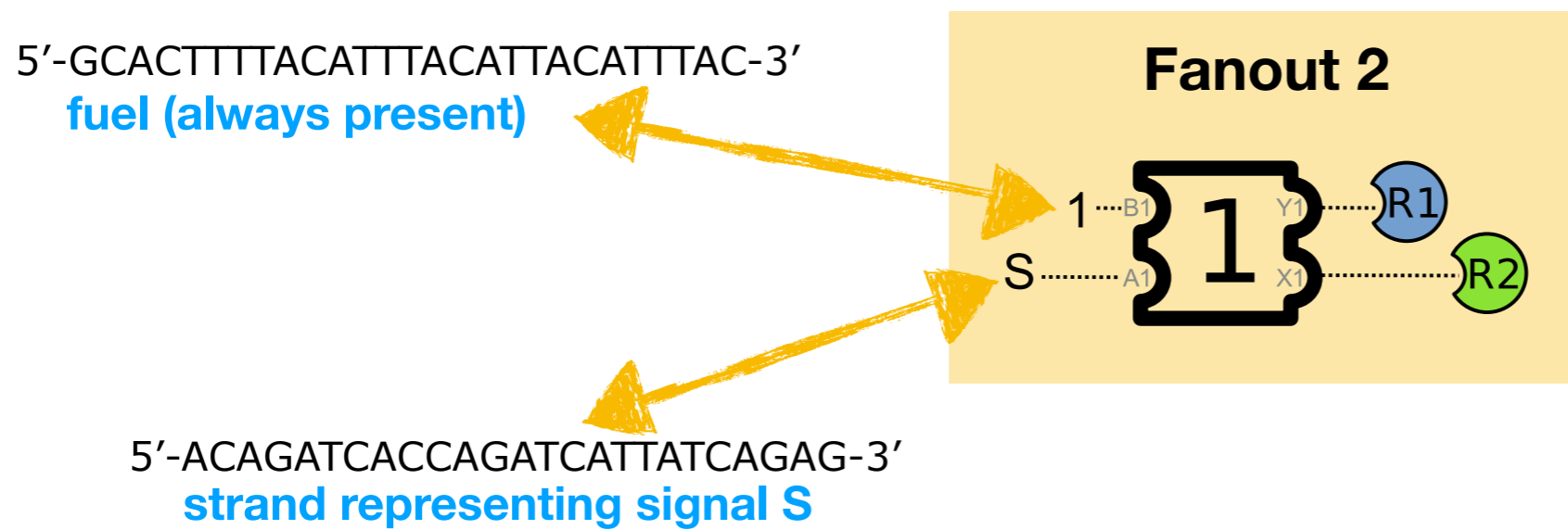
# AND gate



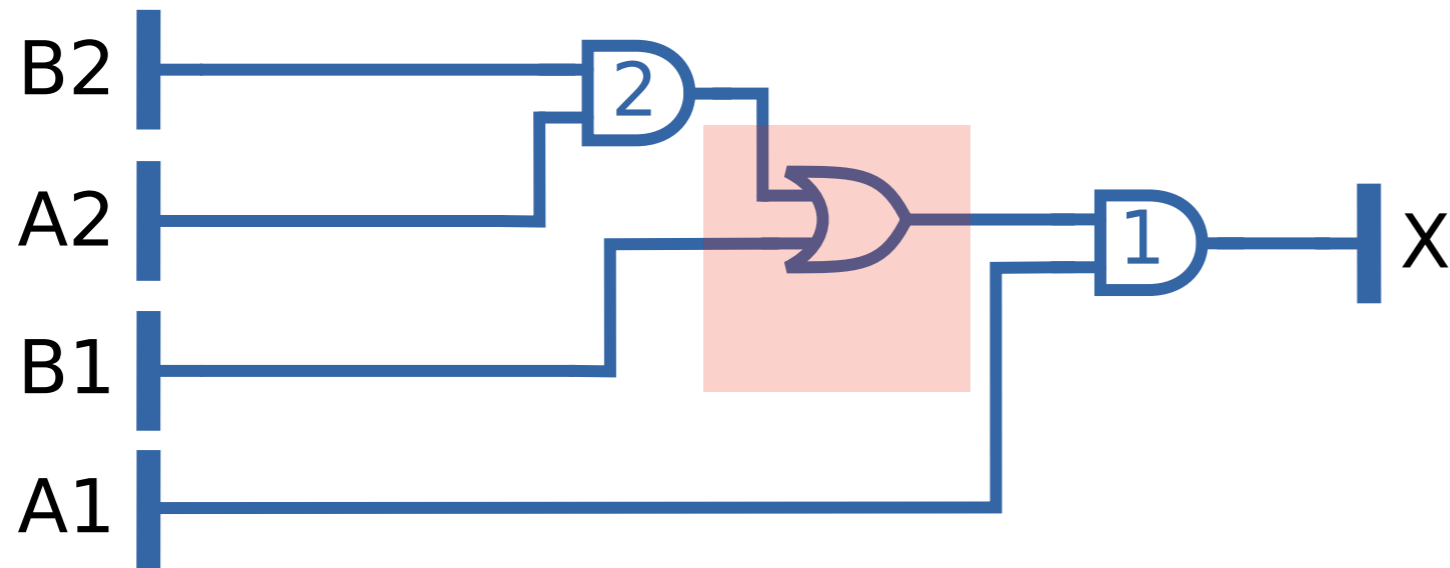
# Signal Fanout Gates



# Signal Fanout Gates

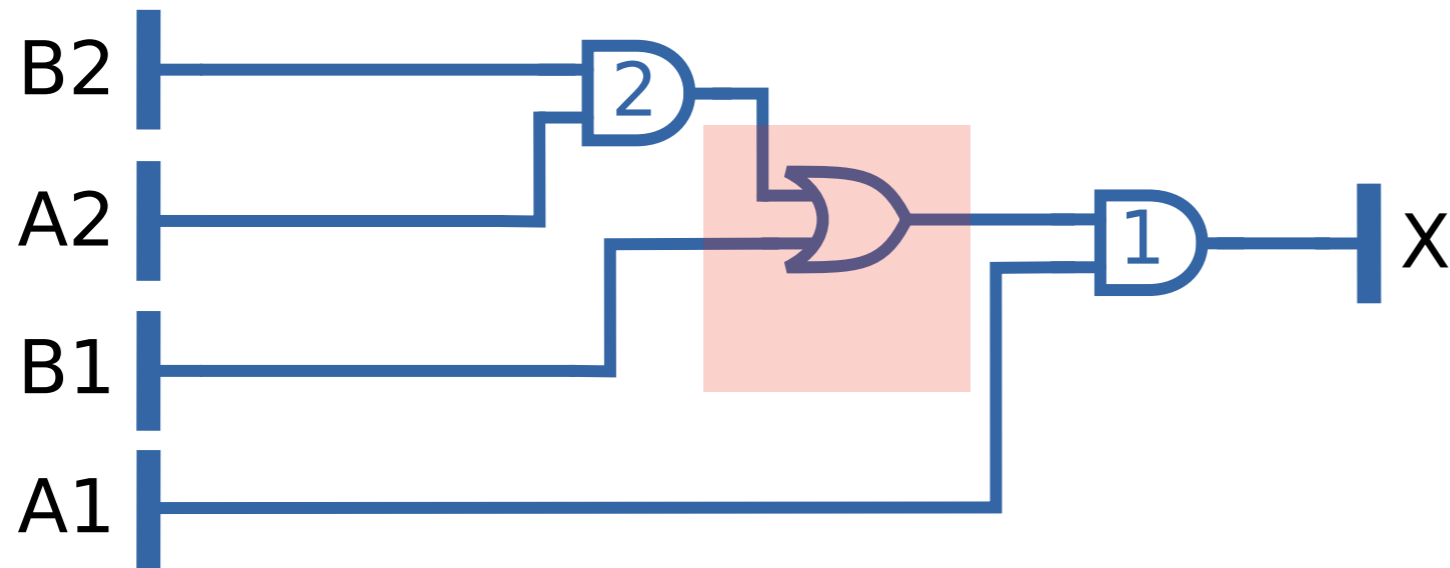


# Handling OR gates

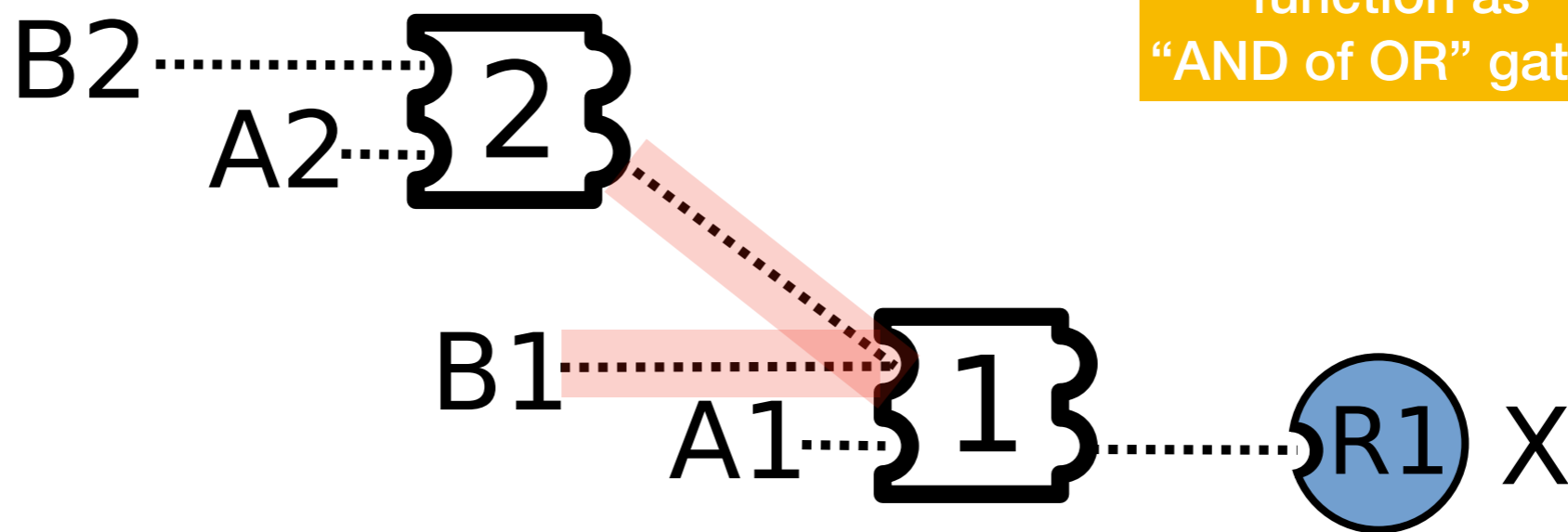


**AND( A1, OR( B1, AND( A2, B2 ) ) )**

# Handling OR gates

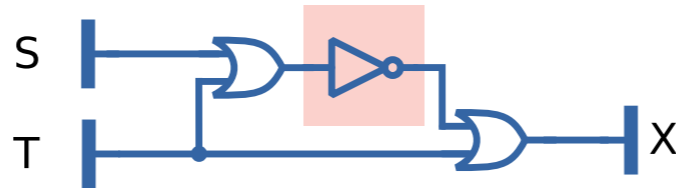


Reaction gates  
function as  
"AND of OR" gates



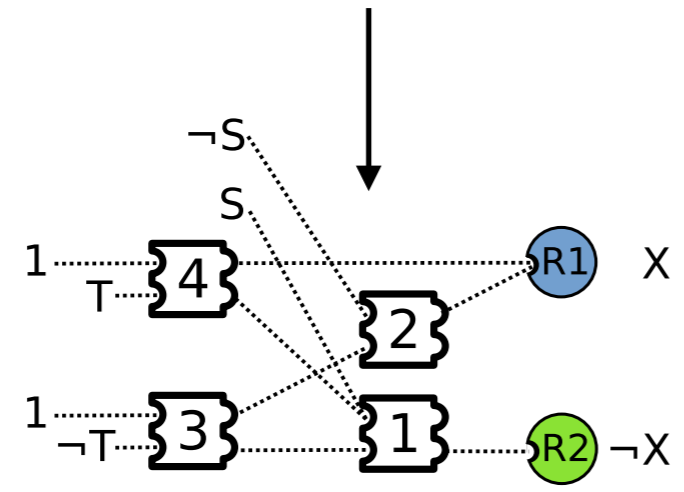
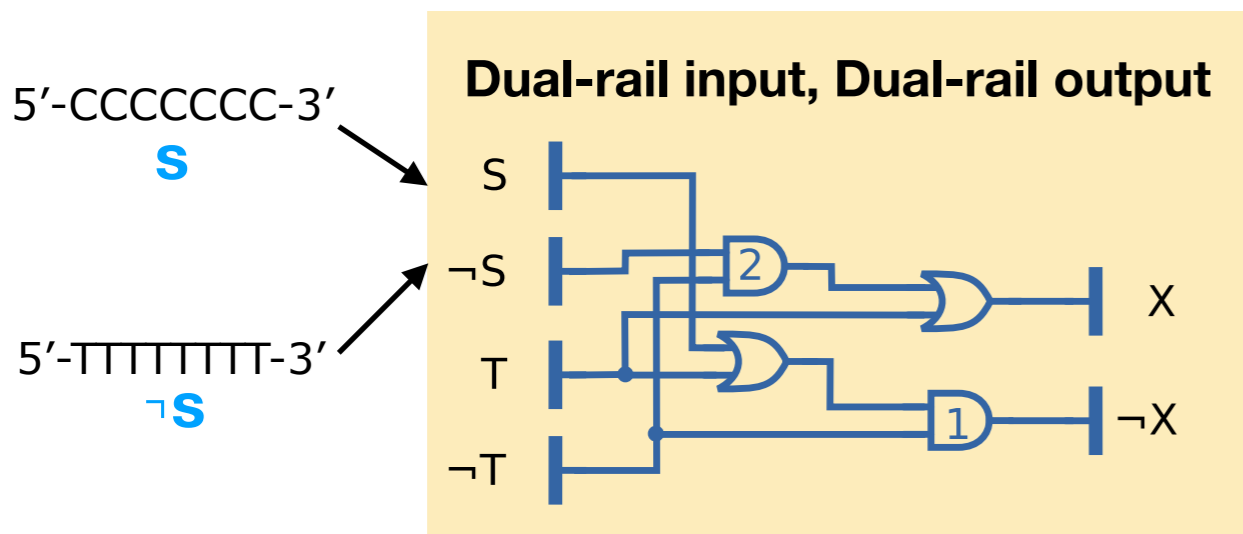
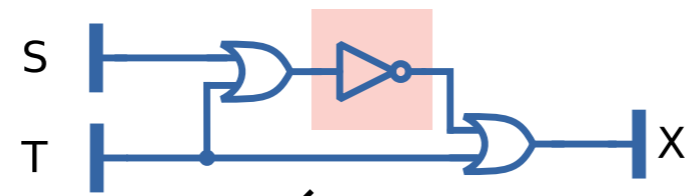
**AND( A1, OR( B1, AND( A2, B2 ) ) )**

# Handling NOT gates



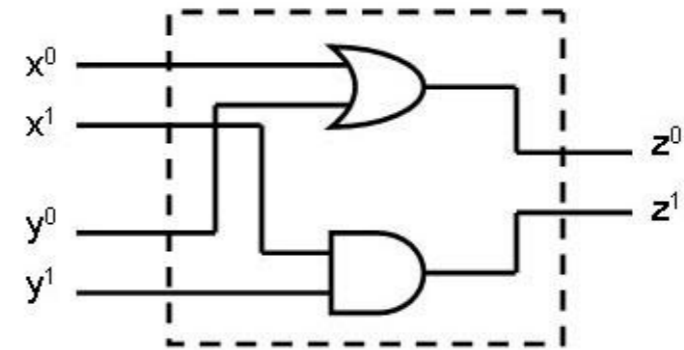
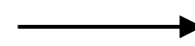
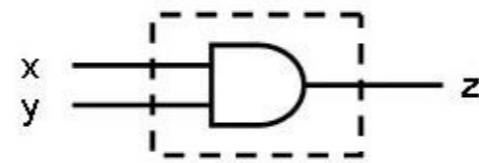


# Handling NOT gates

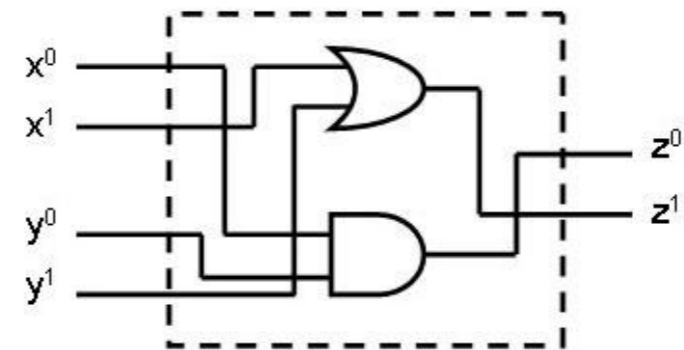
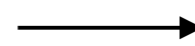
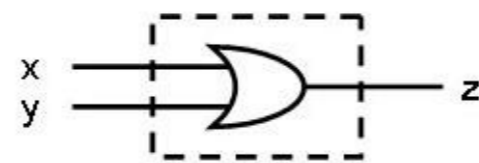


# Dual rail logic

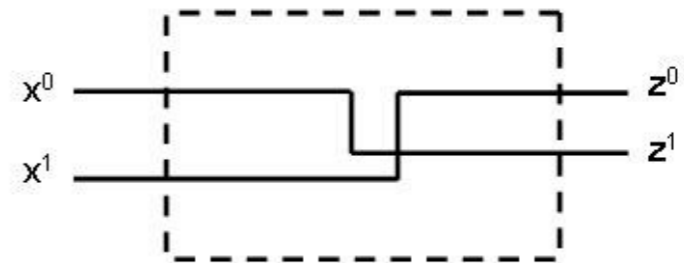
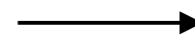
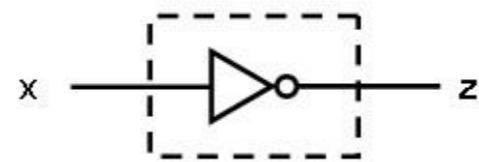
AND



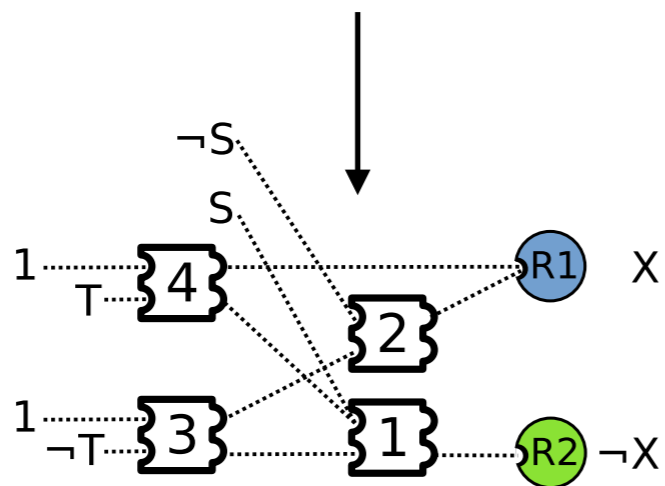
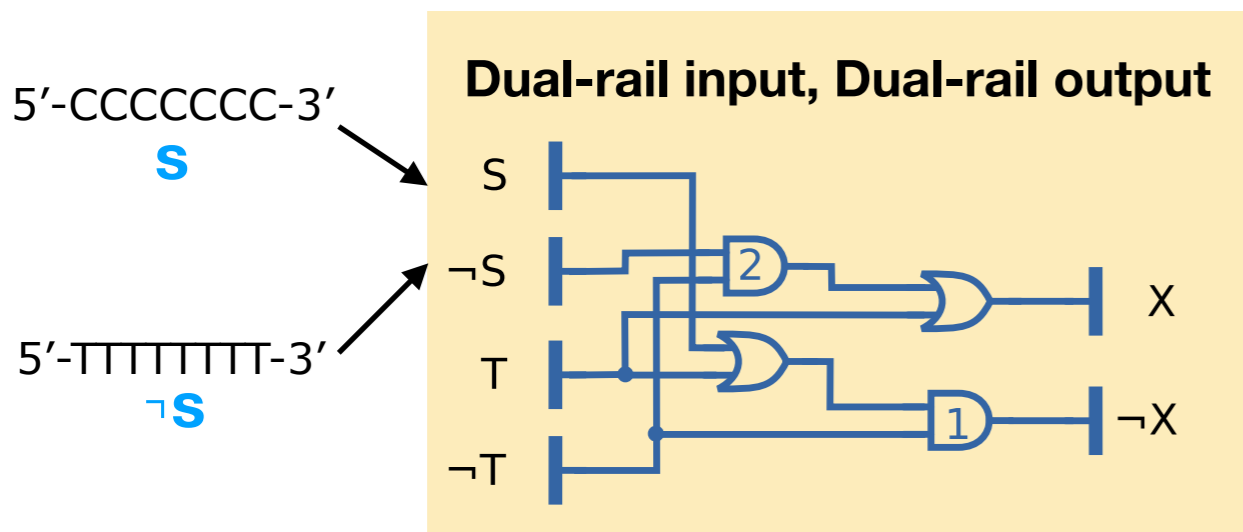
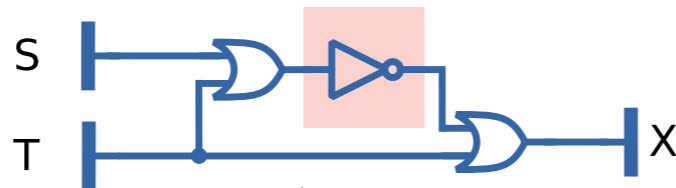
OR



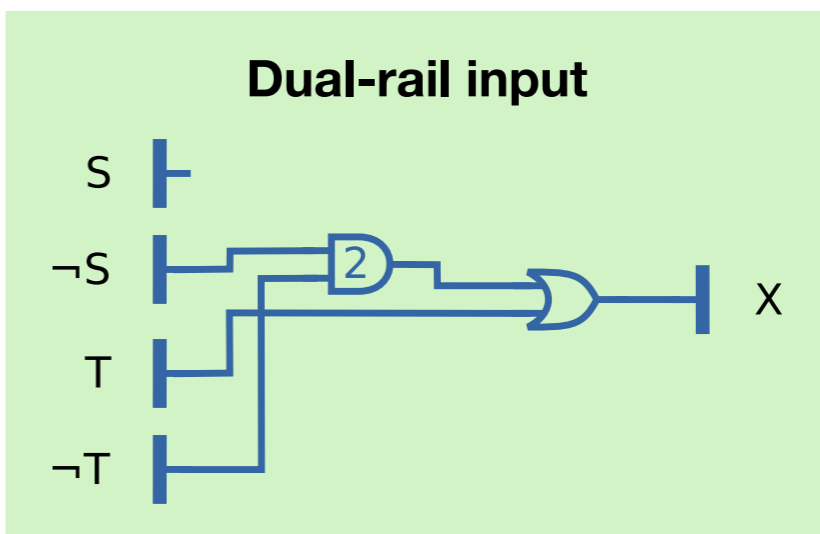
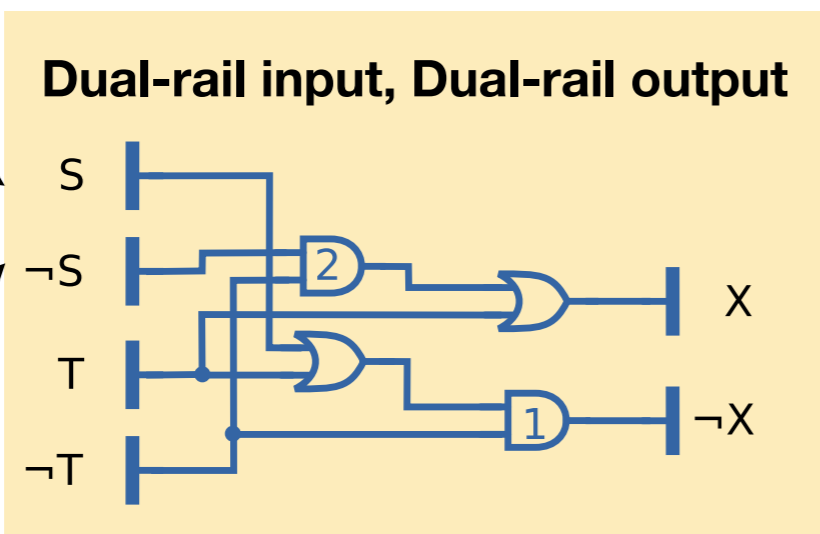
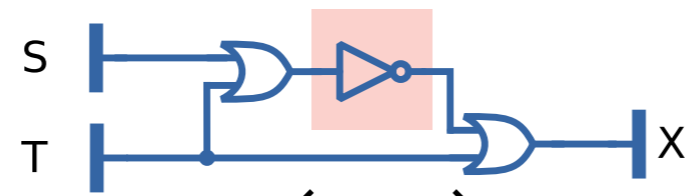
NOT



# Handling NOT gates

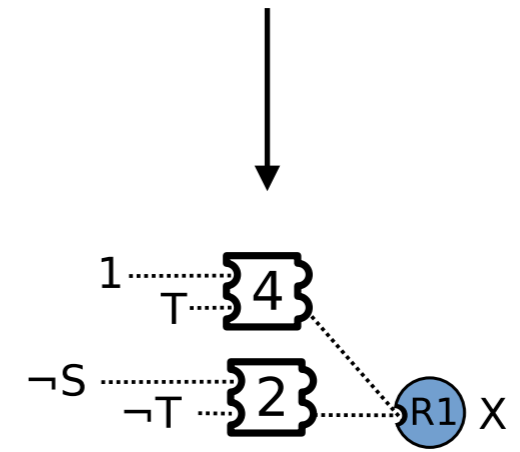
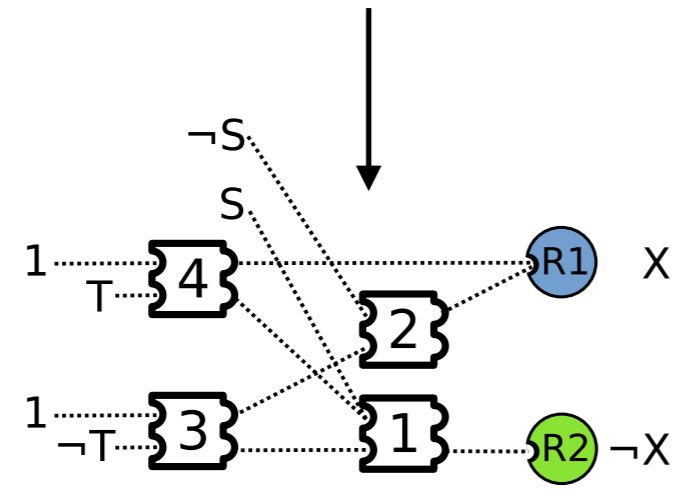


# Handling NOT gates

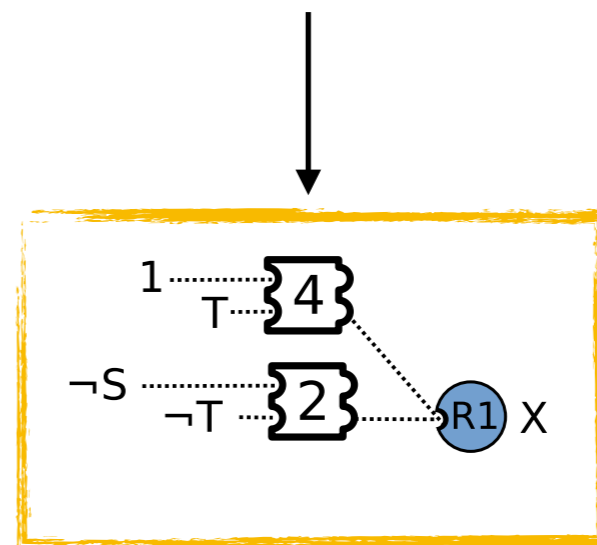
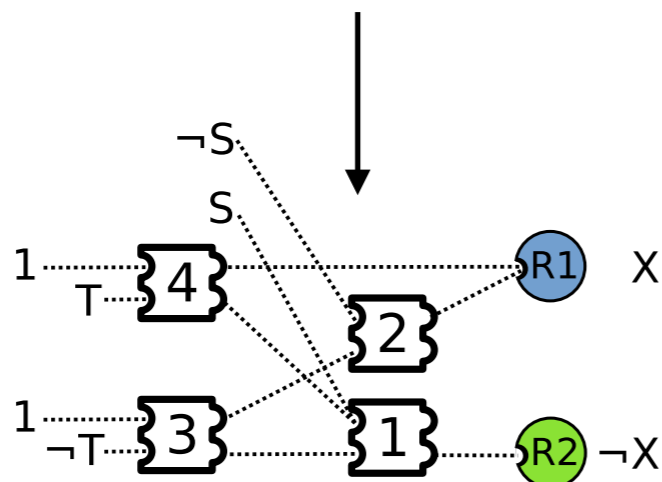
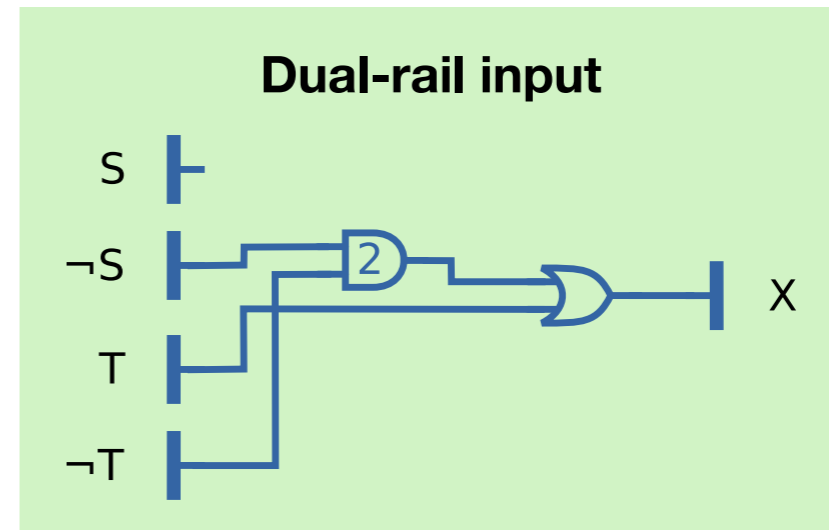
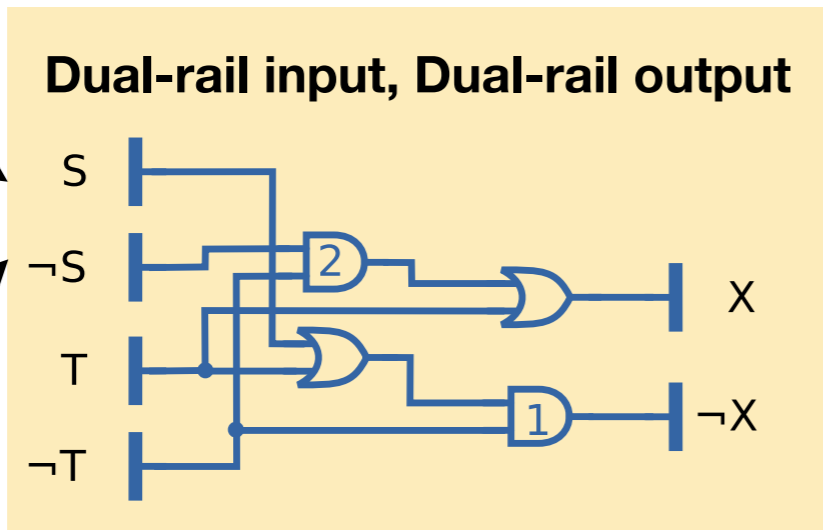
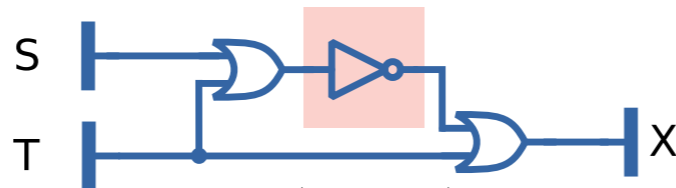


5'-CCCCCCC-3'  
**S**

5'-TTTTTTT-3'  
**¬S**



# Handling NOT gates



With reaction gates, wires,  
and dual-rail encoding, we can  
build any combinatorial circuit

# Tutorial Outline

- ▶ Review of strand displacement
- ▶ Building and composing logic gates
- ▶ **Tools for designing and verifying circuits**
- ▶ Robustness of strand displacement

# How do you design the circuit?

2-input MUX			
A	B	s	out
0	0	0	0
0	1	0	1
1	0	0	0
1	1	0	1
0	0	1	0
0	1	1	0
1	0	1	1
1	1	1	1

2-output DEMUX			
in	r	X	Y
0	0	0	0
1	0	0	1
0	1	0	0
1	1	1	0

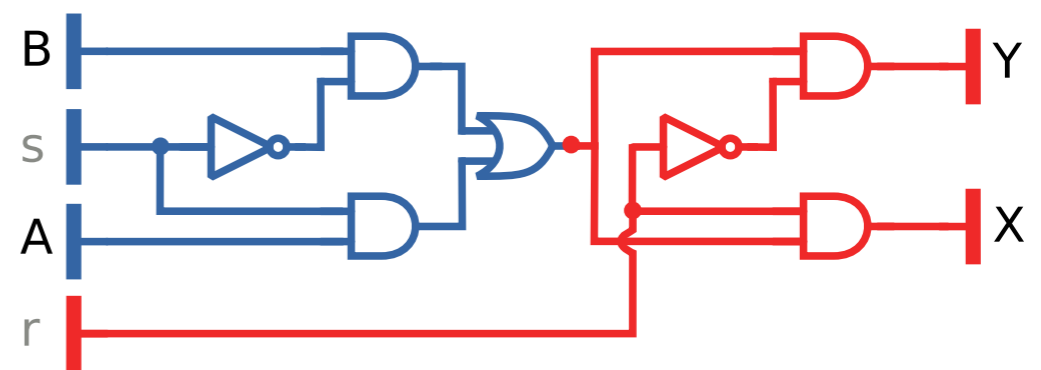




# How do you design the circuit?

2-input MUX				2-output DEMUX			
A	B	s	out	in	r	X	Y
0	0	0	0	0	0	0	0
0	1	0	1	1	0	0	1
1	0	0	0	0	1	0	0
1	1	0	1	1	1	1	0
0	0	1	0	0	0	1	0
0	1	1	0	0	1	1	0
1	0	1	1	0	0	1	1
1	1	1	1	0	1	1	1

Compile from Verilog, or truth table, into AND-OR-NOT circuit

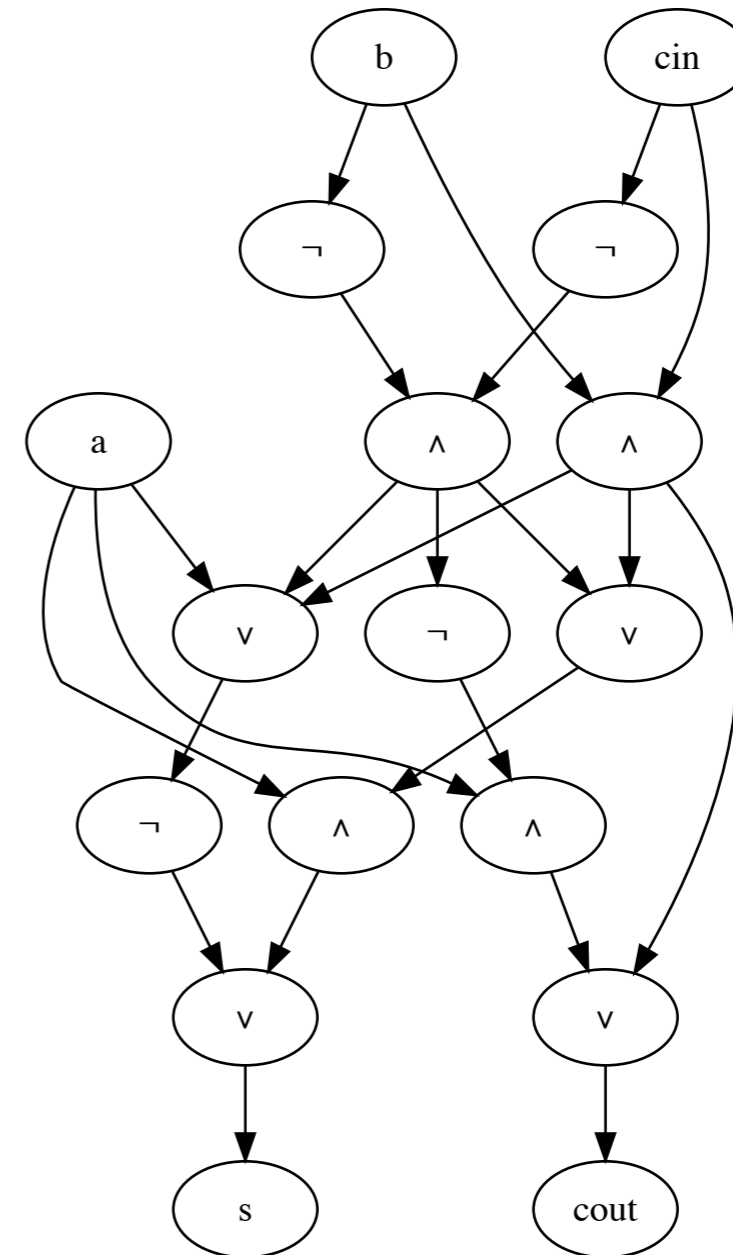


# How do you design the circuit?

Inputs			Outputs	
<b>A</b>	<b>B</b>	<b>C<sub>in</sub></b>	<b>C<sub>out</sub></b>	<b>S</b>
0	0	0	0	0
0	0	1	0	1
0	1	0	0	1
0	1	1	1	0
1	0	0	0	1
1	0	1	1	0
1	1	0	1	0
1	1	1	1	1

# How do you design the circuit?

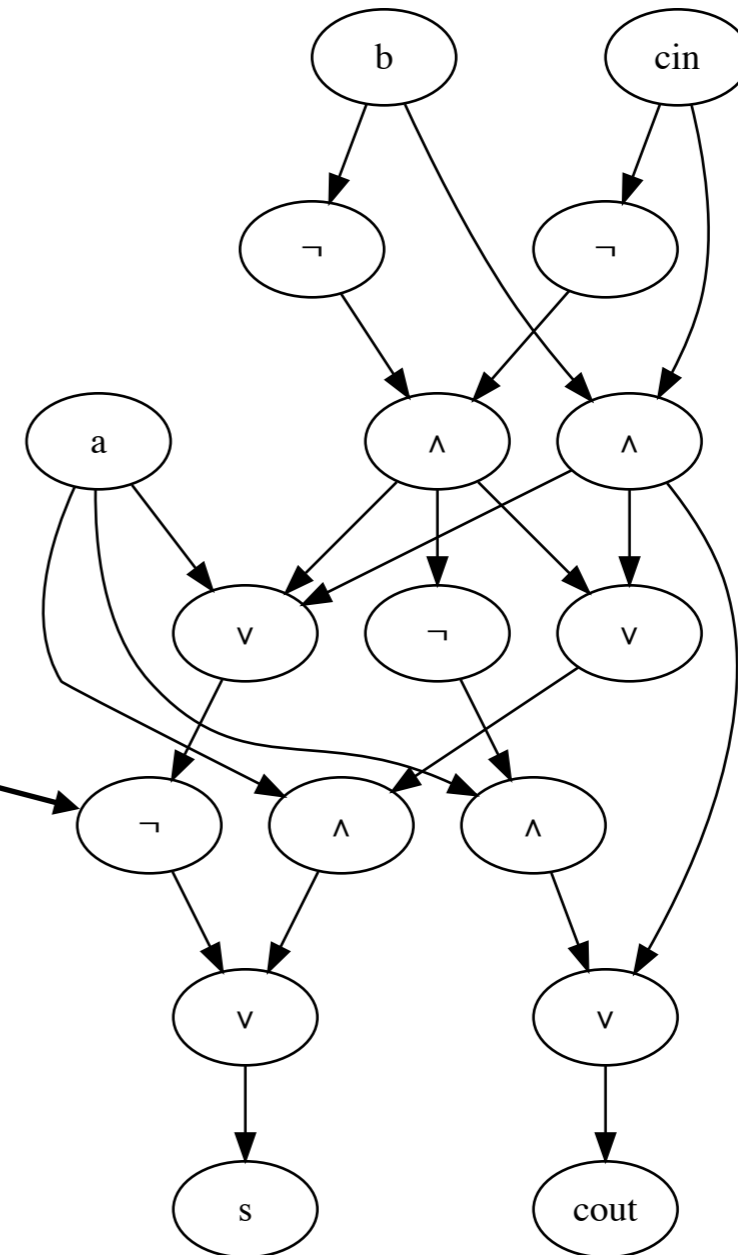
✓ Find minimized AND-OR-NOT circuit using **ABC**



# How do you design the circuit?

- ✓ Find minimized AND-OR-NOT circuit using **ABC**

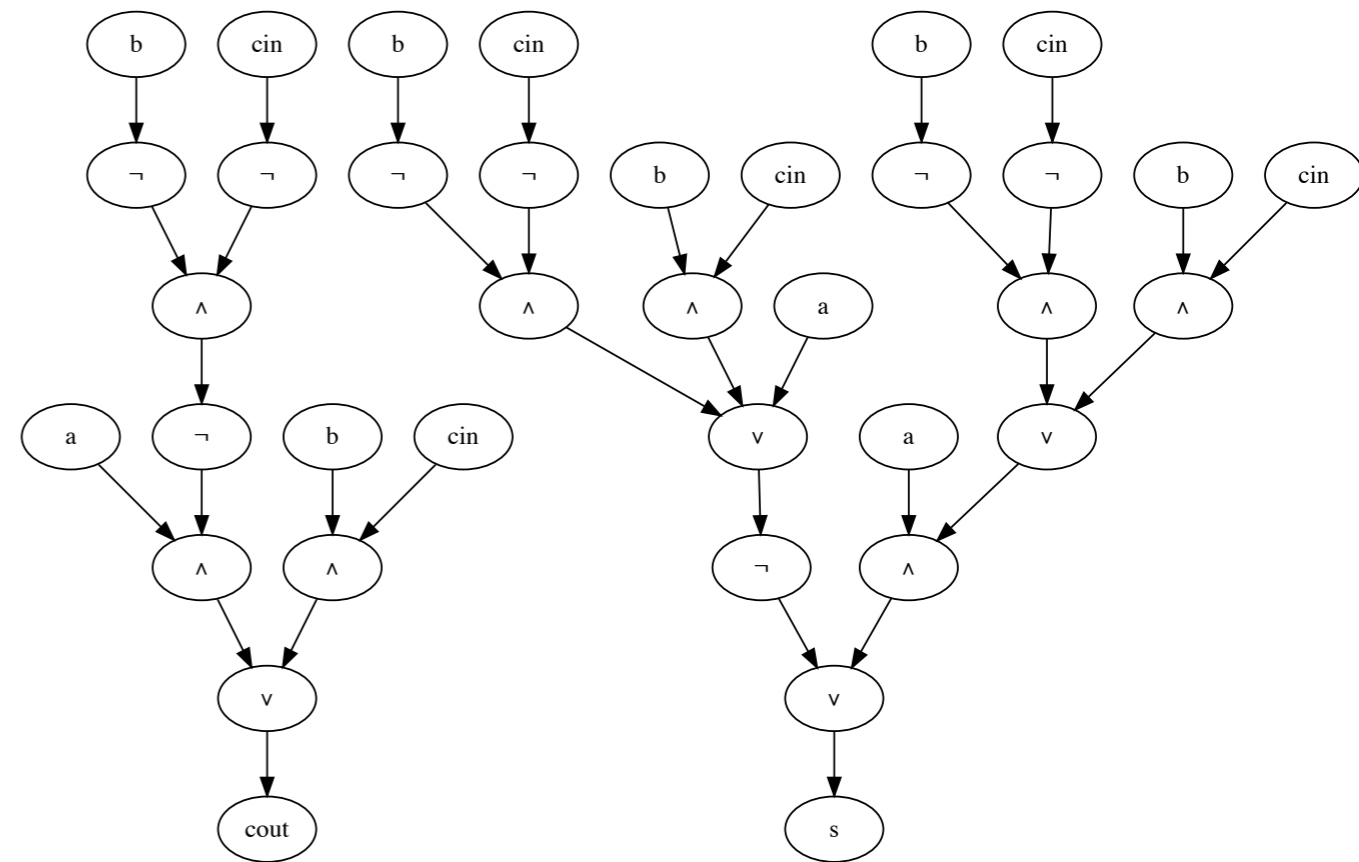
Need to remove explicit NOT gates



# How do you design the circuit?

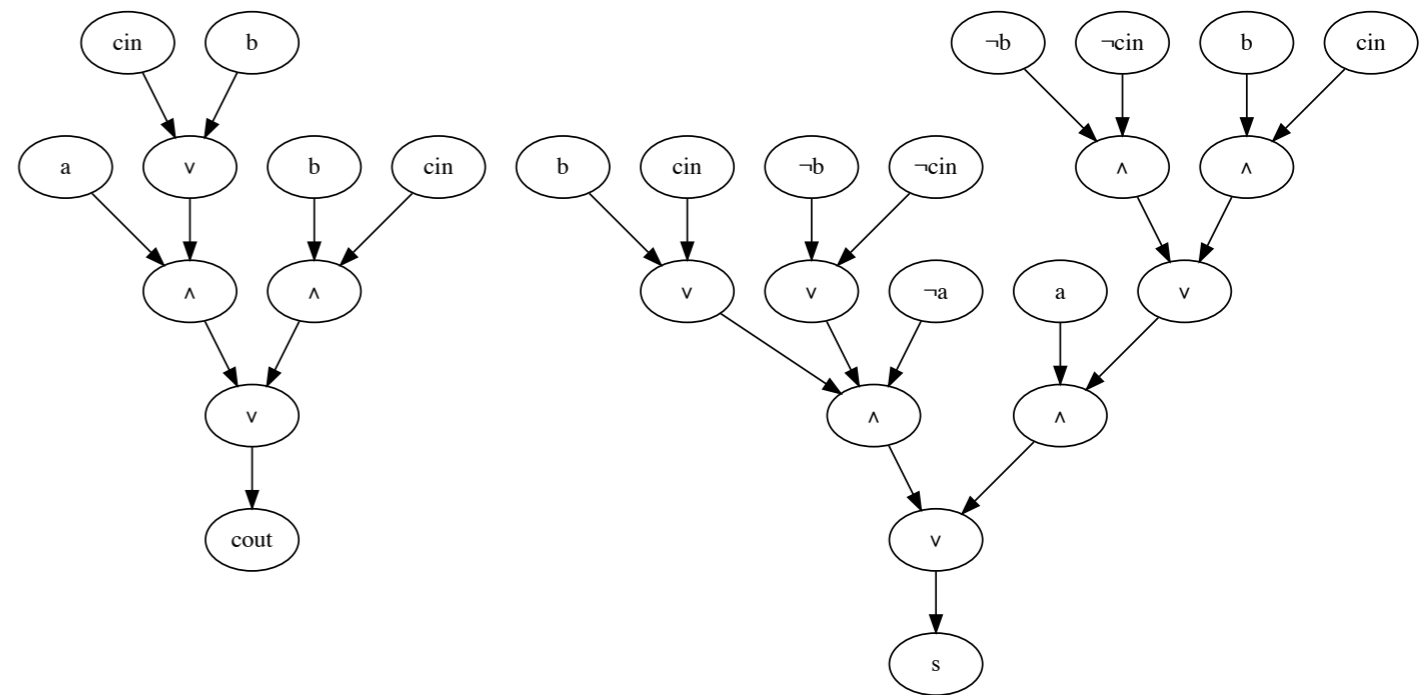
✓ Find minimized AND-OR-NOT circuit using ABC

✓ “Tree-ify” circuit



# How do you design the circuit?

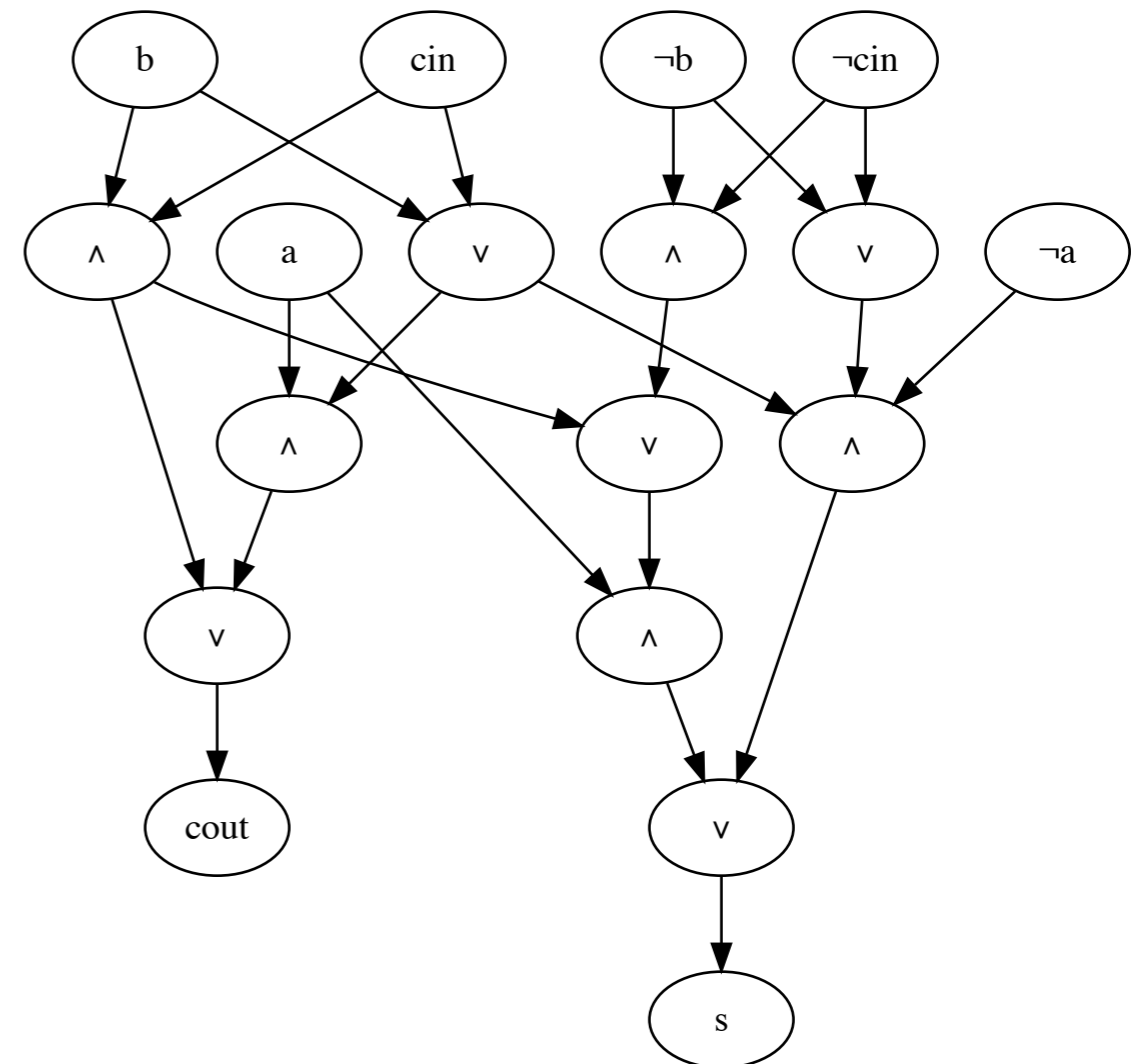
- ✓ Find minimized AND-OR-NOT circuit using ABC
- ✓ “Tree-ify” circuit
- ✓ Push negations to literal level (dual-rail inputs)



# How do you design the circuit?

- ✓ Find minimized AND-OR-NOT circuit using ABC
- ✓ “Tree-ify” circuit
- ✓ Push negations to literal level (dual-rail inputs)
- ✓ Compress circuit

Circuit now using  
dual-rail input



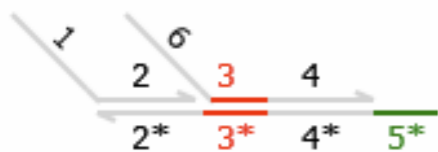
# From circuit to DSD system

DSD: formal language for describing and modeling strand displacement cascades

<http://lepton.research.microsoft.com/webdna/>

$\langle 1 \rangle [2]: \langle 6 \rangle [3^{\wedge} 4]: 5^{\wedge}$

=



Phillips, Cardelli, *Journal of Royal Society Interface*, 2009



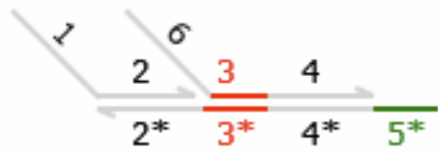
# From circuit to DSD system

DSD: formal language for describing and modeling strand displacement cascades

<http://lepton.research.microsoft.com/webdna/>

$\langle 1 \rangle [2] : \langle 6 \rangle [3^{\wedge} 4] : 5^{\wedge} *$

=



The screenshot shows the webdna interface with a code editor on the left and a graphical representation of a strand displacement reaction on the right. The code includes directives for simulation and species definitions. The graphical representation shows a strand with segments y1, t, y1, x and its interaction with another strand.

## formal semantics

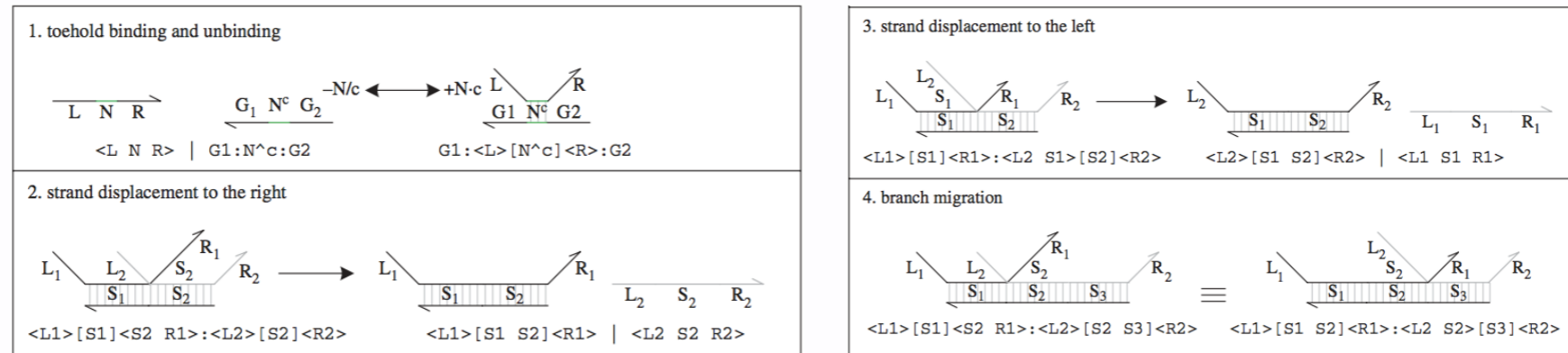
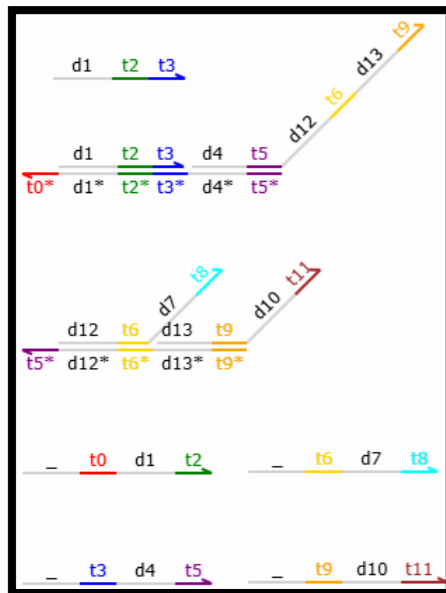


Figure 2. Reduction and branch migration rules of the strand displacement language. For each rule, the graphical representation at the top is equivalent to the program code at the bottom.

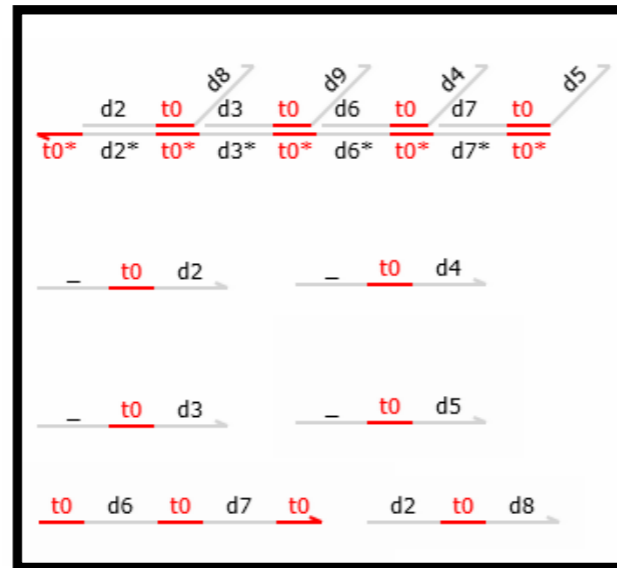
# From circuit to DSD system

$$A + B \rightarrow C + D$$

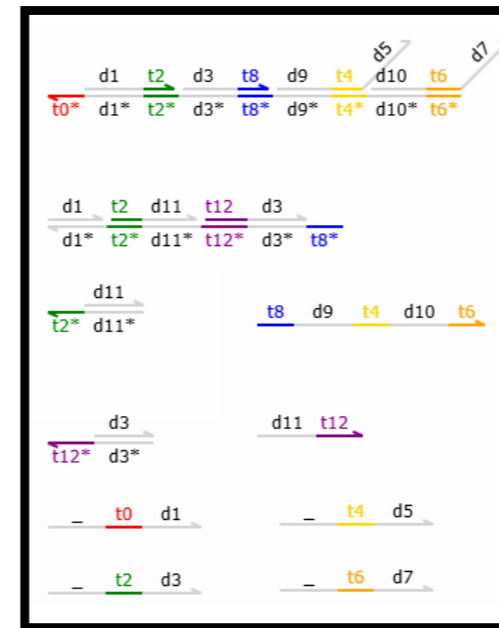
Soloveichik  
et al. (2010)



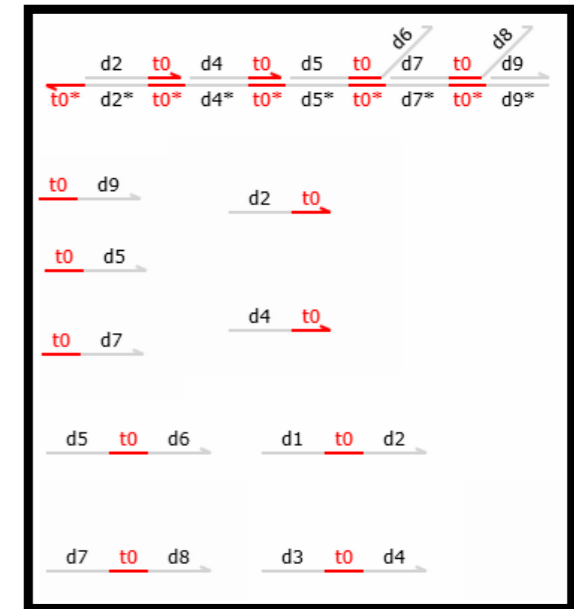
Lakin  
et al. (2012)



Cardelli (2011)



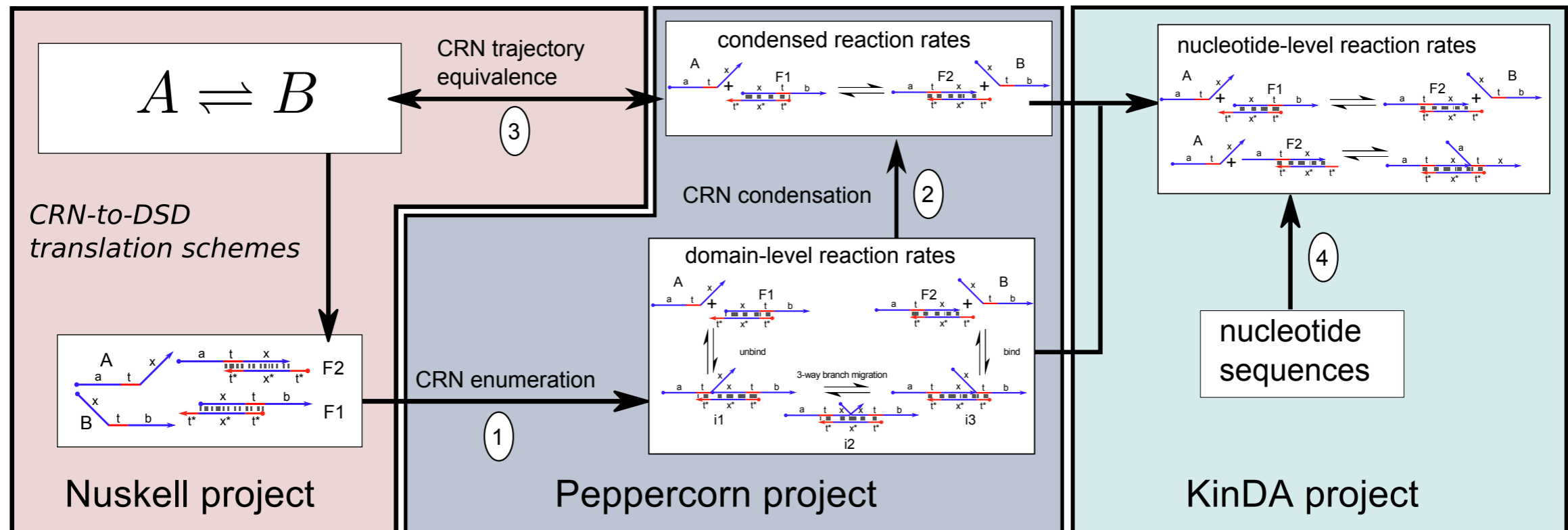
Qian et al. (2011)



Chen et al. (2012), Cardelli (2013), Srinivas (2015), Lakin et al. (2016), ...

Images drawn using VisualDSD, Lakin et al. (2012)

# The Nuskell compiler framework



Badelt et al. (2017) - Nuskell

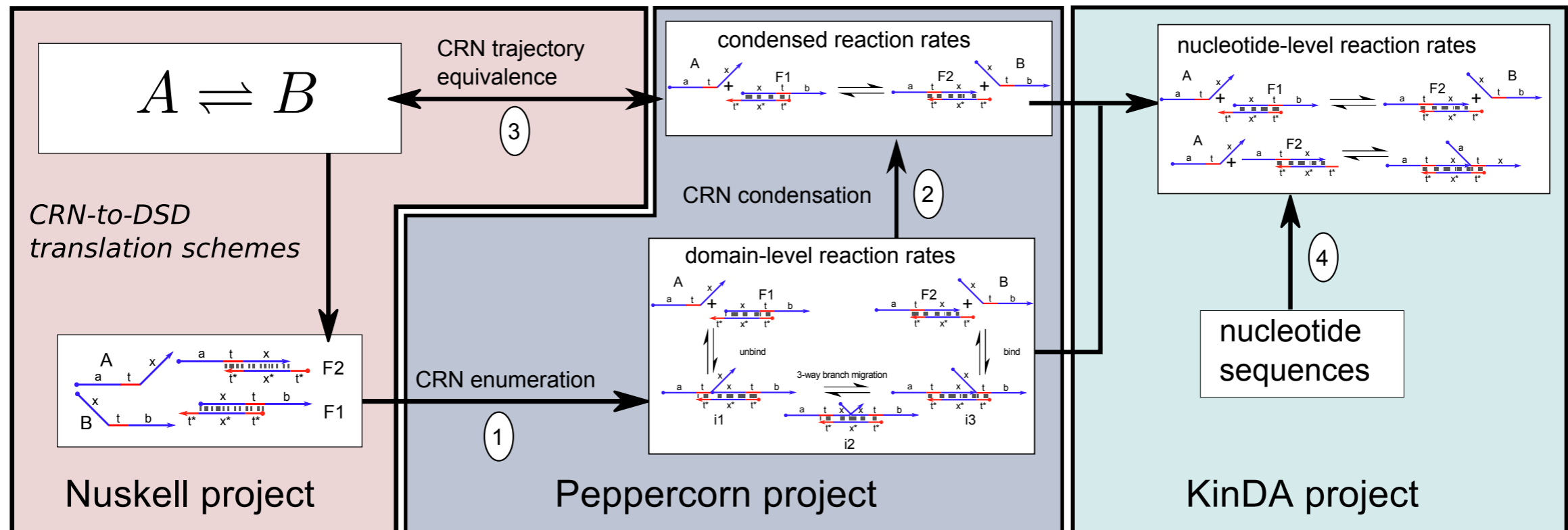
Grun et al. (2014) - Peppercorn

Shin et al. (2017) - CRN pathway decomposition equivalence

Johnson et al. (2018) - CRN bisimulation equivalence

Berleant et al. (submitted) - KinDA

# The Nuskell compiler framework



Badelt et al. (2017) - Nuskell

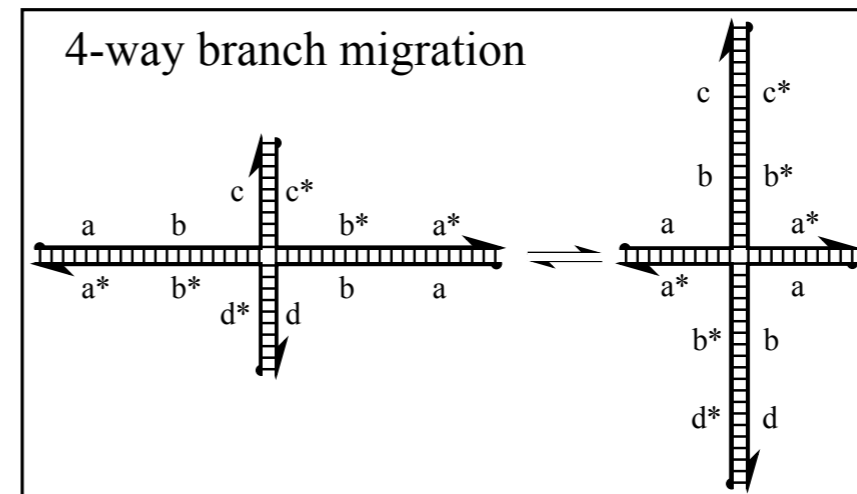
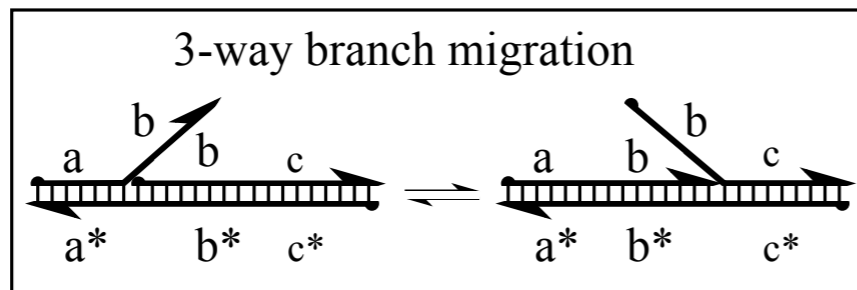
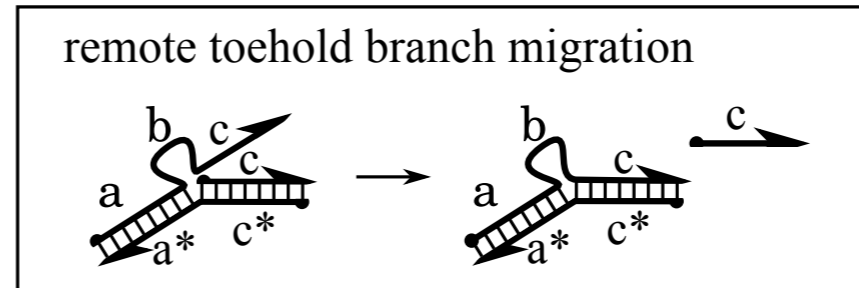
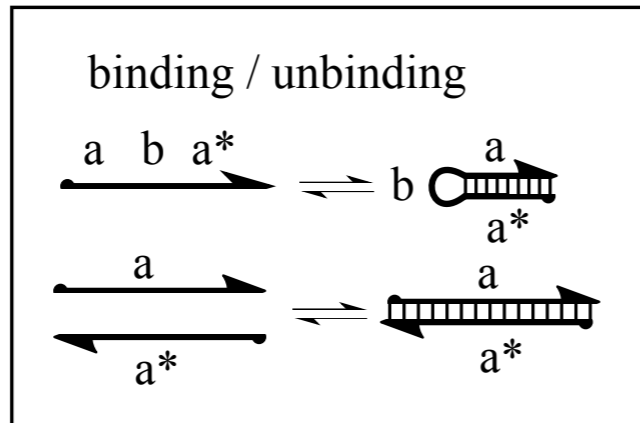
Grun et al. (2014) - Peppercorn

Shin et al. (2017) - CRN pathway decomposition equivalence

Johnson et al. (2018) - CRN bisimulation equivalence

Berleant et al. (submitted) - KinDA

# Reaction Enumeration



# CRN equivalence verification

## formal input CRN

3 species

7 reactions

$A \rightarrow A + A$

$A + A \rightarrow A$

$A + B \rightarrow B + B$

$B \rightarrow$

$A + C \rightarrow$

$C \rightarrow C + C$

$C + C \rightarrow C$

## enumerated CRN

360 species

668 reactions

# CRN equivalence verification

## formal input CRN

3 species

7 reactions

$A \rightarrow A + A$

$A + A \rightarrow A$

$A + B \rightarrow B + B$

$B \rightarrow$

$A + C \rightarrow$

$C \rightarrow C + C$

$C + C \rightarrow C$

## enumerated CRN

360 species

668 reactions

# CRN equivalence verification

## formal input CRN

3 species

7 reactions

```
A      -> A + A
A + A  -> A
A + B  -> B + B
B      ->
A + C  ->
C      -> C + C
C + C  -> C
```

## condensed CRN

42 species

32 reactions

```
f14 + C -> e1428 + f15
e853 + f12 -> C + f13
A + f4 -> f3 + e71
f2 + e25 -> A + f1
A + e25 -> f2 + e7
e996 + f3 -> A + f10
e1428 + f15 -> f14 + C
f3 + e71 -> A + f4
e465 + B -> e418 + f6
e614 + f9 -> e611 + e730
e996 + C -> e1040 + f12
e465 + f5 -> e514 + e368
e308 + f7 -> f8 + B
e418 + B -> e371 + f6
C + f13 -> e853 + f12
A + f1 -> f2 + e25
B + e71 -> e319 + f7
f2 + e7 -> A + e25
e1040 + f11 -> e1162 + e1163 + e1158
e319 + f7 -> B + e71
e308 + f9 -> e614 + e615 + e611
e371 + f6 -> e418 + B
e1040 + f12 -> e996 + C
f8 + B -> e308 + f7
e319 + f5 -> e372 + e371 + e368
f3 + e7 -> A + f0
e853 + f15 -> e1428 + C
e1428 + C -> e853 + f15
A + f10 -> e996 + f3
e1163 + f11 -> e1158 + e1246
e418 + f6 -> e465 + B
A + f0 -> f3 + e7
```

## enumerated CRN

360 species

668 reactions

Are these networks equivalent?

translation scheme: qian2011\_3D\_var1.ts



# CRN equivalence verification

<b>formal input CRN</b>	<b>interpreted CRN</b>	<b>condensed CRN</b>	<b>enumerated CRN</b>
3 species	3 species	42 species	360 species
7 reactions	7 non-trivial reactions	32 reactions	668 reactions
$A \rightarrow A + A$ $A + A \rightarrow A$ $A + B \rightarrow B + B$ $B \rightarrow$ $A + C \rightarrow$ $C \rightarrow C + C$ $C + C \rightarrow C$	$C \rightarrow C$ $C + C \rightarrow C$ $A \rightarrow A$ $A \rightarrow A$ $A + A \rightarrow A + A$ $A \rightarrow A$ $C \rightarrow C$ $A \rightarrow A$ $B \rightarrow B$ $\rightarrow$ $A + C \rightarrow A + C$ $\rightarrow$ $B \rightarrow B$ $B + B \rightarrow B + B$ $C \rightarrow C + C$ $A \rightarrow A$ $B + A \rightarrow A + B$ $A + A \rightarrow A + A$ $A + C \rightarrow$ $A + B \rightarrow B + A$ $B \rightarrow$ $B + B \rightarrow B + B$ $A + C \rightarrow A + C$ $B \rightarrow B$ $A + B \rightarrow B + B$ $A + A \rightarrow A$ $C + C \rightarrow C + C$ $C + C \rightarrow C + C$ $A \rightarrow A$ $\rightarrow$ $B \rightarrow B$ $A \rightarrow A + A$	$f14 + C \rightarrow e1428 + f15$ $e853 + f12 \rightarrow C + f13$ $A + f4 \rightarrow f3 + e71$ $f2 + e25 \rightarrow A + f1$ $A + e25 \rightarrow f2 + e7$ $e996 + f3 \rightarrow A + f10$ $e1428 + f15 \rightarrow f14 + C$ $f3 + e71 \rightarrow A + f4$ $e465 + B \rightarrow e418 + f6$ $e614 + f9 \rightarrow e611 + e730$ $e996 + C \rightarrow e1040 + f12$ $e465 + f5 \rightarrow e514 + e368$ $e308 + f7 \rightarrow f8 + B$ $e418 + B \rightarrow e371 + f6$ $C + f13 \rightarrow e853 + f12$ $A + f1 \rightarrow f2 + e25$ $B + e71 \rightarrow e319 + f7$ $f2 + e7 \rightarrow A + e25$ $e1040 + f11 \rightarrow e1162 + e1163 + e1158$ $e319 + f7 \rightarrow B + e71$ $e308 + f9 \rightarrow e614 + e615 + e611$ $e371 + f6 \rightarrow e418 + B$ $e1040 + f12 \rightarrow e996 + C$ $f8 + B \rightarrow e308 + f7$ $e319 + f5 \rightarrow e372 + e371 + e368$ $f3 + e7 \rightarrow A + f0$ $e853 + f15 \rightarrow e1428 + C$ $e1428 + C \rightarrow e853 + f15$ $A + f10 \rightarrow e996 + f3$ $e1163 + f11 \rightarrow e1158 + e1246$ $e418 + f6 \rightarrow e465 + B$ $A + f0 \rightarrow f3 + e7$	

Johnson et al. (2016) - CRN bisimulation equivalence  
translation scheme: qian2011\_3D\_var1.ts

# CRN equivalence verification

## formal input CRN

3 species

7 reactions

A → A + A  
 A + A → A  
 A + B → B + B  
 B →  
 A + C →  
 C → C + C  
 C + C → C

## interpreted CRN

3 species

7 non-trivial reactions

C → C  
 C + C → C  
 A → A  
 A → A  
 A + A → A + A  
 A → A  
 C → C  
 A → A  
 B → B  
 →  
 A + C → A + C  
 →  
 B → B  
 B + B → B + B  
 C → C + C  
 A → A  
 B + A → A + B  
 A + A → A + A  
 A + C →  
 A + B → B + A  
 B →  
 B + B → B + B  
 A + C → A + C  
 B → B  
 A + B → B + B  
 A + A → A  
 C + C → C + C  
 C + C → C + C  
 A → A  
 →  
 B → B  
 A → A + A

## condensed CRN

42 species

32 reactions

f14 + C → e1428 + f15  
 e853 + f12 → C + f13  
 A + f4 → f3 + e71  
 f2 + e25 → A + f1  
 A + e25 → f2 + e7  
 e996 + f3 → A + f10  
 e1428 + f15 → f14 + C  
 f3 + e71 → A + f4  
 e465 + B → e418 + f6  
 e614 + f9 → e611 + e730  
 e996 + C → e1040 + f12  
 e465 + f5 → e514 + e368  
 e308 + f7 → f8 + B  
 e418 + B → e371 + f6  
 C + f13 → e853 + f12  
 A + f1 → f2 + e25  
 B + e71 → e319 + f7  
 f2 + e7 → A + e25  
 e1040 + f11 → e1162 + e1163 + e1158  
 e319 + f7 → B + e71  
 e308 + f9 → e614 + e615 + e611  
 e371 + f6 → e418 + B  
 e1040 + f12 → e996 + C  
 f8 + B → e308 + f7  
 e319 + f5 → e372 + e371 + e368  
 f3 + e7 → A + f0  
 e853 + f15 → e1428 + C  
 e1428 + C → e853 + f15  
 A + f10 → e996 + f3  
 e1163 + f11 → e1158 + e1246  
 e418 + f6 → e465 + B  
 A + f0 → f3 + e7

## enumerated CRN

360 species

668 reactions

Johnson et al. (2016) - CRN bisimulation equivalence  
 translation scheme: qian2011\_3D\_var1.ts

# CRN equivalence verification

## formal input CRN

3 species

7 reactions

```
A      -> A + A
A + A -> A
A + B -> B + B
B      ->
A + C ->
C      -> C + C
C + C -> C
```

## interpreted CRN

3 species

7 non-trivial reactions

```
C      -> C
C + C -> C
A      -> A
A      -> A
A + A -> A + A
A      -> A
C      -> C
A      -> A
B      -> B
->
A + C -> A + C
->
B      -> B
B + B -> B + B
C      -> C + C
A      -> A
B + A -> A + B
A + A -> A + A
A + C ->
A + B -> B + A
B      ->
B + B -> B + B
A + C -> A + C
B      -> B
A + B -> B + B
A + A -> A
C + C -> C + C
C + C -> C + C
A      -> A
->
B      -> B
A      -> A + A
```

## condensed CRN

42 species

32 reactions

```
f14 + C -> e1428 + f15
e853 + f12 -> C + f13
A + f4 -> f3 + e71
f2 + e25 -> A + f1
A + e25 -> f2 + e7
e996 + f3 -> A + f10
e1428 + f15 -> f14 + C
f3 + e71 -> A + f4
e465 + B -> e418 + f6
e614 + f9 -> e611 + e730
e996 + C -> e1040 + f12
e465 + f5 -> e514 + e368
e308 + f7 -> f8 + B
e418 + B -> e371 + f6
C + f13 -> e853 + f12
A + f1 -> f2 + e25
B + e71 -> e319 + f7
f2 + e7 -> A + e25
e1040 + f11 -> e1162 + e1163 + e1158
e319 + f7 -> B + e71
e308 + f9 -> e614 + e615 + e611
e371 + f6 -> e418 + B
e1040 + f12 -> e996 + C
f8 + B -> e308 + f7
e319 + f5 -> e372 + e371 + e368
f3 + e7 -> A + f0
e853 + f15 -> e1428 + C
e1428 + C -> e853 + f15
A + f10 -> e996 + f3
e1163 + f11 -> e1158 + e1246
e418 + f6 -> e465 + B
A + f0 -> f3 + e7
```

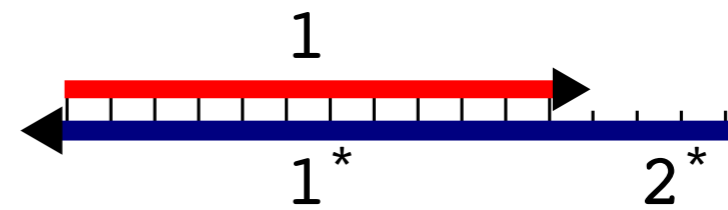
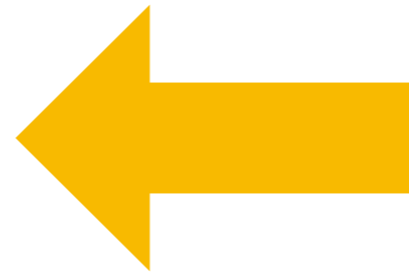
## enumerated CRN

360 species

668 reactions

Johnson et al. (2016) - CRN bisimulation equivalence  
translation scheme: qian2011\_3D\_var1.ts

# Designing Sequences



# Designing Sequences



## NUPACK

Analysis

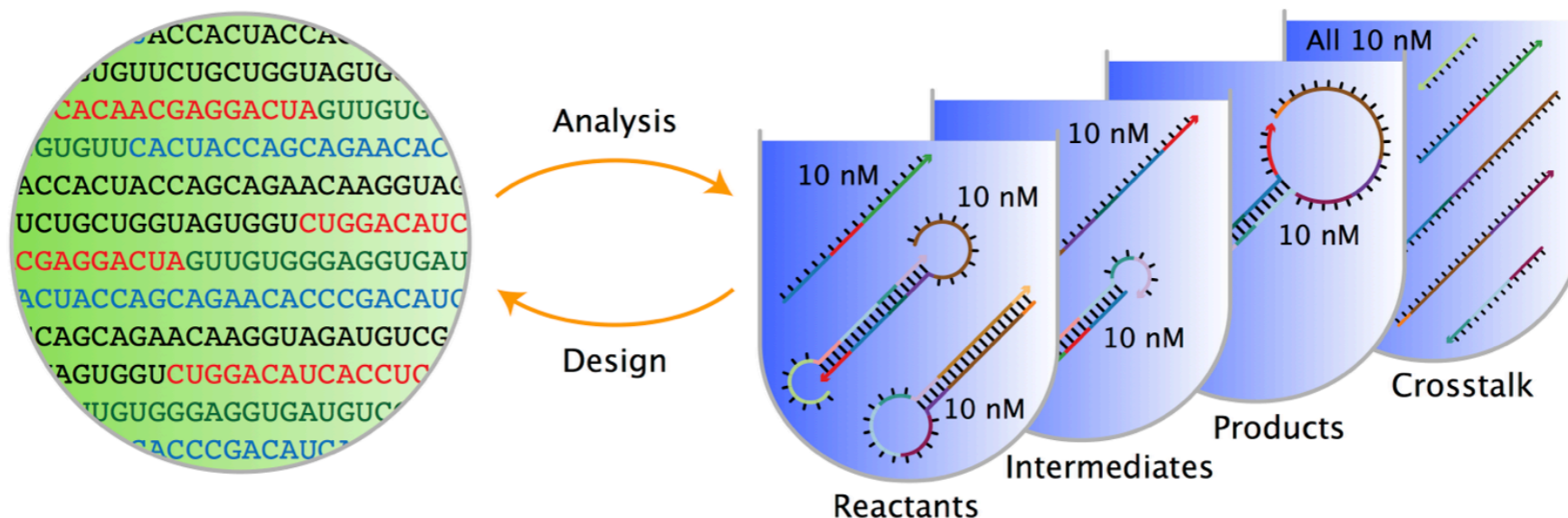
Design

Utilities

Downloads

**NUPACK** is a growing software suite for the analysis and design of nucleic acid structures, devices, and systems.

The NUPACK web application enables analysis and design of the equilibrium base-pairing properties of one or more test tubes of interacting nucleic acid strands:



Please [cite](#) the web application and algorithms appropriately; usage statistics are an important component in helping to secure funding for NUPACK development. We are happy to provide advice and [technical support](#).

— The NUPACK Team

**News:** Constrained multistate test tube design for reaction pathway engineering is now published! ([pdf](#), [supp info](#), [source code](#), [user guide](#))

# Designing Sequences

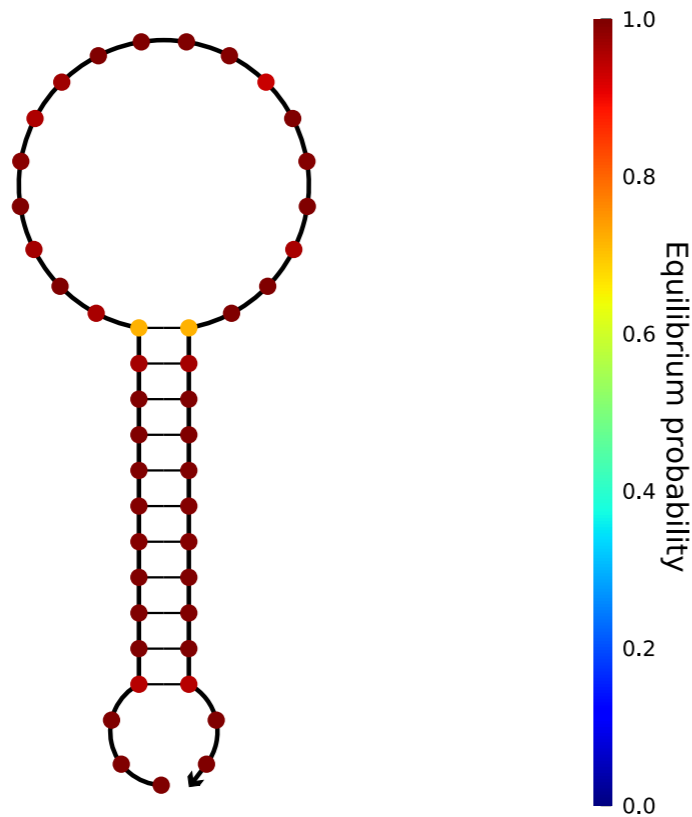


input X

poor sequence  
for a signal strand

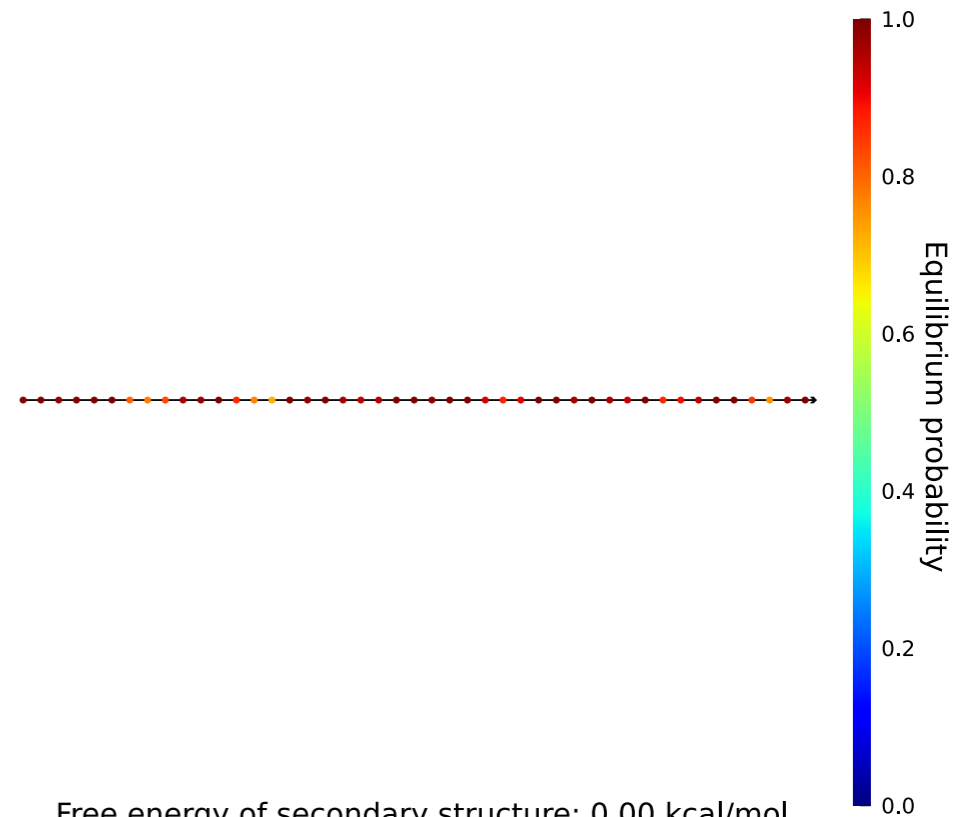
good sequence  
for a signal strand

MFE structure at 25.0 C



Free energy of secondary structure: -10.70 kcal/mol

MFE structure at 25.0 C



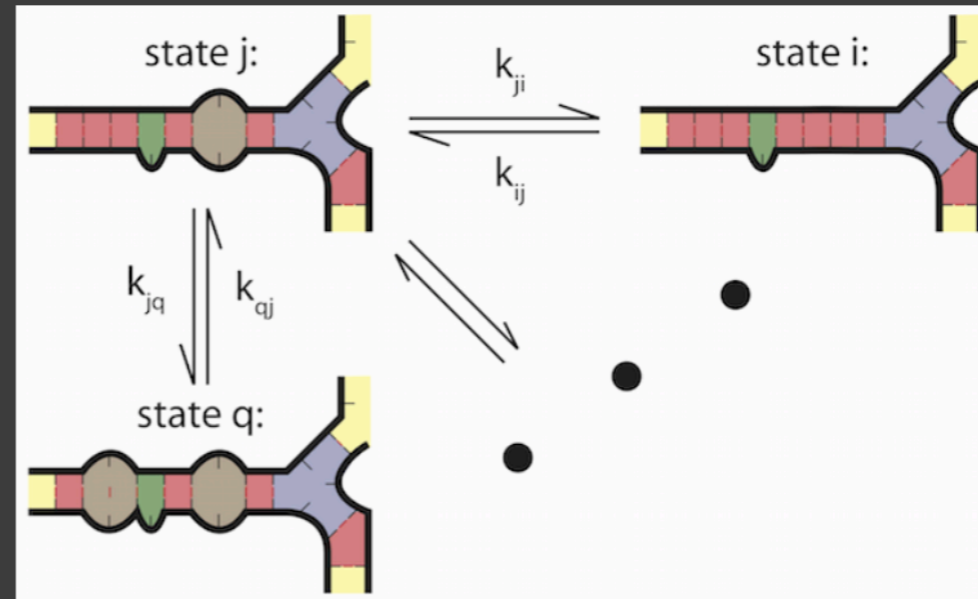
Free energy of secondary structure: 0.00 kcal/mol

# Multistrand.org to determine reaction rates

Multistrand is a software package for simulating the kinetics of multiple interacting nucleic acid strands. It is developed at the Winfree lab at the California Institute of Technology.

› DNA and Natural Algorithms Group @ Caltech

[Live demo](#)



## Key Features

- Kinetic simulations of nucleic acids as random walk on thermodynamic energy model
- Supports multiple interacting strands
- Equilibrium consistent with [NUPACK](#)
- Various usage modes to study kinetic trajectories
- Distributed as a Python package
- MIT License

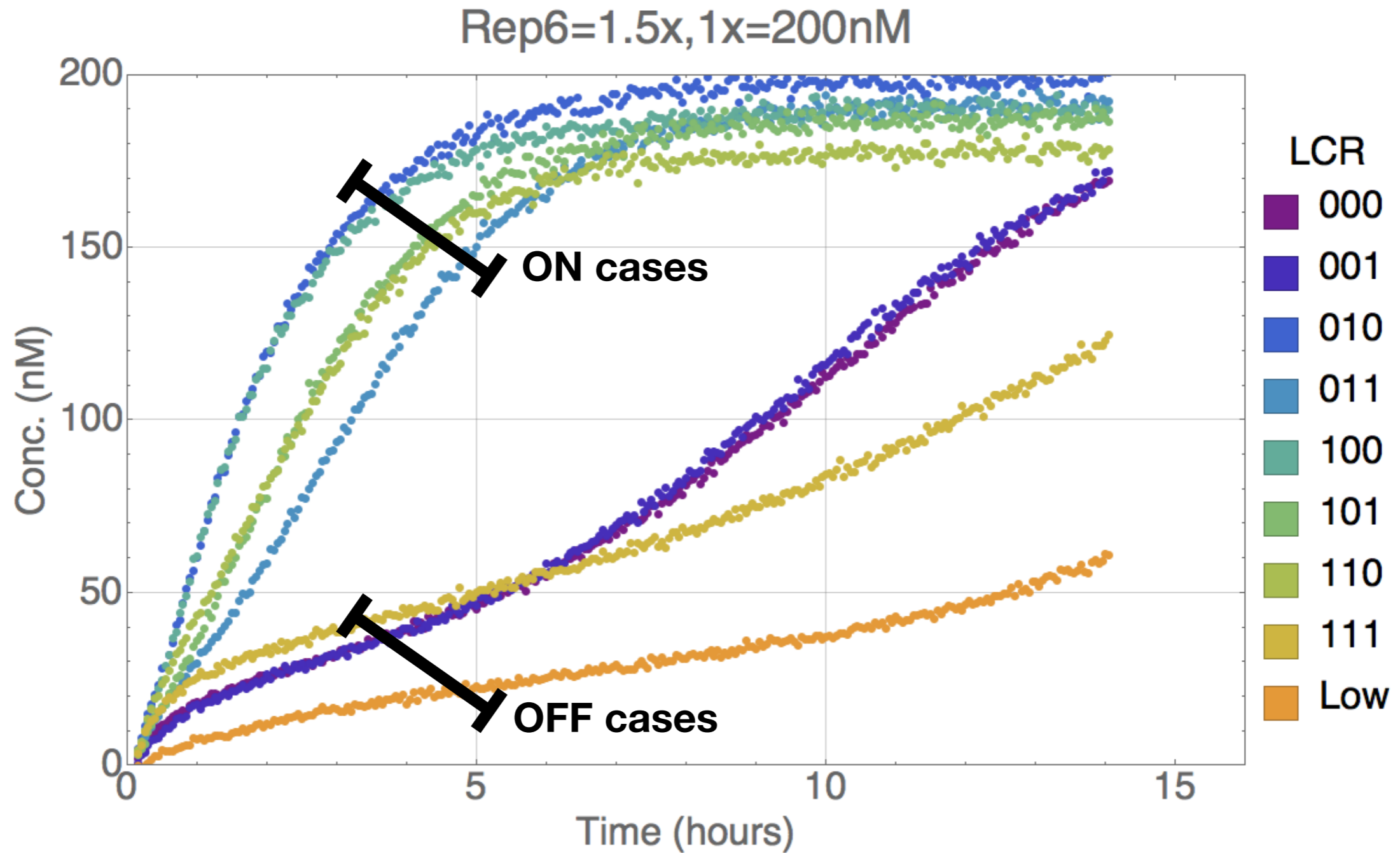


# Tutorial Outline

- ▶ Review of strand displacement
- ▶ Building and composing logic gates
- ▶ Tools for designing and verifying circuits
- ▶ **Robustness of strand displacement**



# Why is this circuit not *robust*?

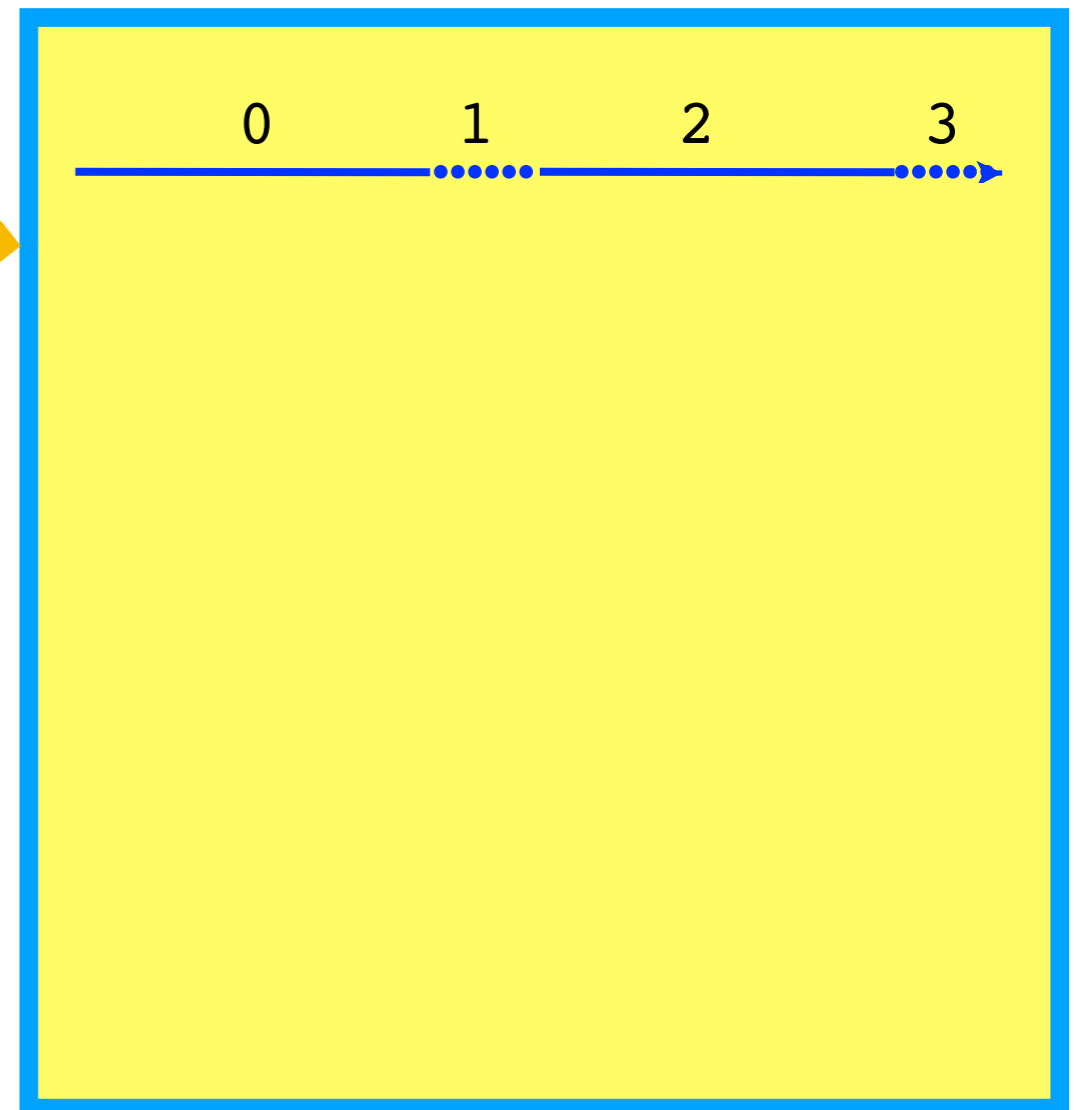


What causes signal *leak*?



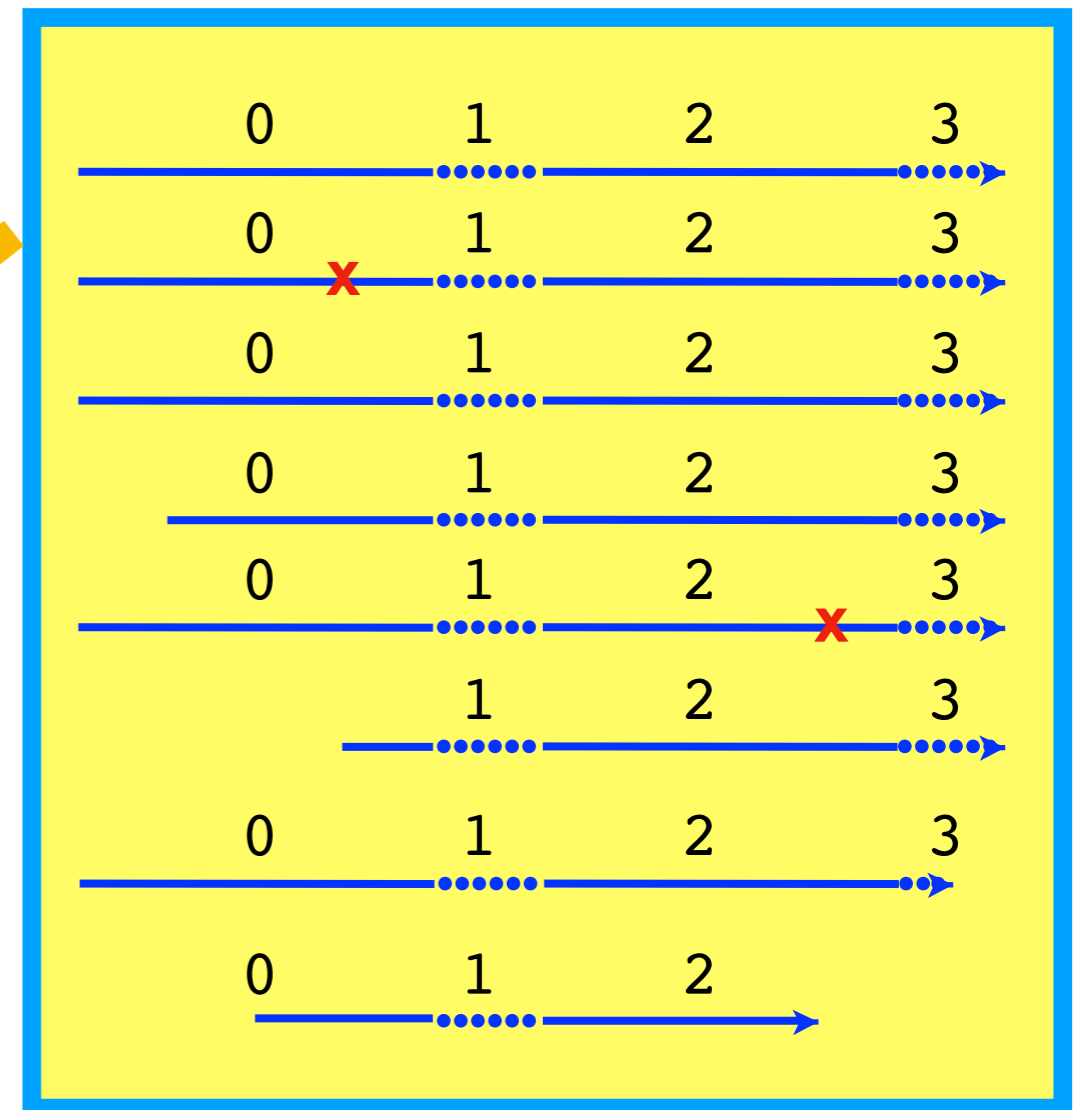
# Problem 1: Molecules are not perfect

**Imperfect strands from imperfect synthesis**



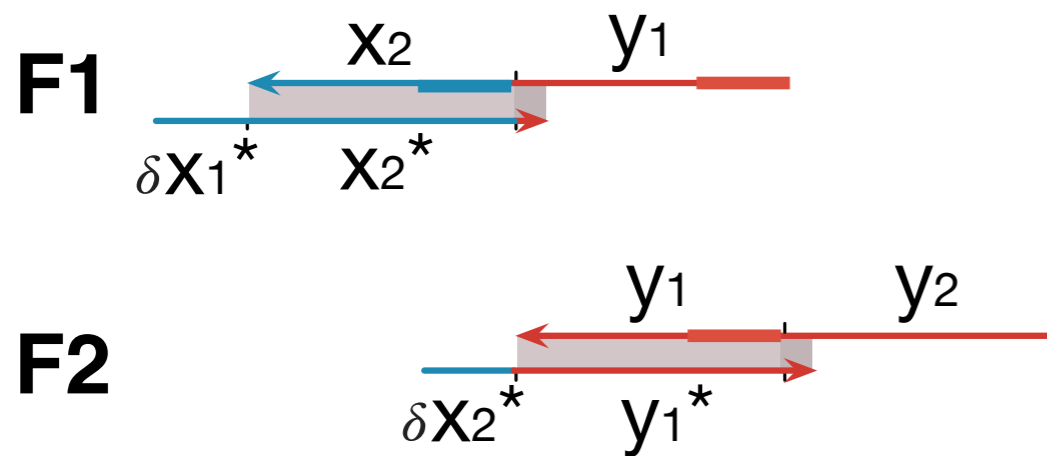
# Problem 1: Molecules are not perfect

## Imperfect strands from imperfect synthesis



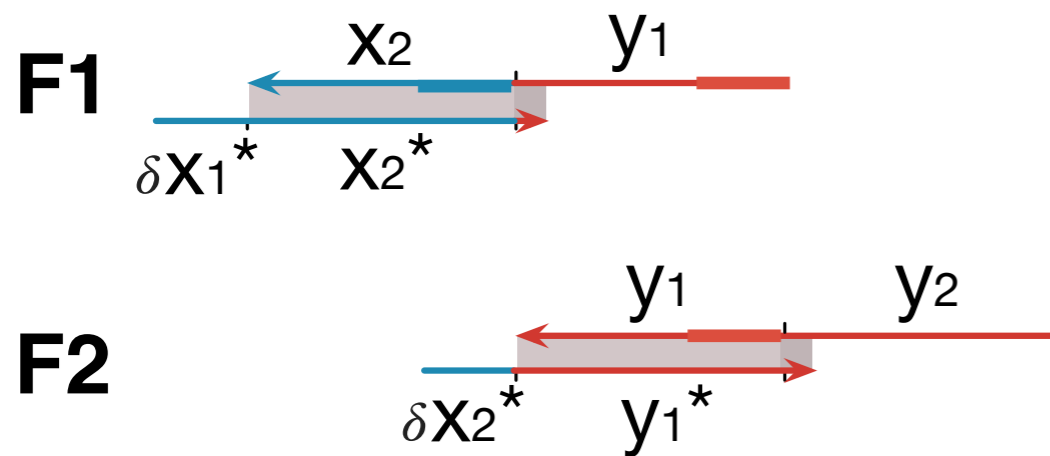
# Problem 1: Molecules are not perfect

translator cascade  
with perfect molecules

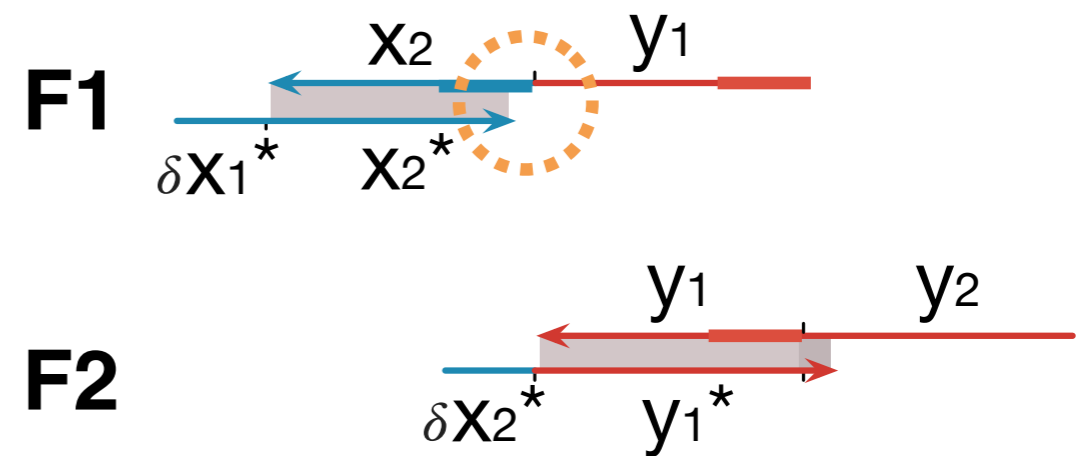


# Problem 1: Molecules are not perfect

translator cascade  
with perfect molecules

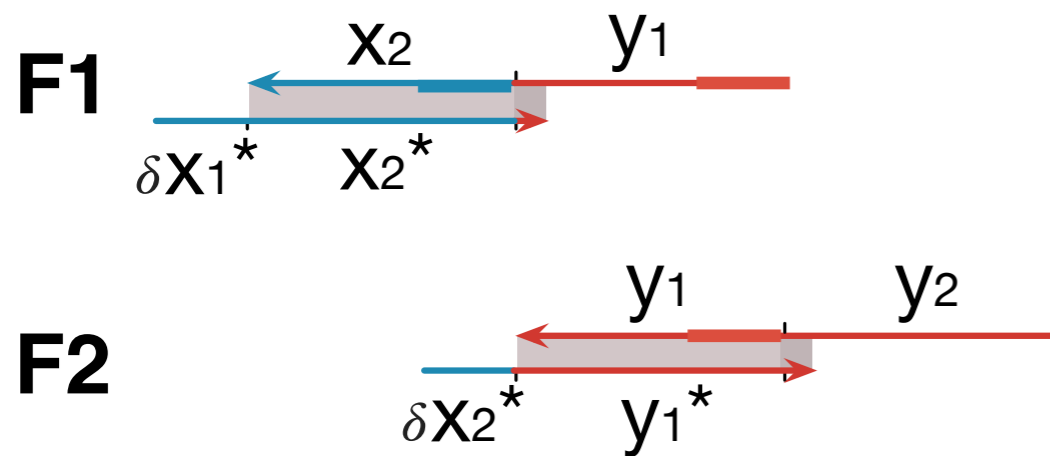


translator cascade  
with imperfect molecules

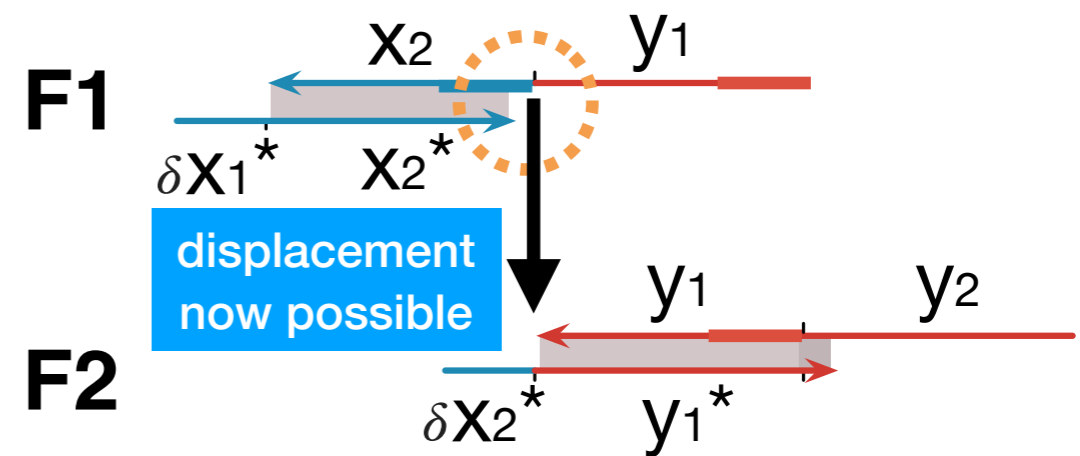


# Problem 1: Molecules are not perfect

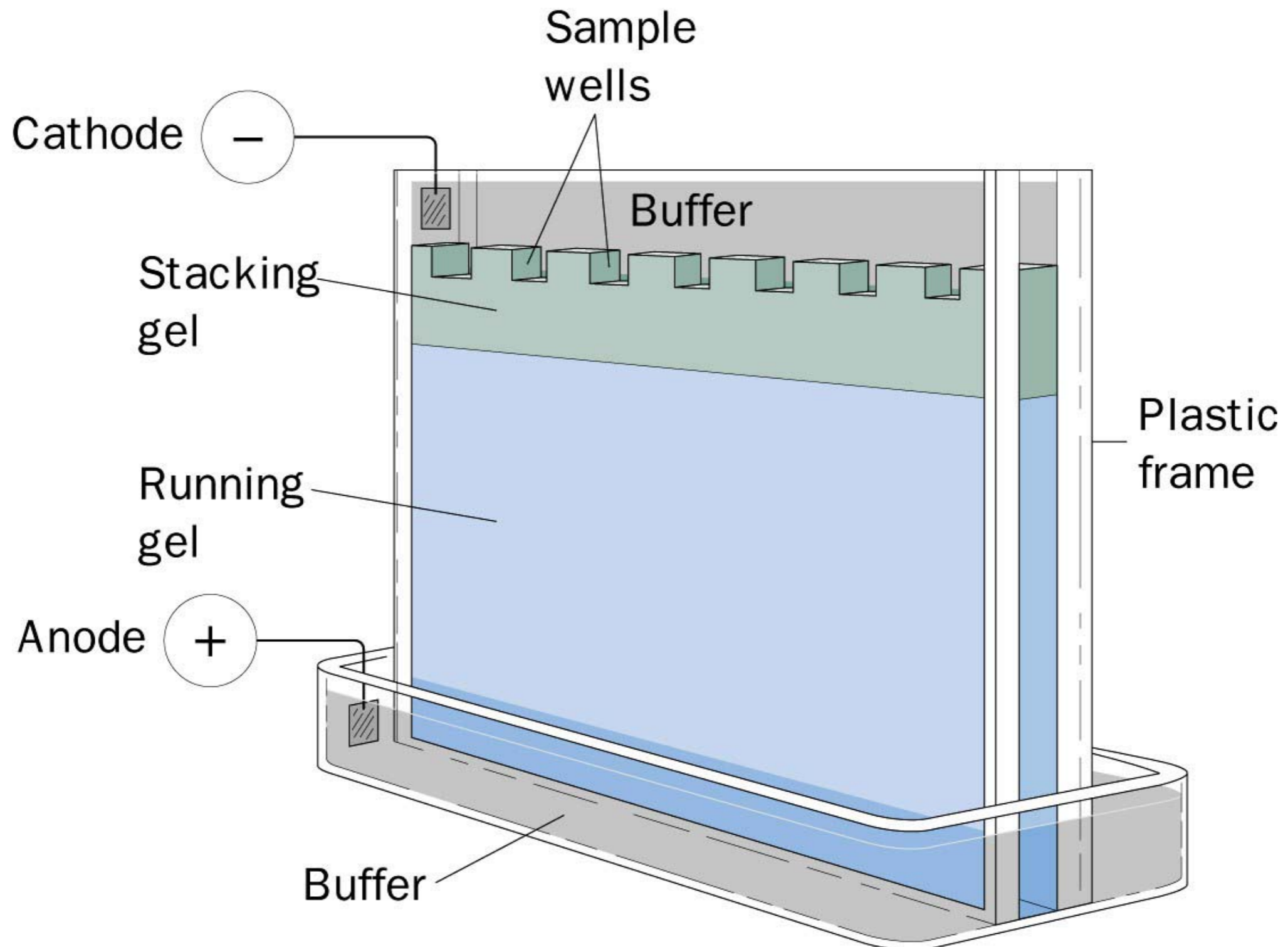
translator cascade  
with perfect molecules



translator cascade  
with imperfect molecules

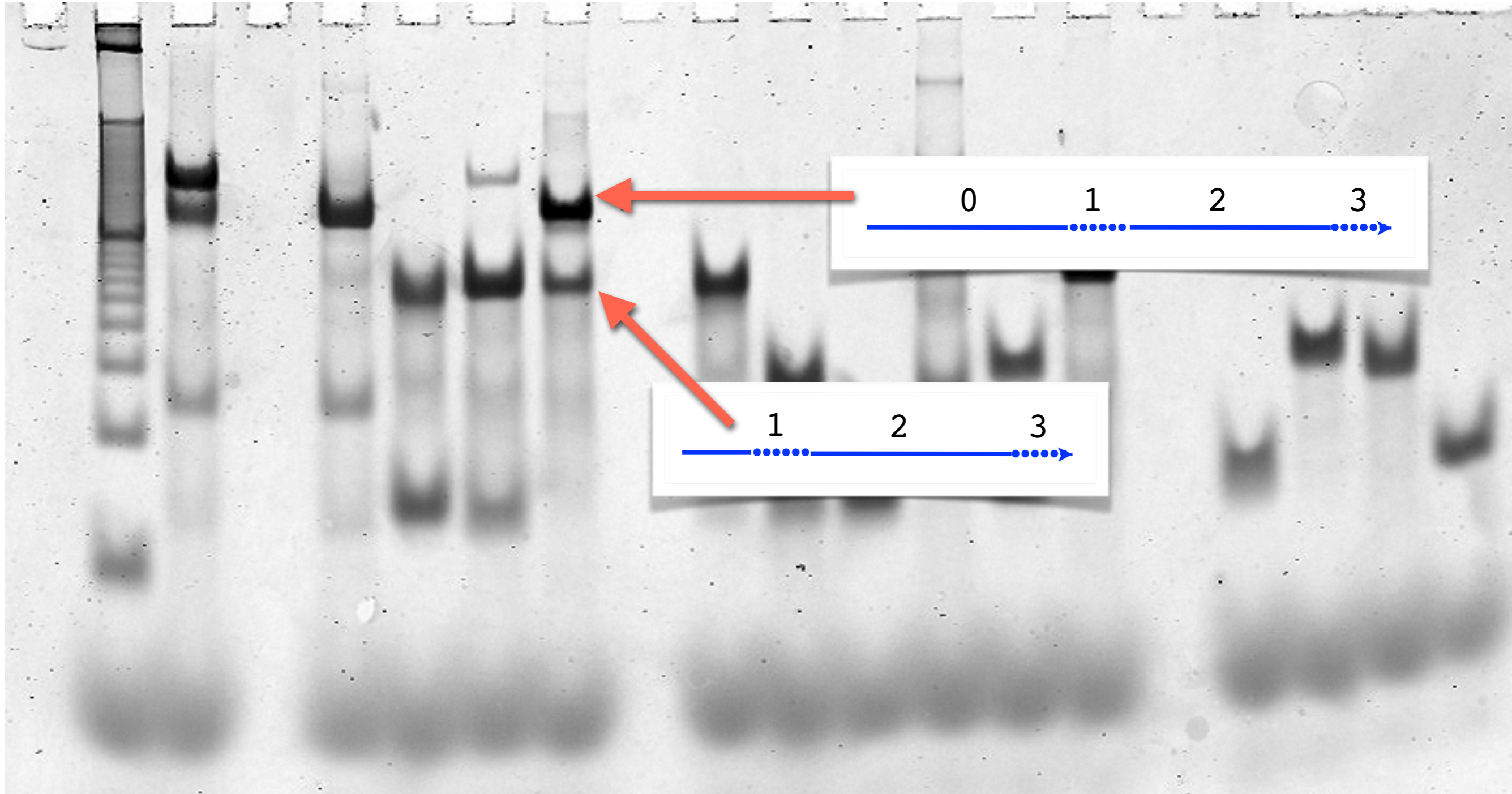


# (Partial) solution to Problem 1



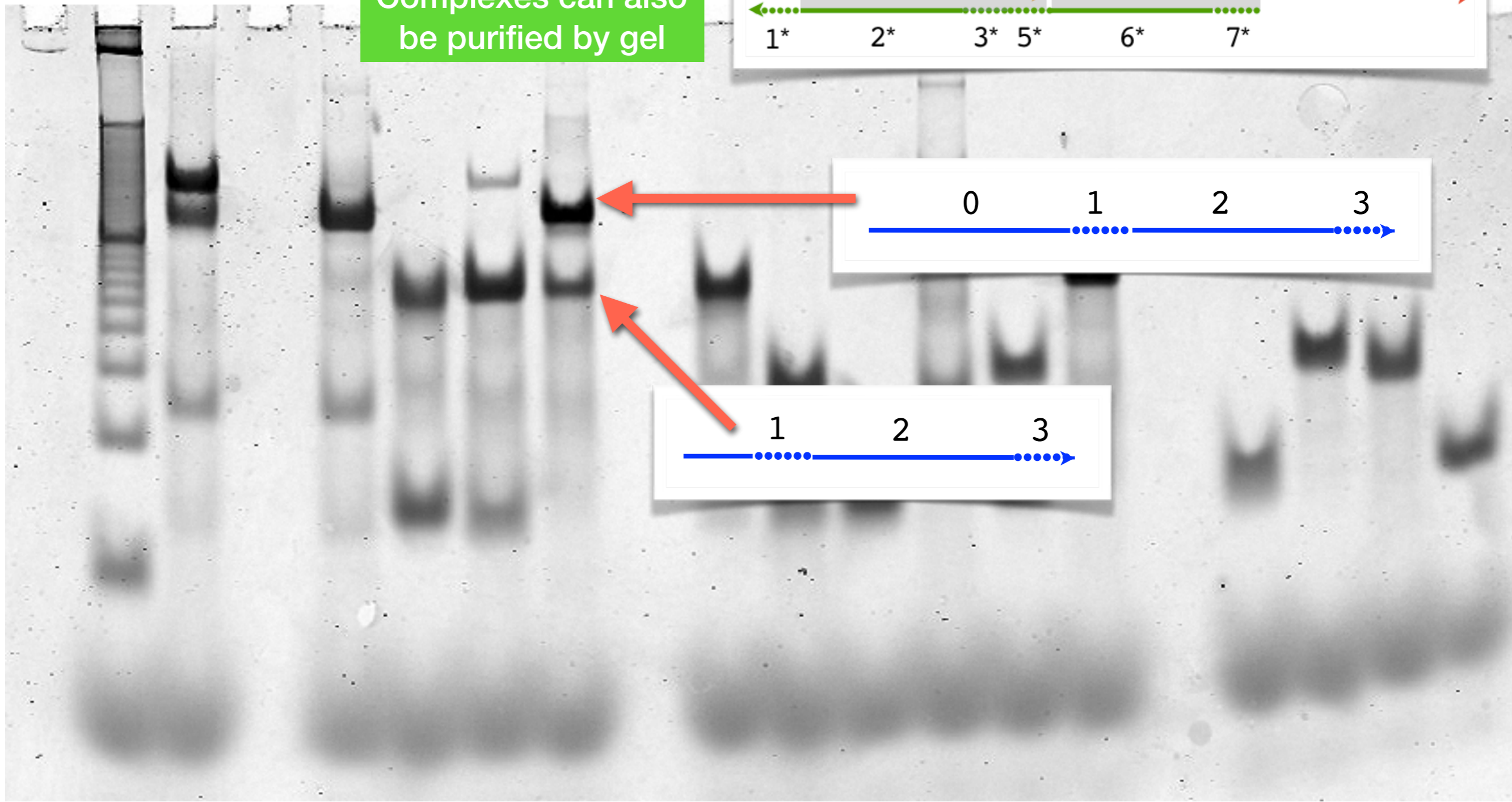
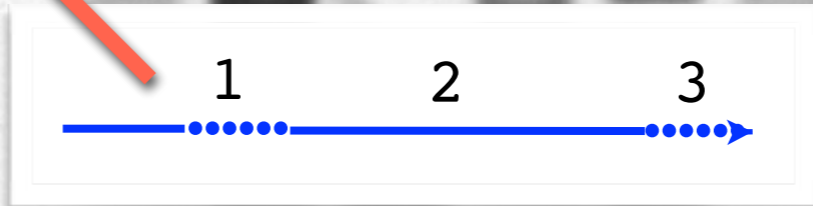
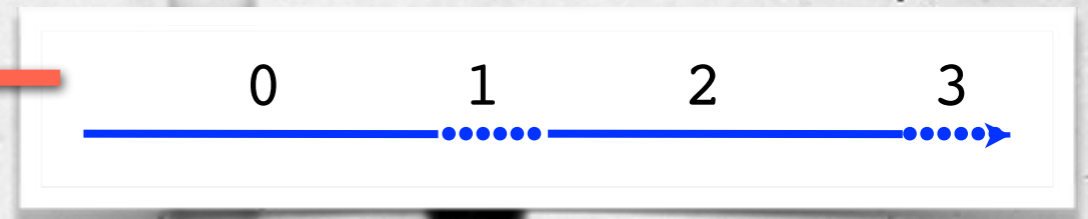


# (Partial) solution to Problem 1

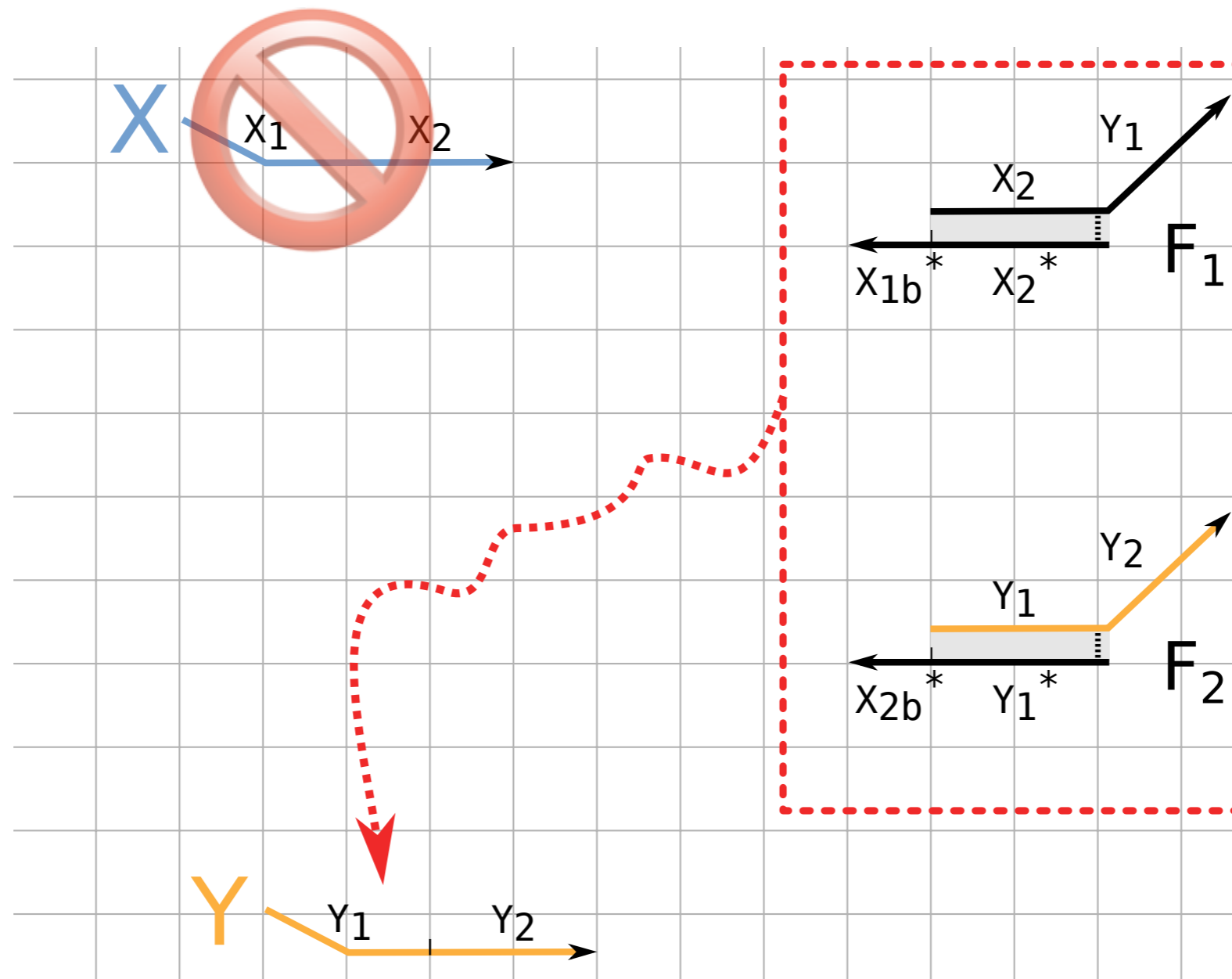
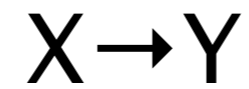


# (Partial) solution to Problem 1

Complexes can also be purified by gel

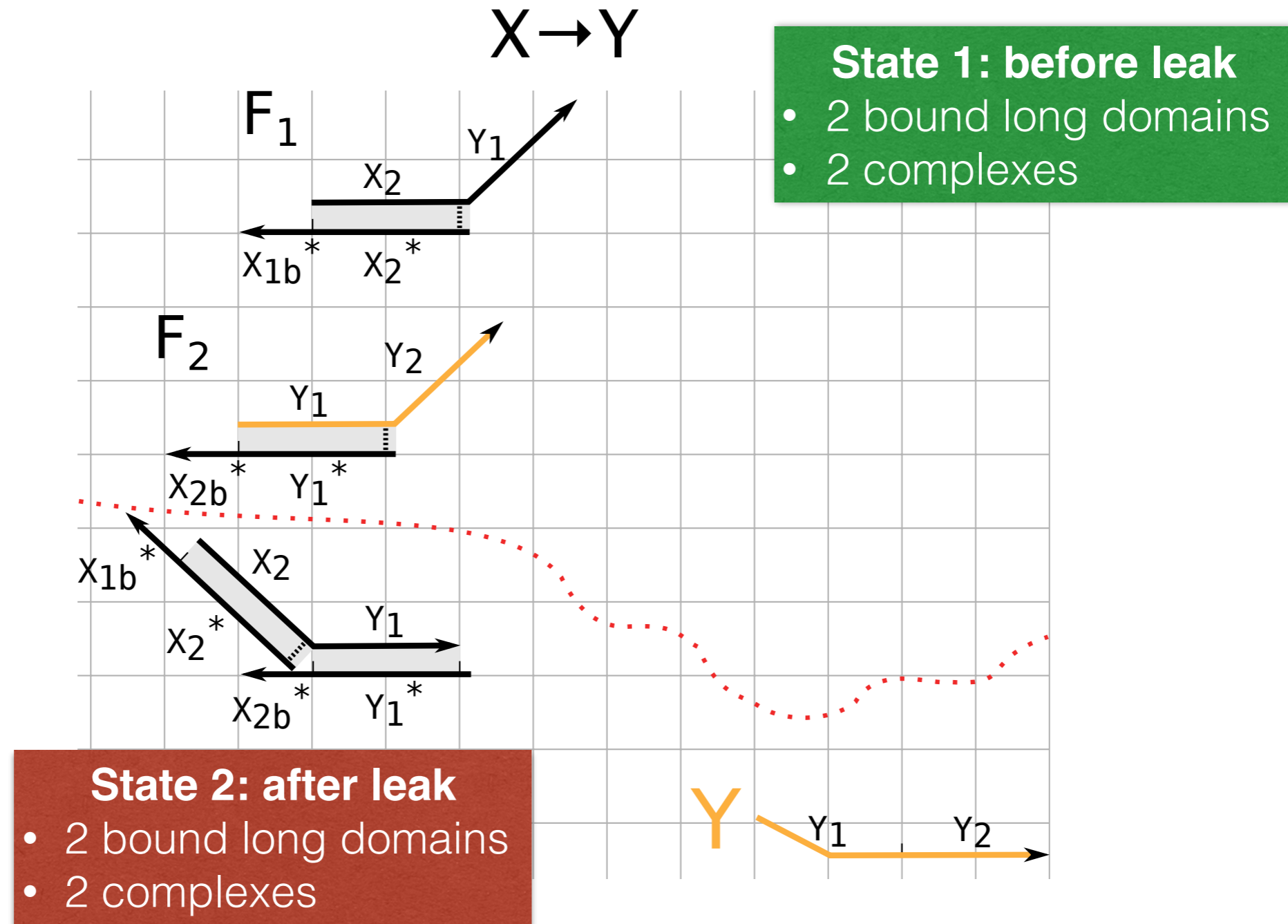


# Problem 2: Spurious reactions occur (even with perfect molecules)

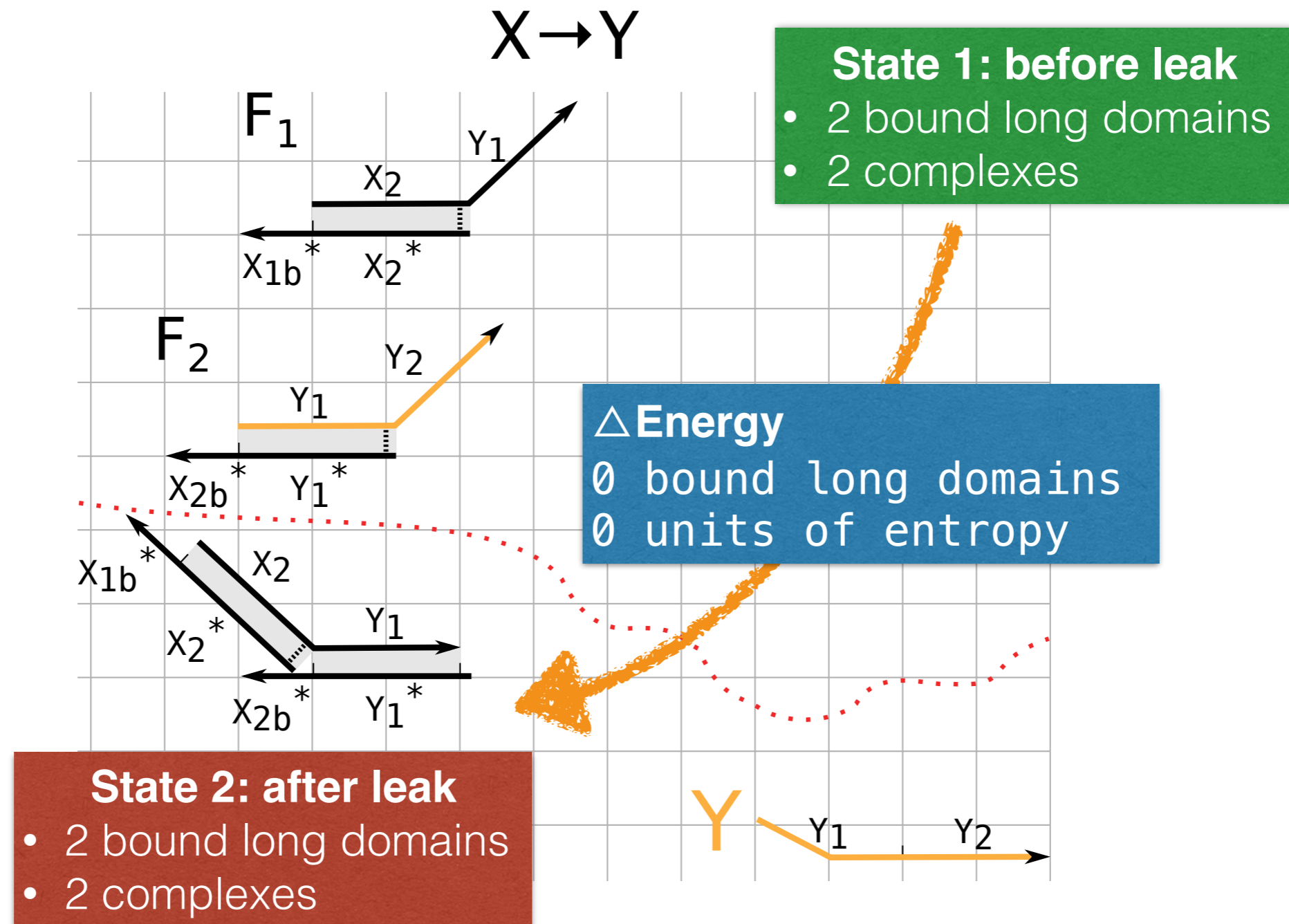


Y has been spuriously “produced”

# Some rough energy accounting



# Some rough energy accounting



# A Motivating Question

Can we rationally design  
*composable, leakless*  
DSD gates?

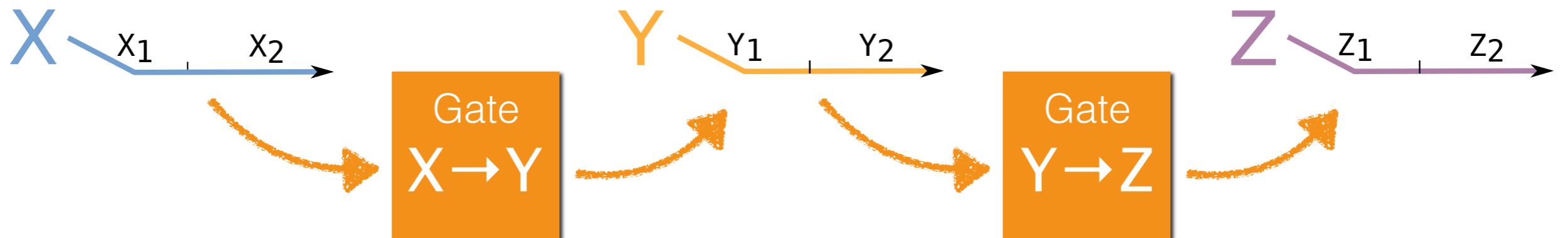
# A Motivating Question

Can we rationally design  
composable, leakless  
DSD gates?



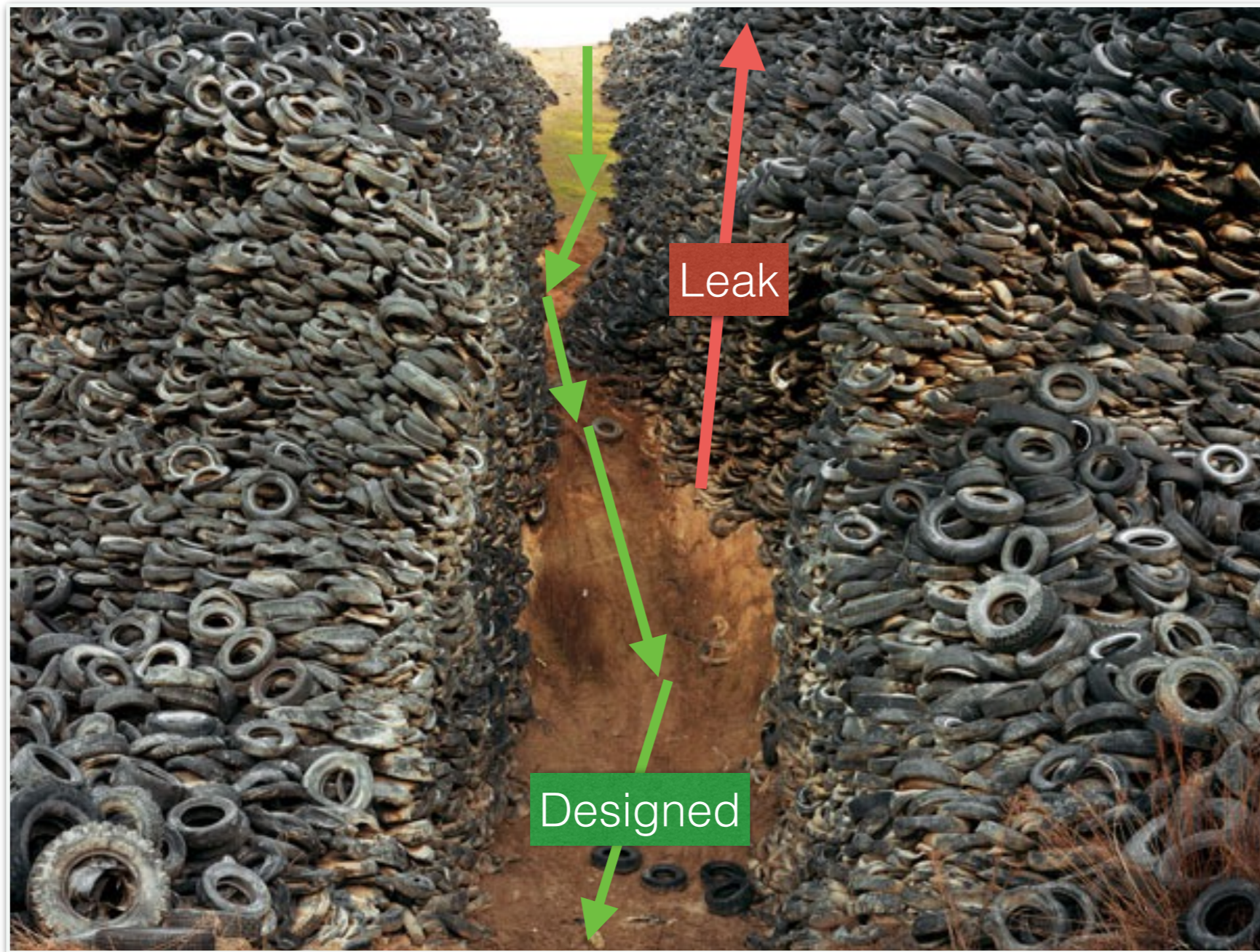
# A Motivating Question

Can we rationally design  
composable, leakless  
DSD gates?



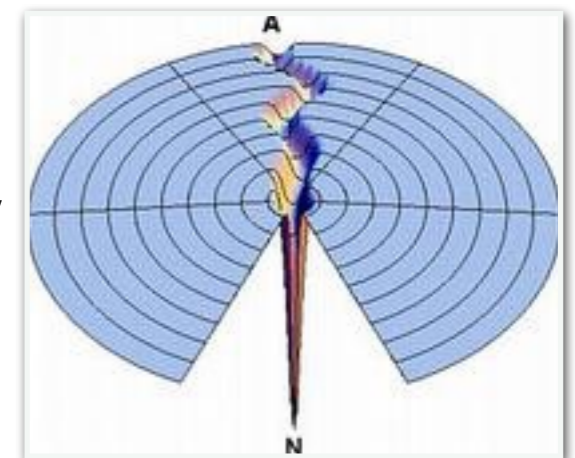


# What do we mean by *leakless*?



**“Golf funnel with deep groove” pathway**

K. Dill & Bromberg (2002). *Molecular Driving Forces*.



# (Partial) solution to Problem 2

For a redundancy parameter  $\mathbf{N}$ , there exist **translator** and **AND** gates using  $\mathbf{N}$  long domains that have the following property:

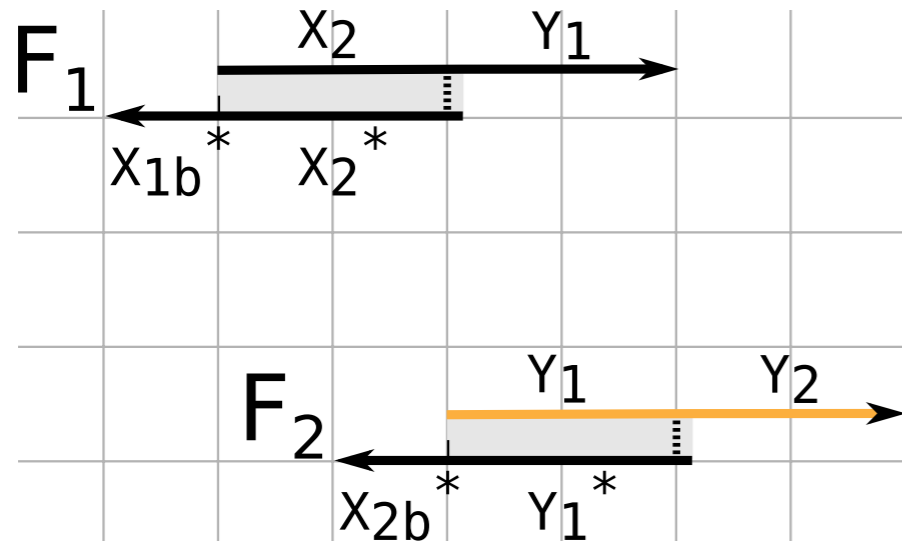
*even at thermodynamic equilibrium,*

the net leak decreases exponentially with  $\mathbf{N}$ .

Thachuk, Winfree, David Soloveichik. (2015)  
*Leakless DNA strand displacement.* DNA 21.



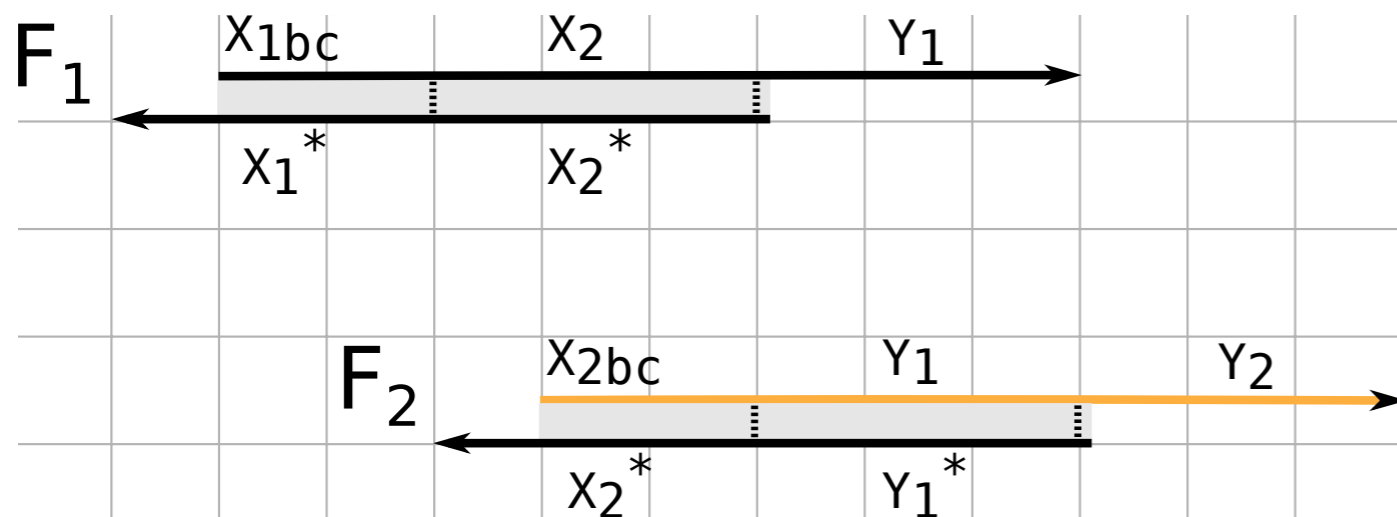
## Typical translator using “Single Long Domain” (SLD)



- Designed pathways: bimolecular
- Leak pathways: bimolecular

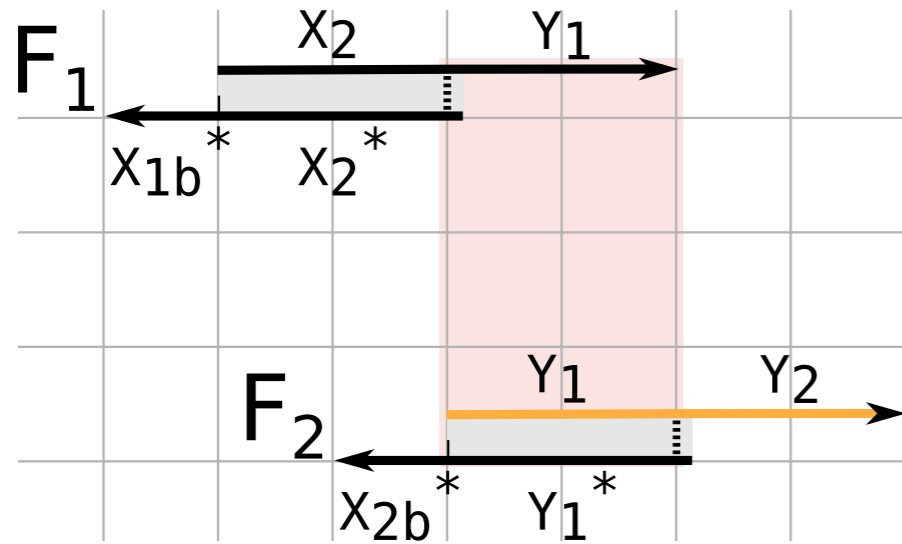
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## DLD translator using “Double Long Domain” (DLD)



- Designed pathways: bimolecular
- Leak pathways: **trimolecular**

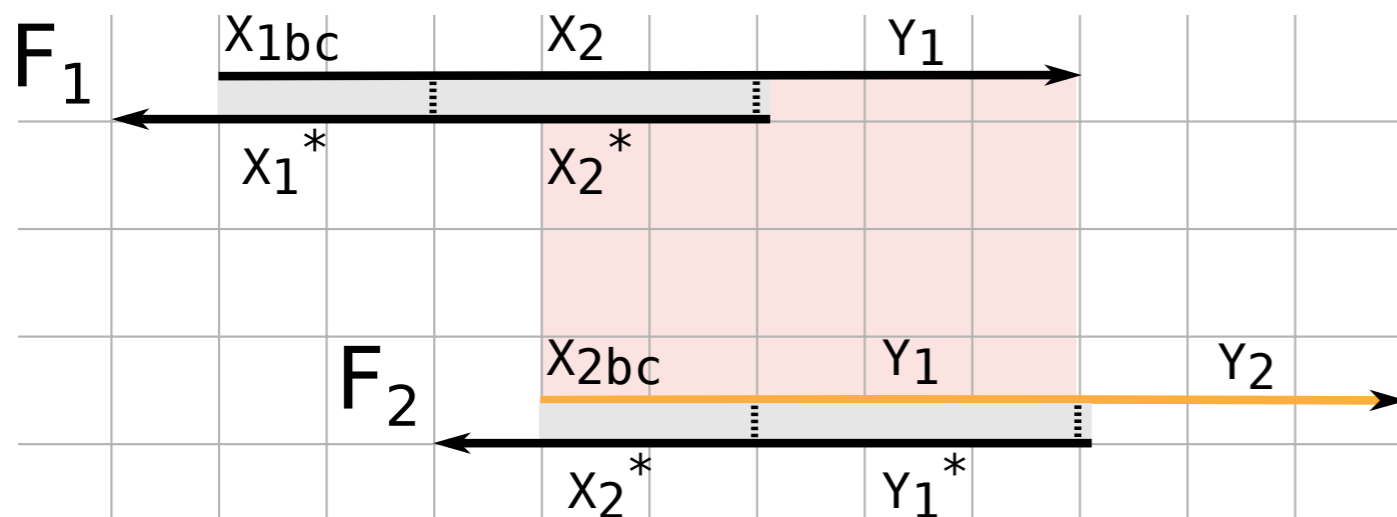
## Typical translator using “Single Long Domain” (SLD)



- Designed pathways: bimolecular
- Leak pathways: bimolecular

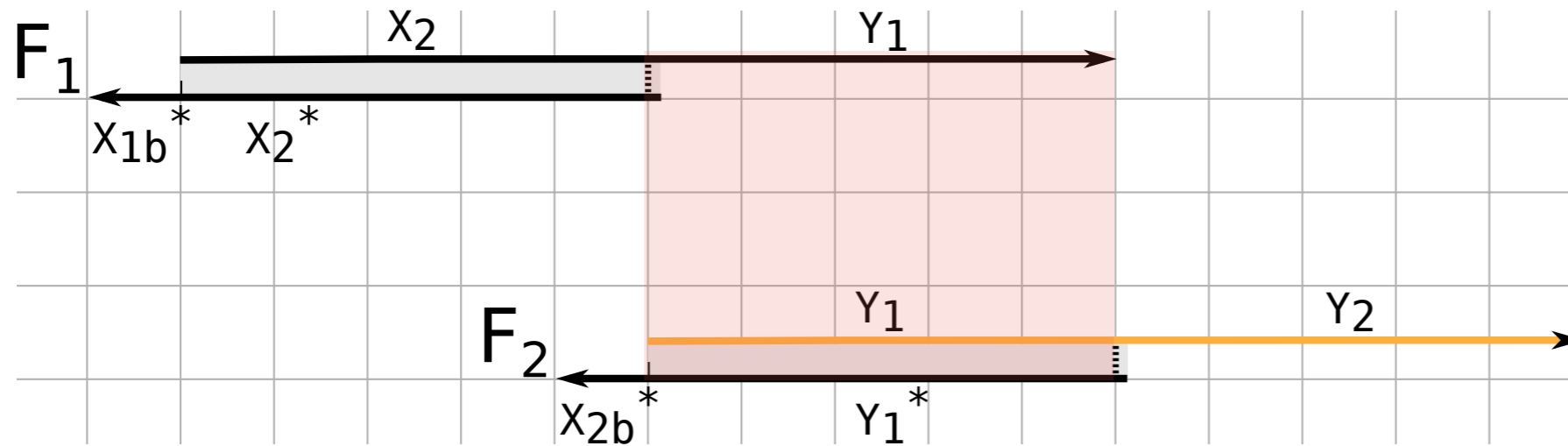
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## DLD translator using “Double Long Domain” (DLD)



- Designed pathways: bimolecular
- Leak pathways: **trimolecular**

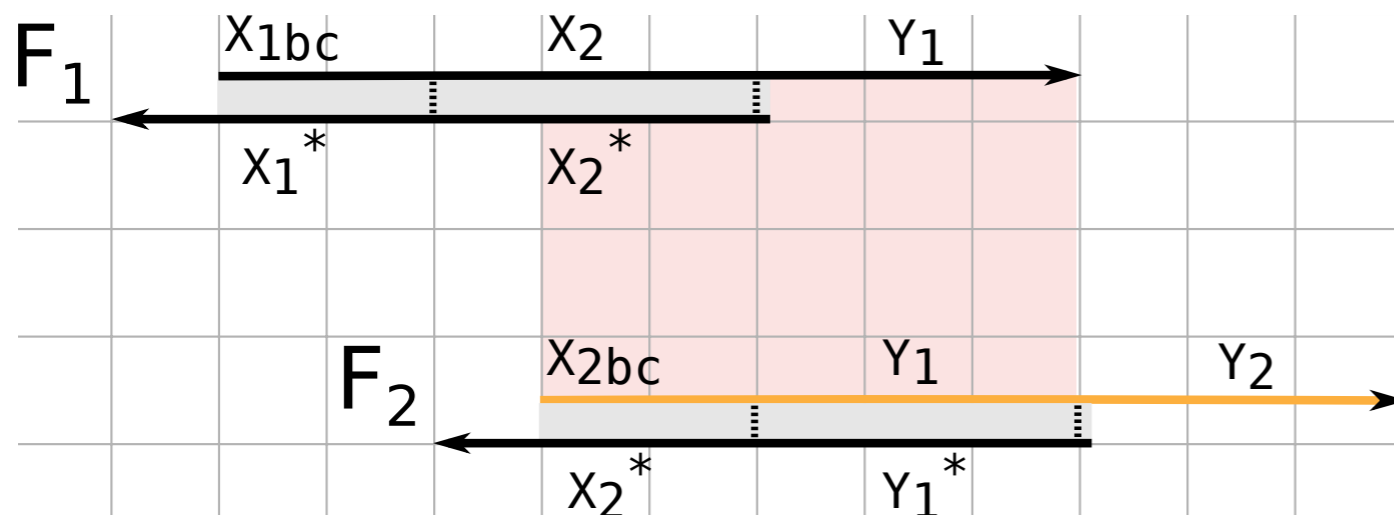
## Typical translator using “Single Long Domain” (SLD)



- Designed pathways: bimolecular
- Leak pathways: bimolecular

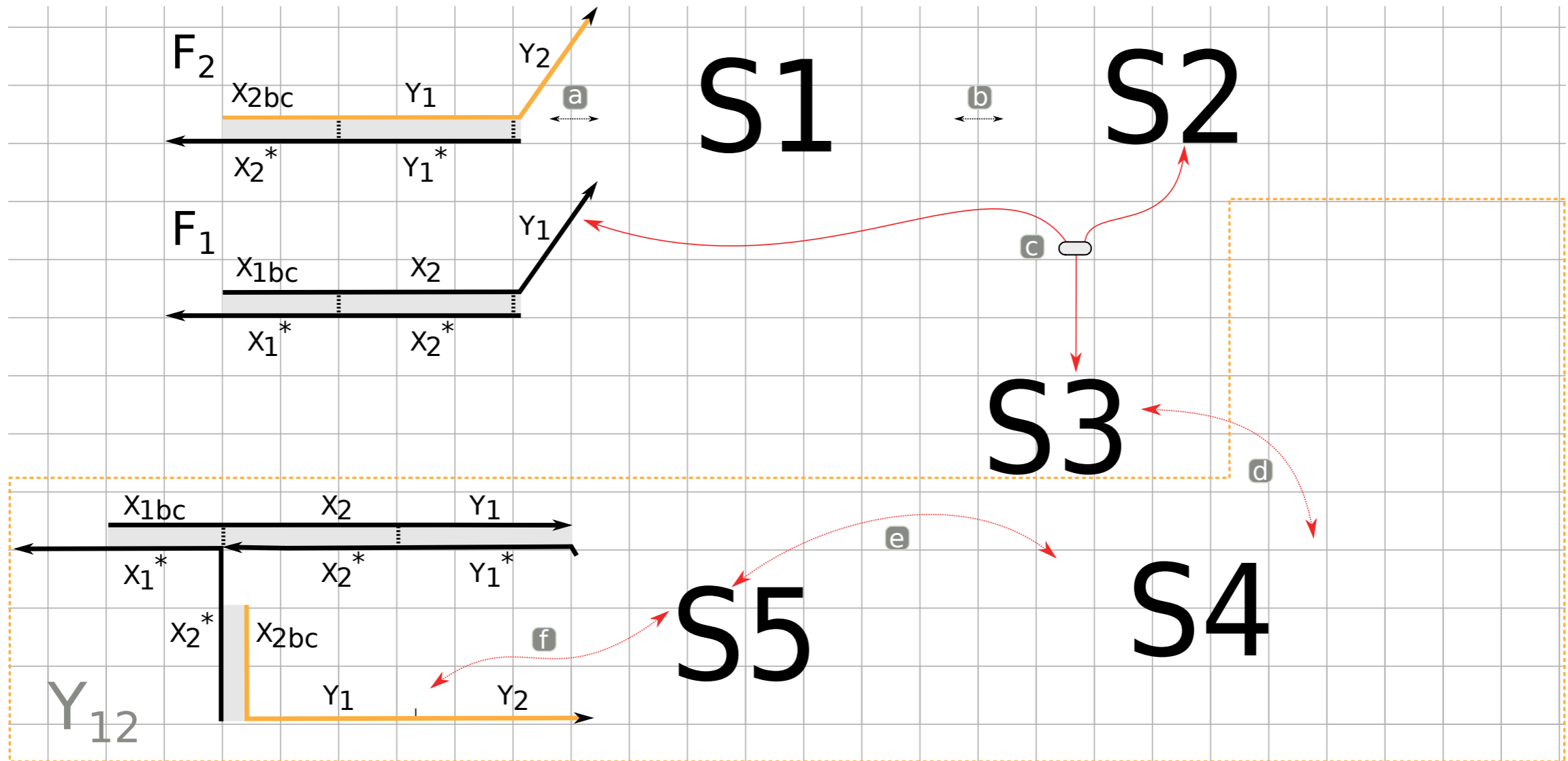
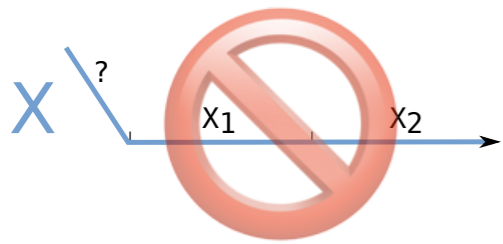
Lengthening recognition domains  
does not help

## DLD translator using “Double Long Domain” (DLD)

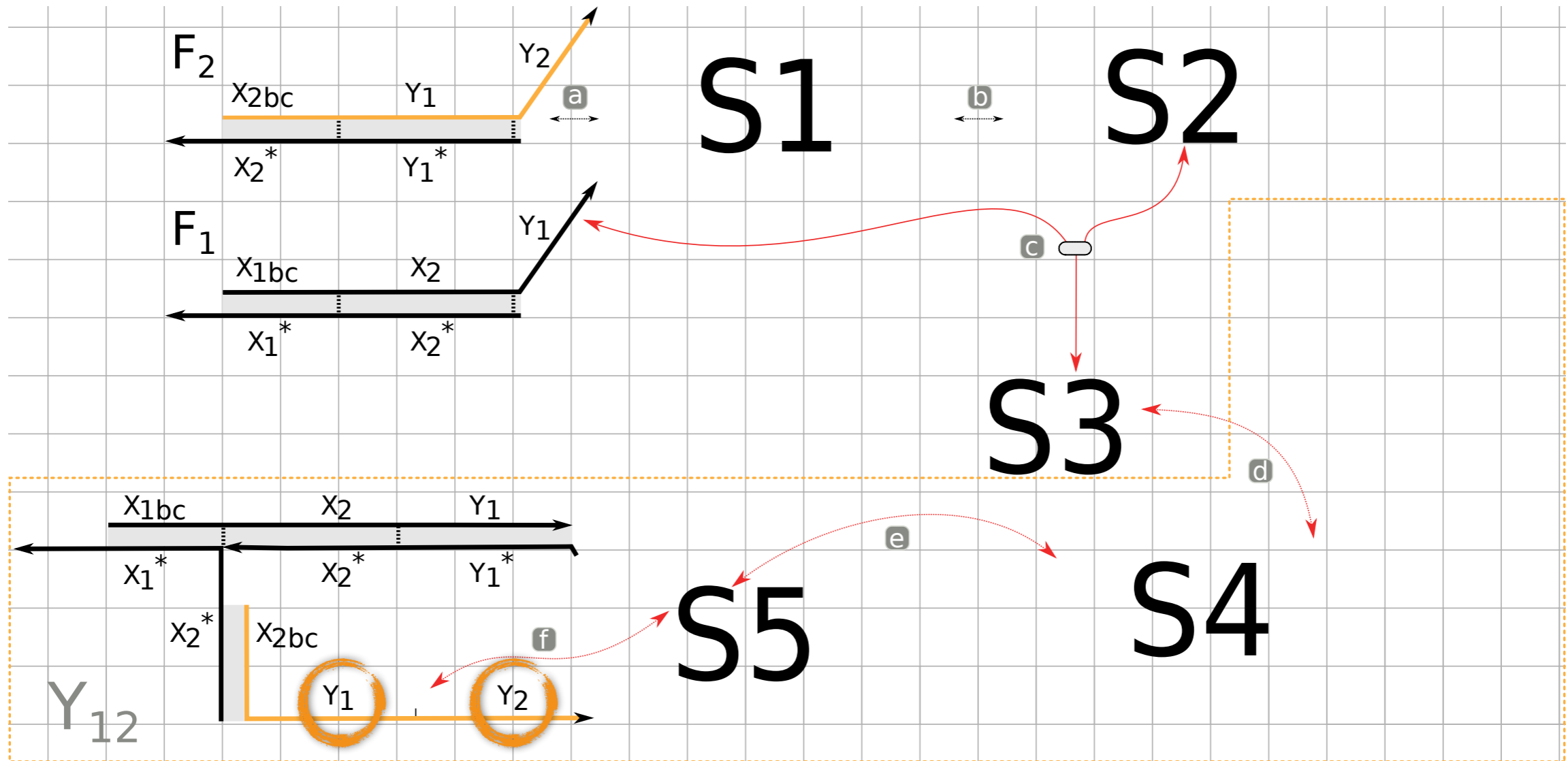
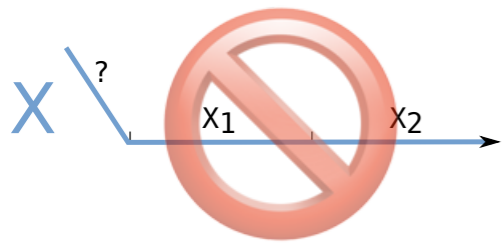


- Designed pathways: bimolecular
- Leak pathways: **trimolecular**

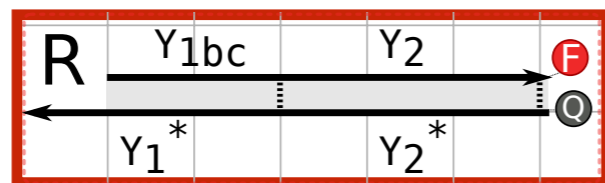
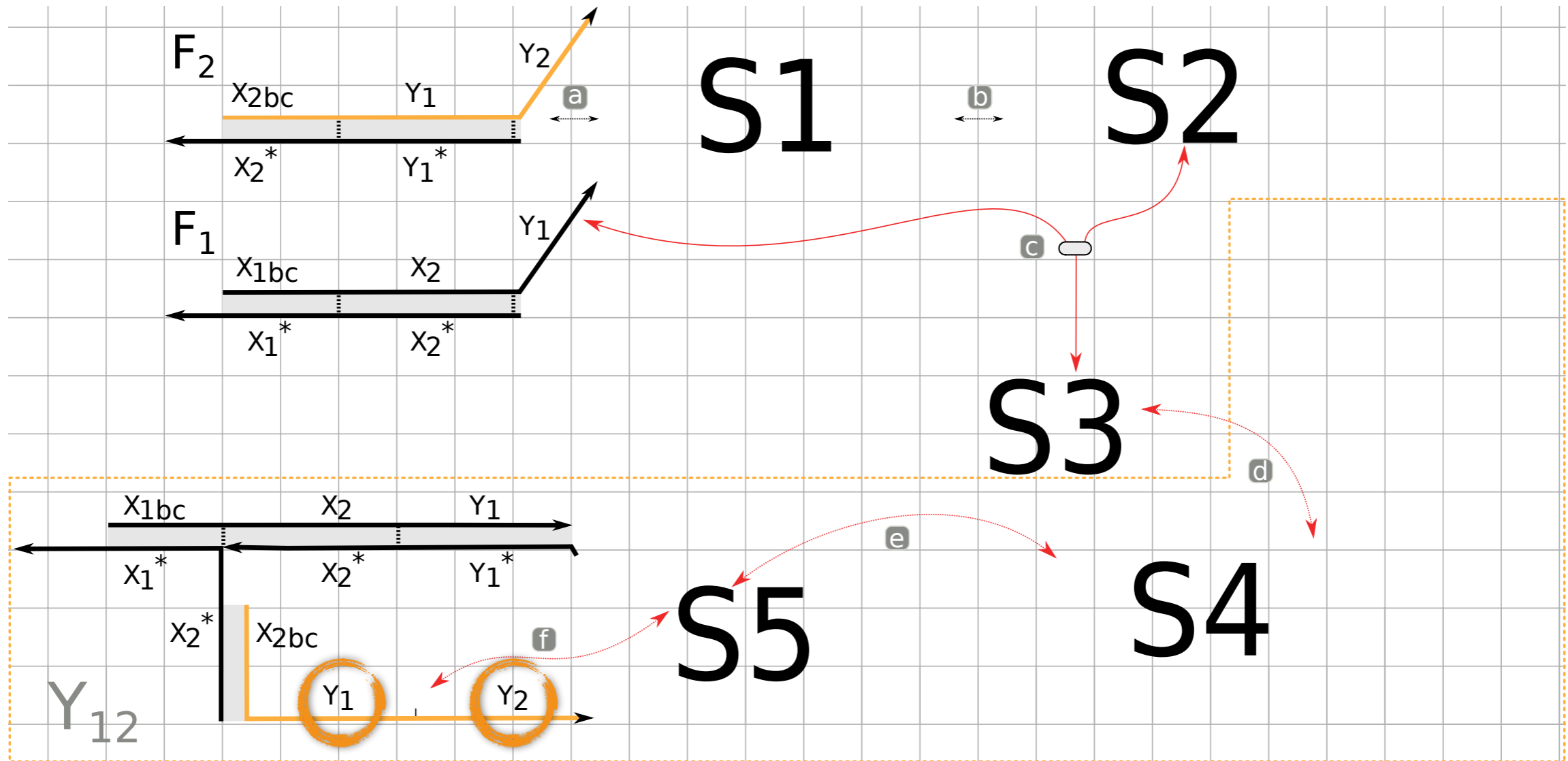
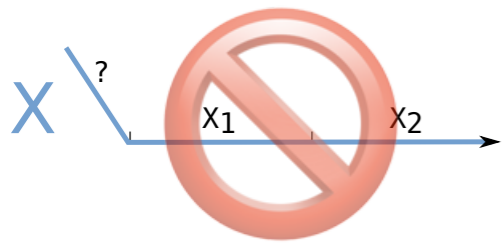
# DLD translators are intrinsically less “leaky”



# DLD translators are intrinsically less “leaky”



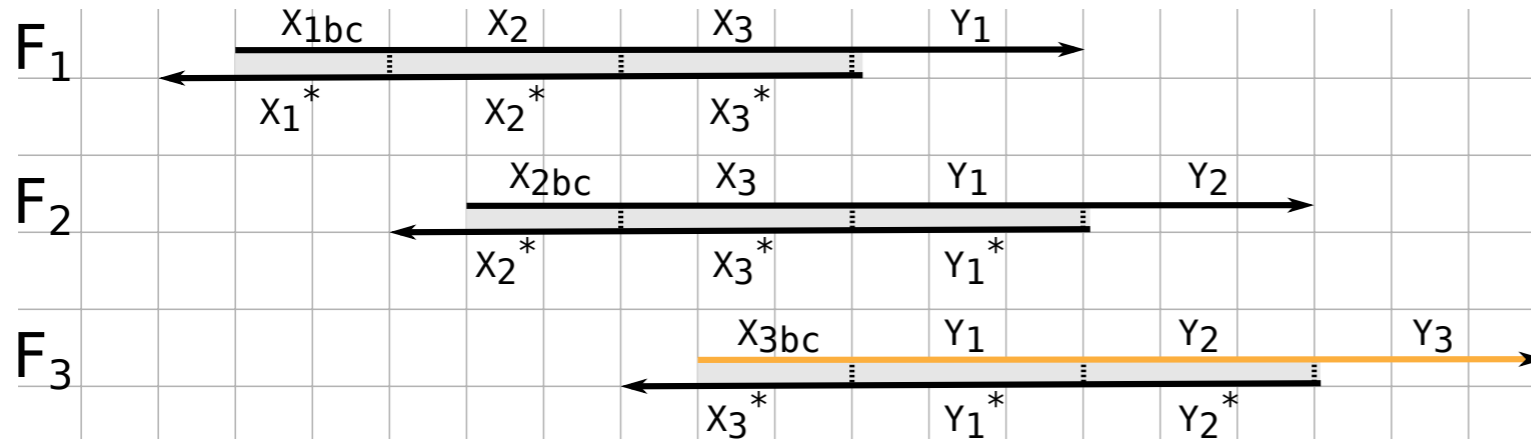
# DLD translators are intrinsically less “leaky”



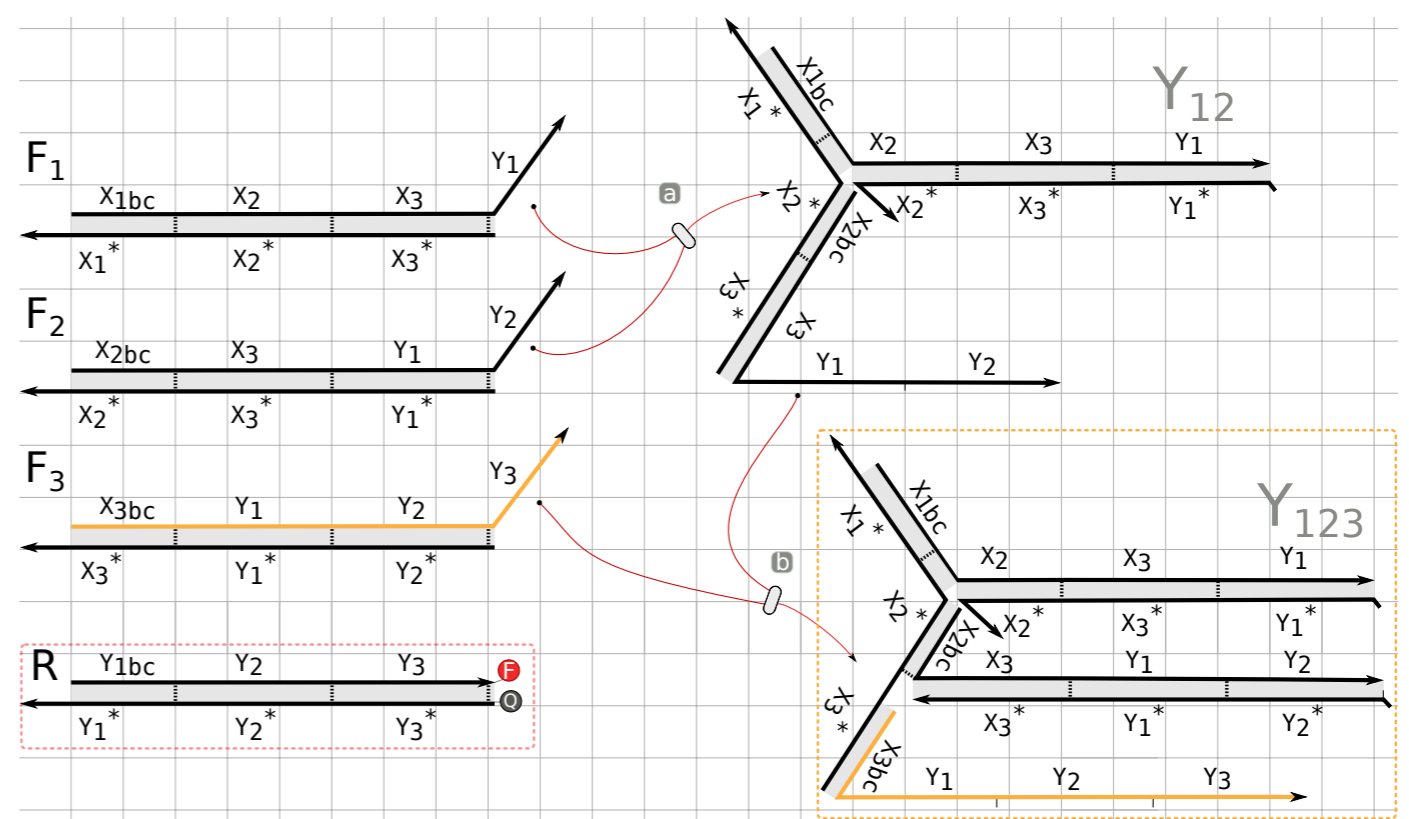


Can we generalize the  
DLD motif?

# Translator using Triple Long Domain (TLD) motif

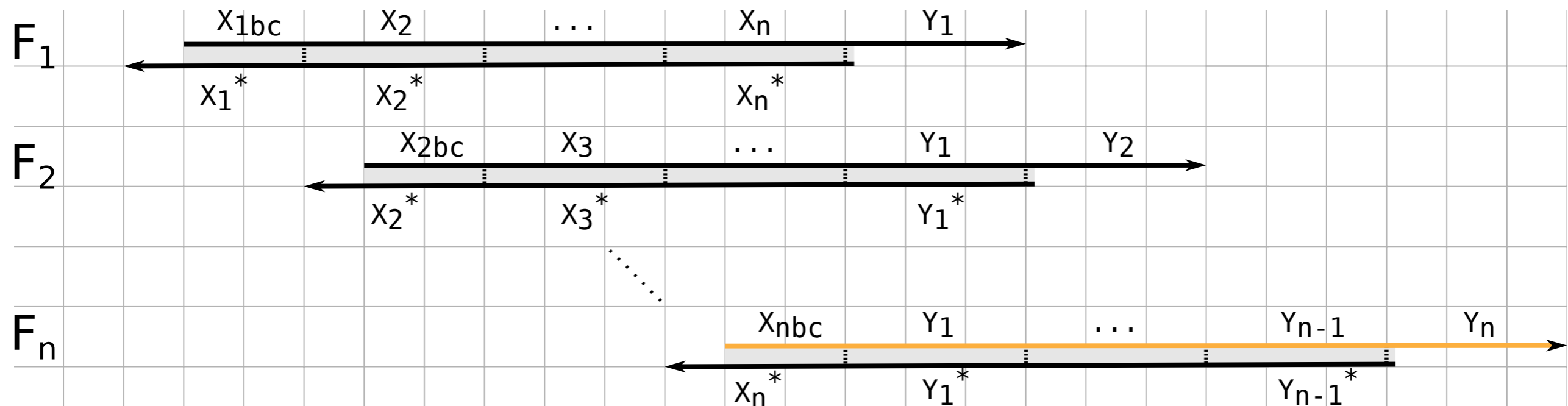


Three fuel complexes must combine to activate output signal.



$\Delta$ Energy  
 0 bound long domains  
 -2 units of entropy

# Translator using $N$ Long Domain (NLD) motif



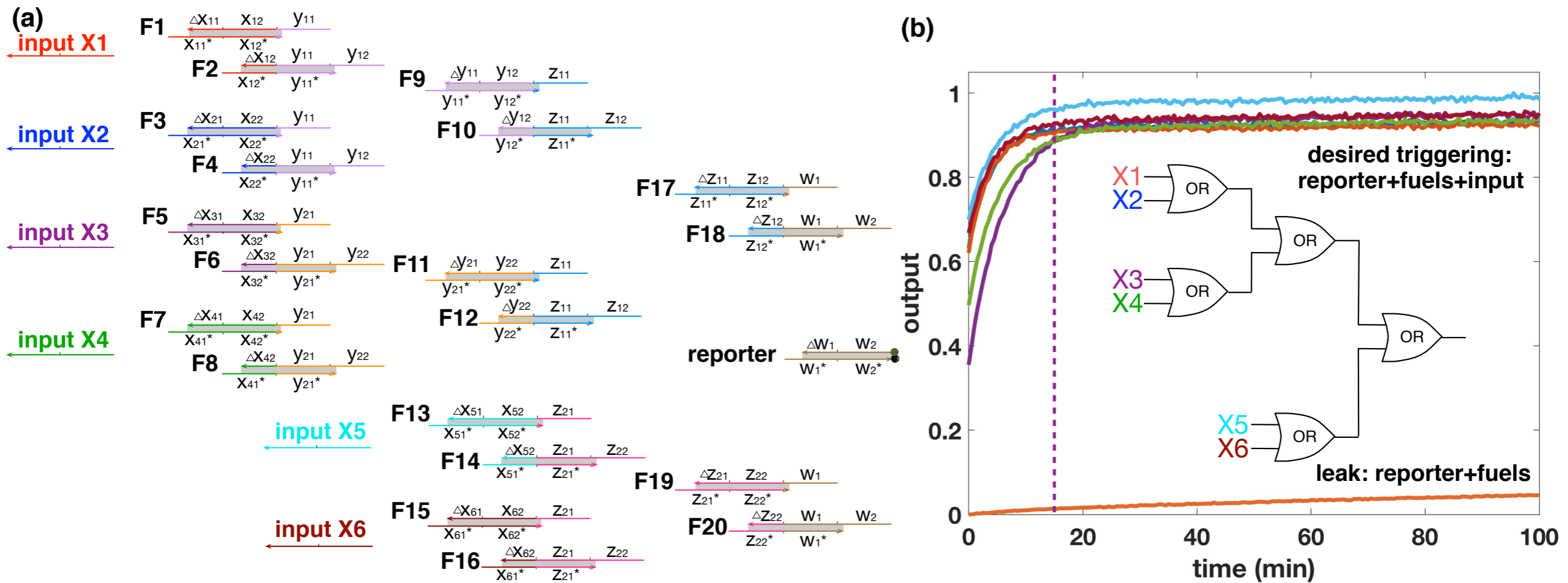
$N$  fuel complexes must combine to activate output signal.

$\Delta$ Energy to leak state

0 bound long domains  
 $-(N-1)$  units of entropy



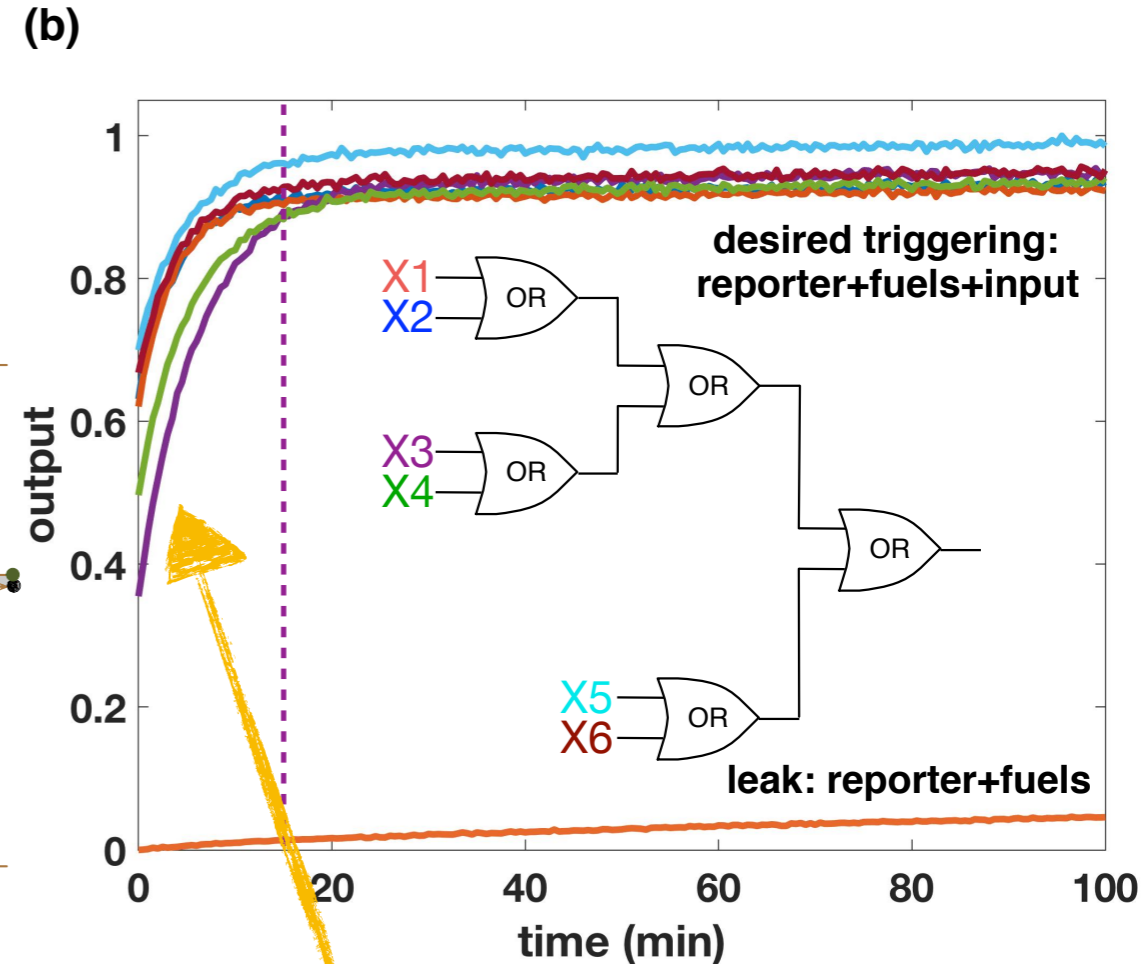
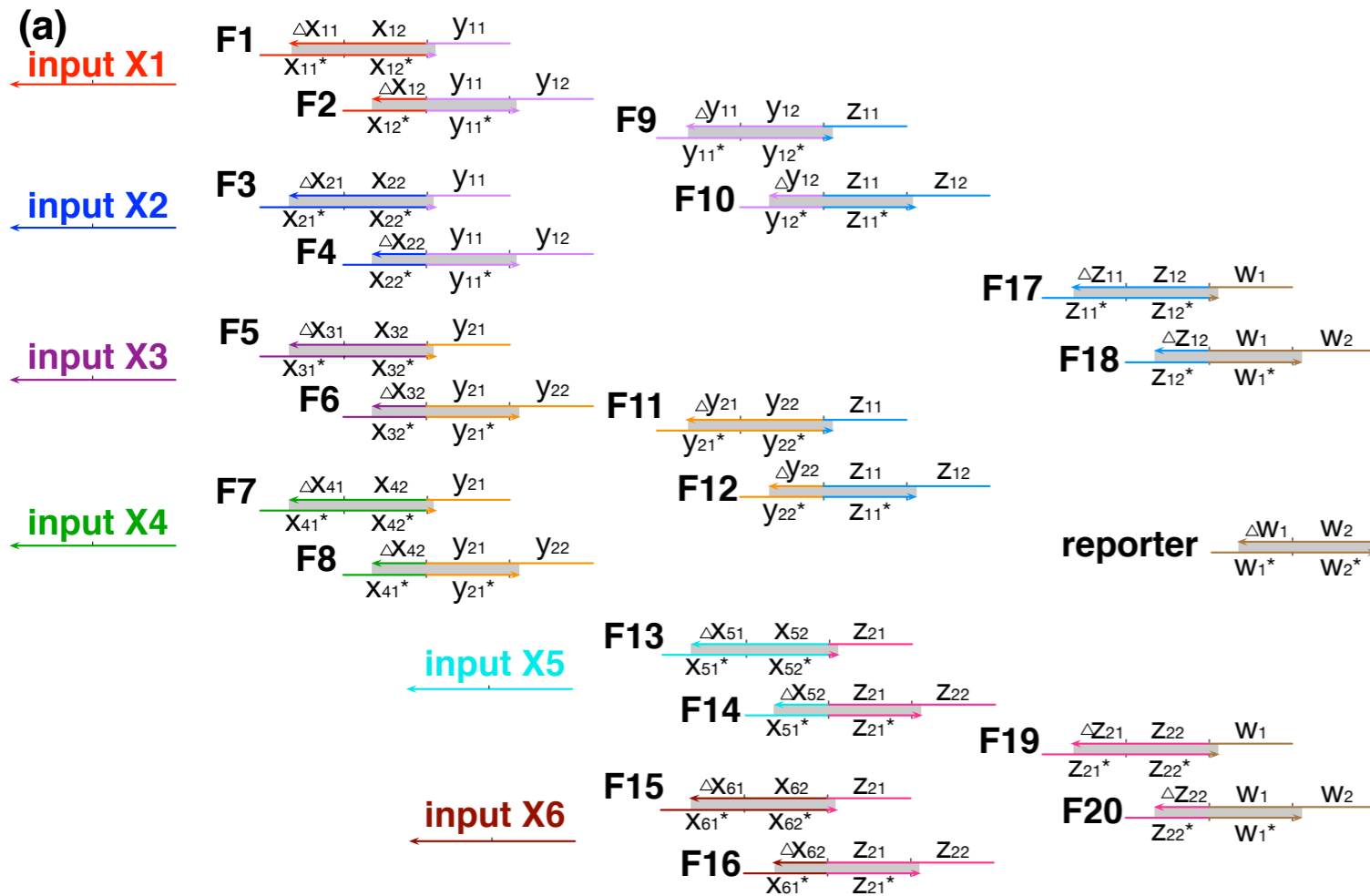
# Building OR circuits from DLD translators



[fuel]=[input]=1000nM  
[reporter]=500nM



# Building OR circuits from DLD translators



Half-time completion ~6 minutes  
No signal restoration used.

[fuel]=[input]=1000nM  
[reporter]=500nM

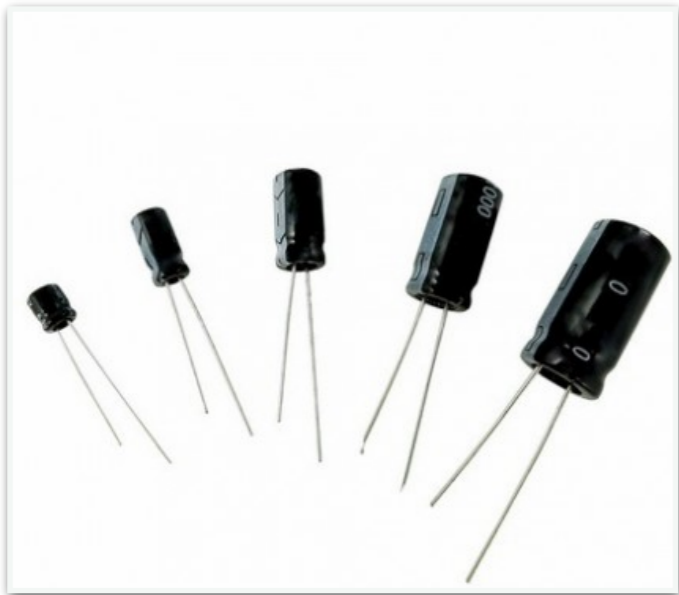
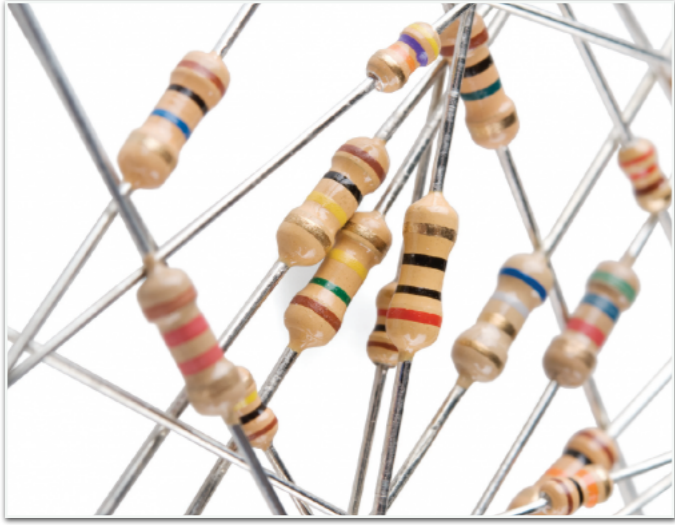
# Tutorial Outline

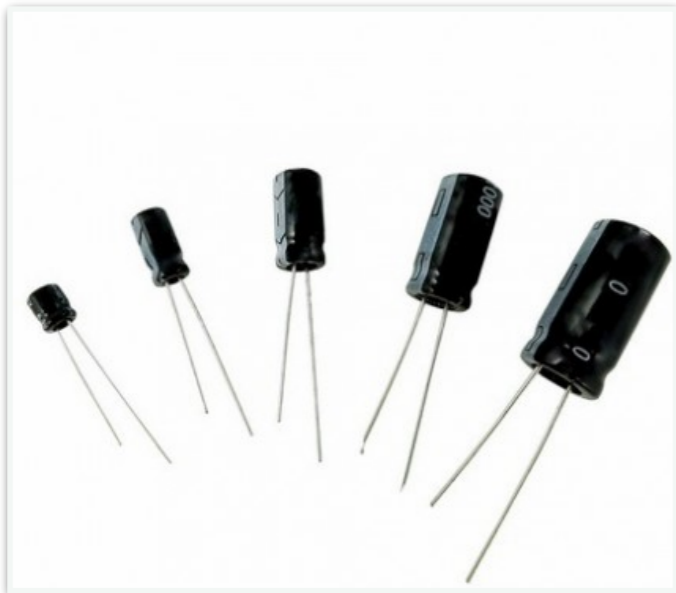
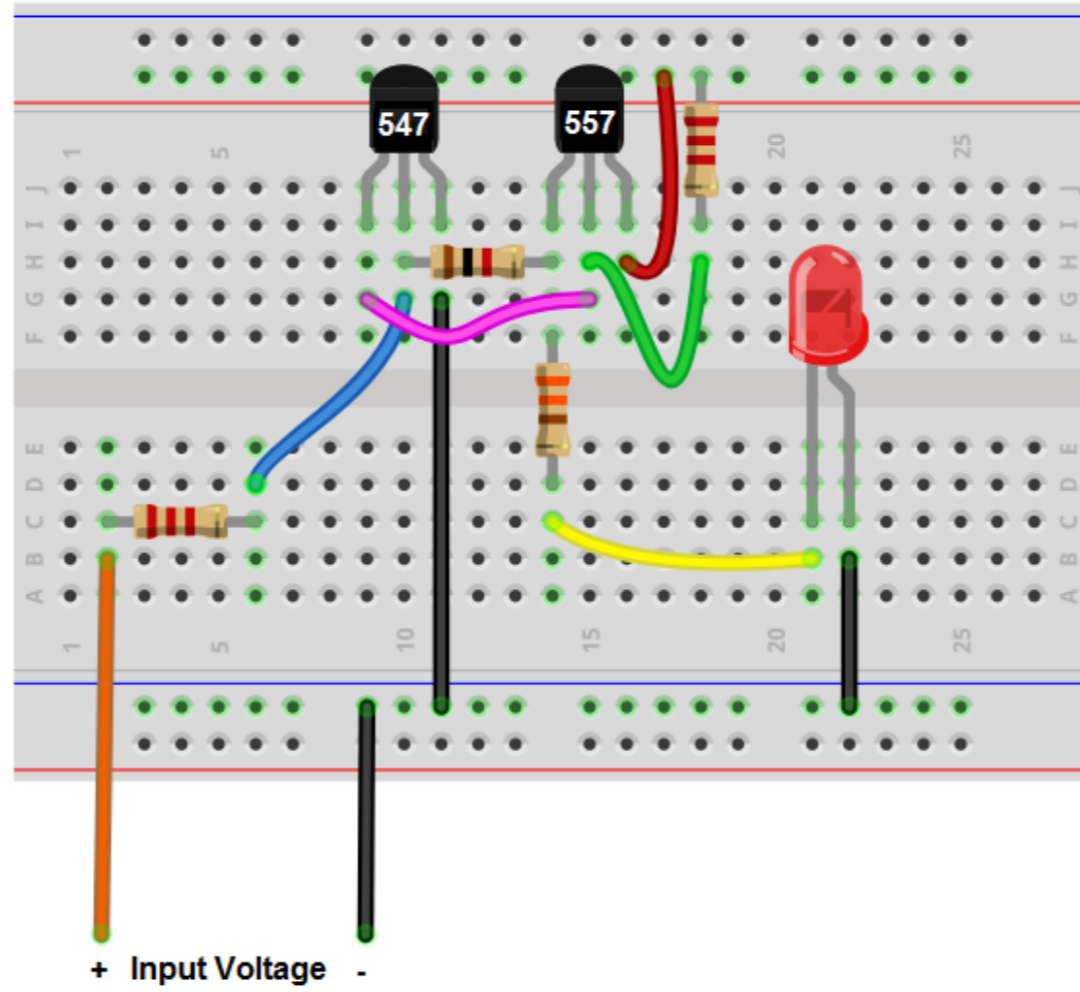
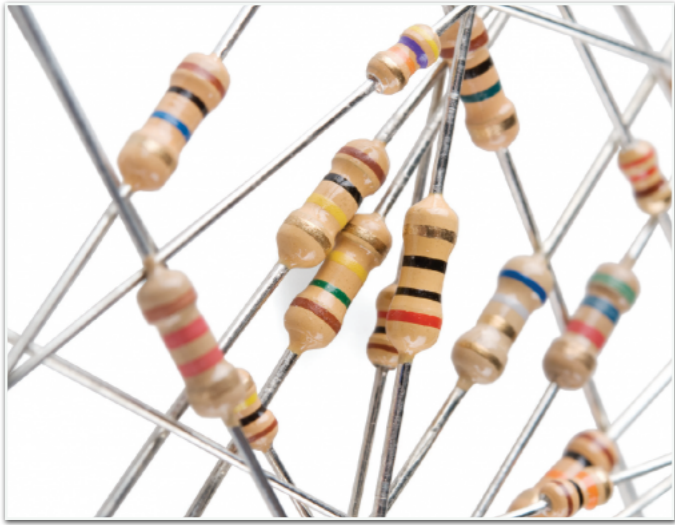
- ▶ Review of strand displacement
- ▶ Building and composing logic gates
- ▶ Tools for designing and verifying circuits
- ▶ Robustness of strand displacement
- ▶ **(Bonus) DSD circuits the easy way**

Does it need to be this  
difficult to build a circuit?







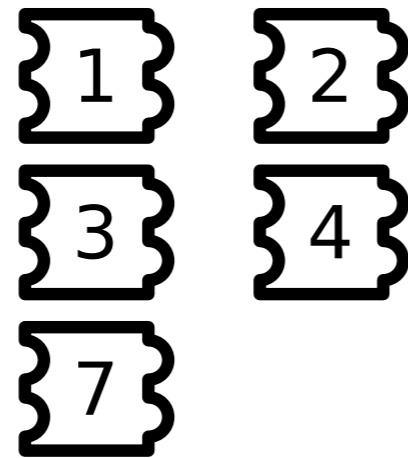


# Molecular breadboard 1.0

input signals

A1 B1  
A2 B2  
A3 B3  
A4 B4  
A7 B7

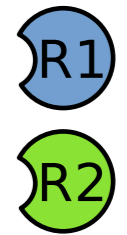
reaction gates



wires

X1.....R1    Y3.....A2  
Y1.....R2    Y3.....B2  
X2.....B1    X4.....B1  
X2.....R2    X4.....B2  
Y2.....R1    Y4.....A2  
X3.....B1    Y4.....R2  
X3.....B4    X7.....A1  
X3.....R2

reporters



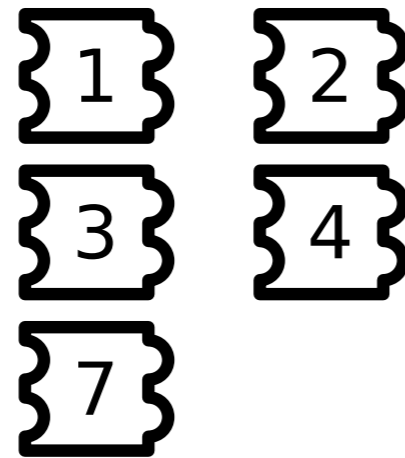
Built using leakless motif

# Molecular breadboard 1.0

input signals

A1 B1  
A2 B2  
A3 B3  
A4 B4  
A7 B7

reaction gates



wires

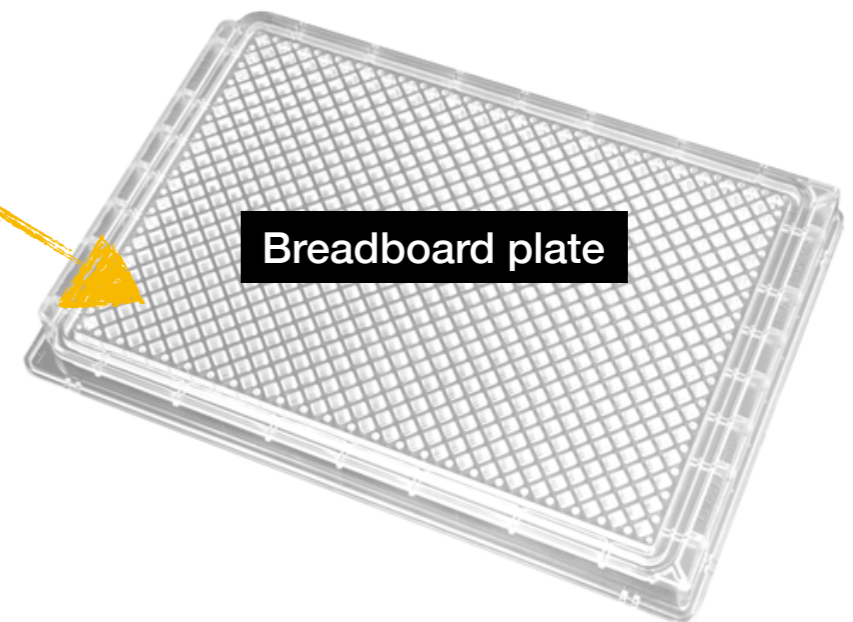
X1.....R1 Y3.....A2  
Y1.....R2 Y3.....B2  
X2.....B1 X4.....B1  
X2.....R2 X4.....B2  
Y2.....R1 Y4.....A2  
X3.....B1 Y4.....R2  
X3.....B4 X7.....A1  
X3.....R2

reporters



Load breadboard components onto 384-well plate

Built using leakless motif

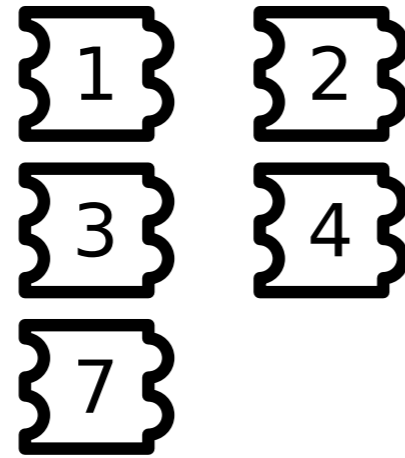


# Molecular breadboard 1.0

input signals

A1 B1  
A2 B2  
A3 B3  
A4 B4  
A7 B7

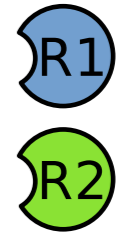
reaction gates



wires

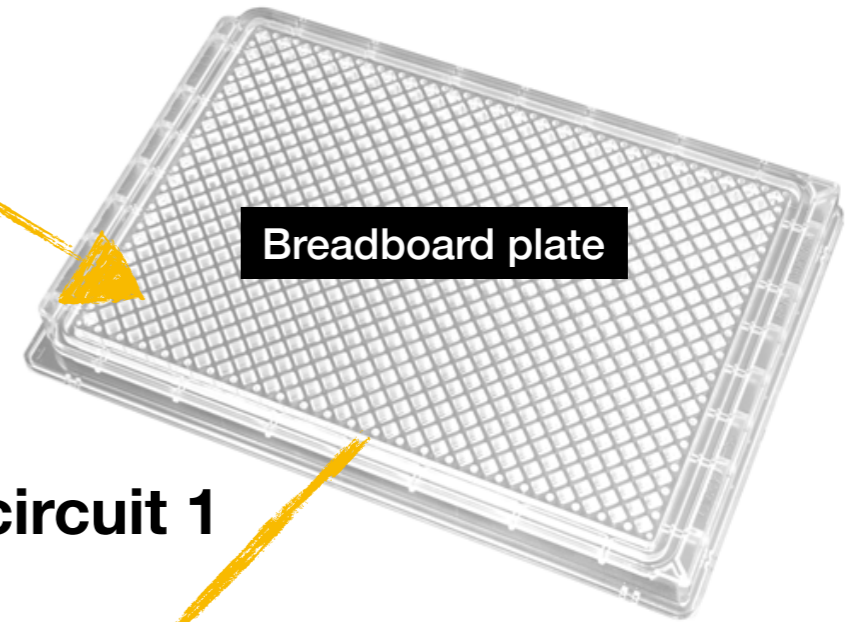
X1.....R1 Y3.....A2  
Y1.....R2 Y3.....B2  
X2.....B1 X4.....B1  
X2.....R2 X4.....B2  
Y2.....R1 Y4.....A2  
X3.....B1 Y4.....R2  
X3.....B4 X7.....A1  
X3.....R2

reporters

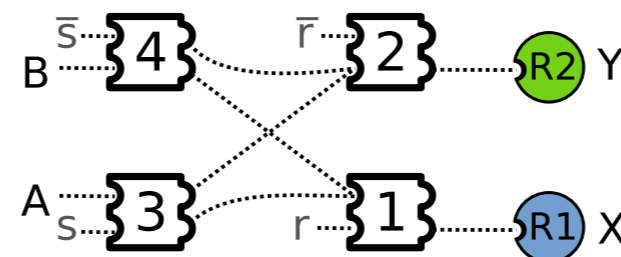


Load breadboard components onto 384-well plate

Built using leakless motif



circuit 1

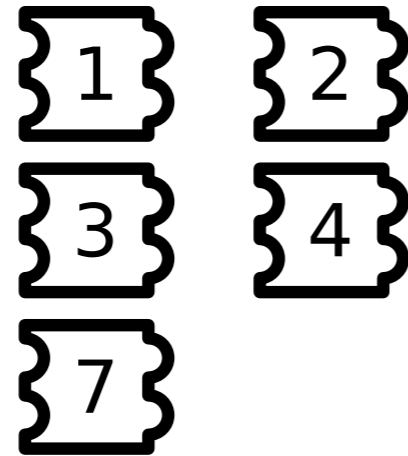


# Molecular breadboard 1.0

input signals

A1 B1  
A2 B2  
A3 B3  
A4 B4  
A7 B7

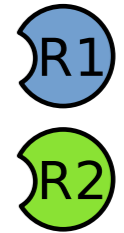
reaction gates



wires

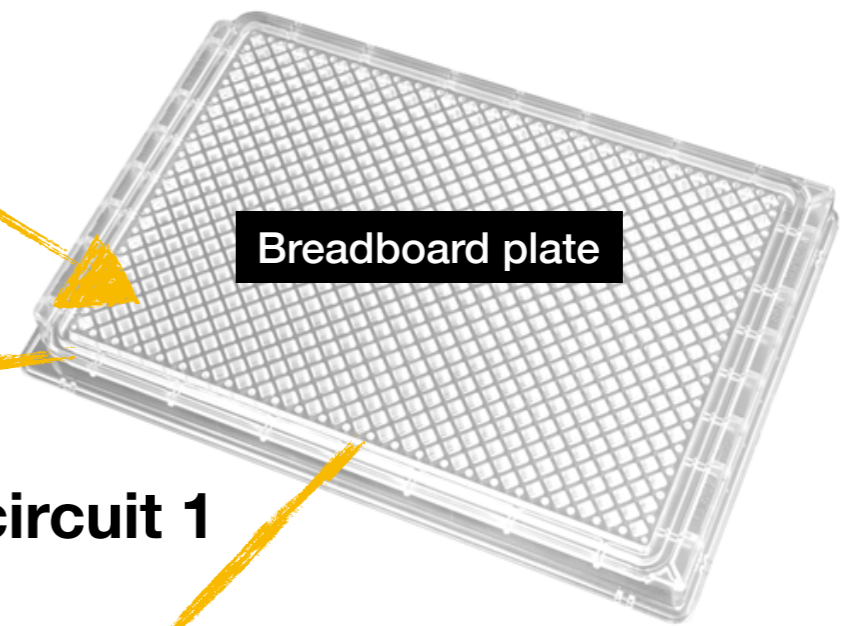
X1.....R1 Y3.....A2  
Y1.....R2 Y3.....B2  
X2.....B1 X4.....B1  
X2.....R2 X4.....B2  
Y2.....R1 Y4.....A2  
X3.....B1 Y4.....R2  
X3.....B4 X7.....A1  
X3.....R2

reporters

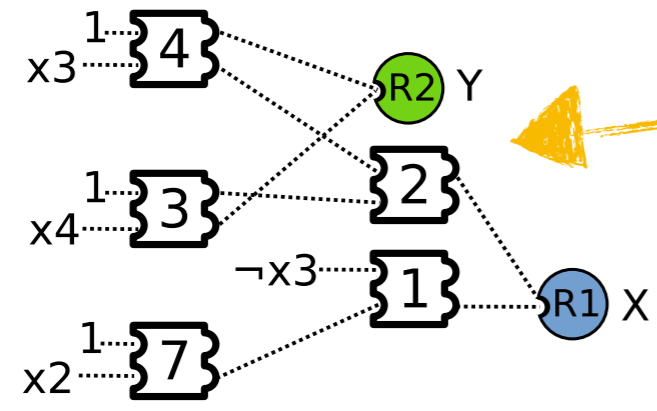


Load breadboard components onto 384-well plate

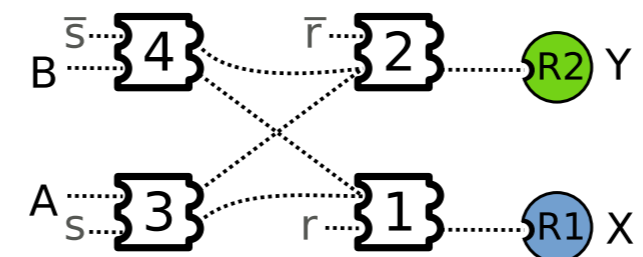
Built using leakless motif



circuit 2



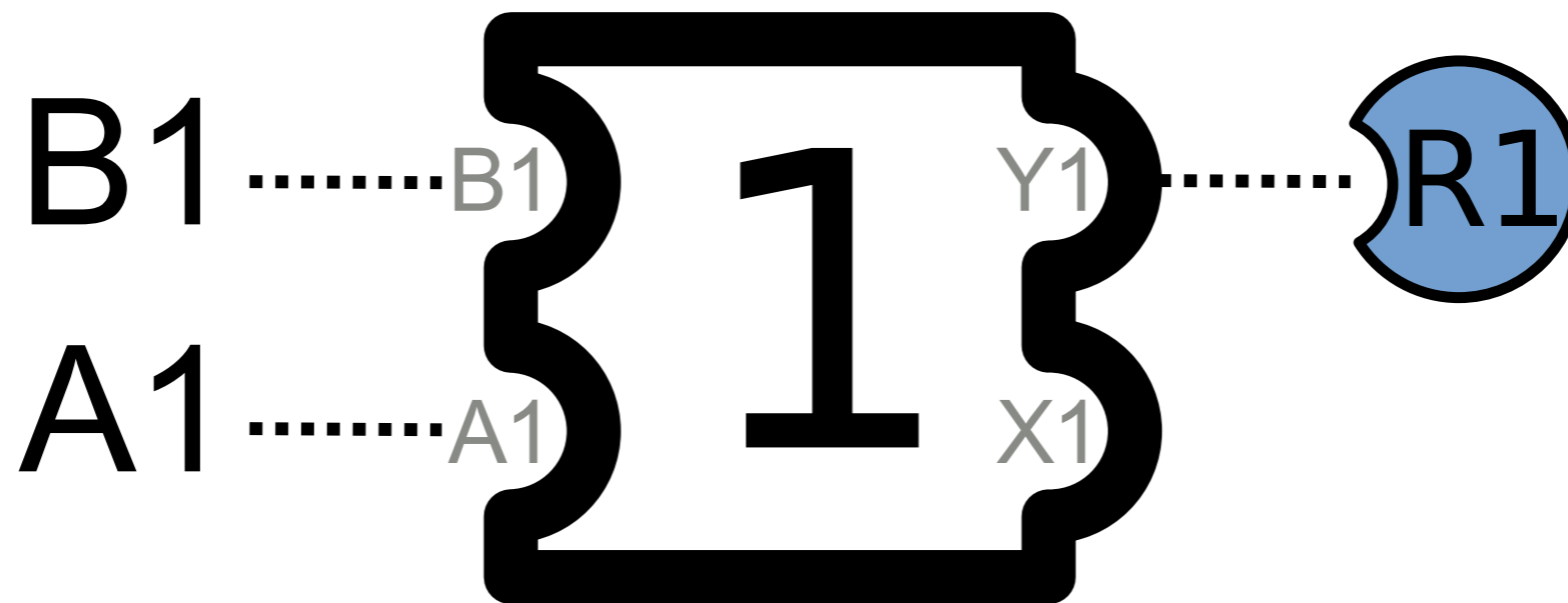
circuit 1



# Testing breadboard components

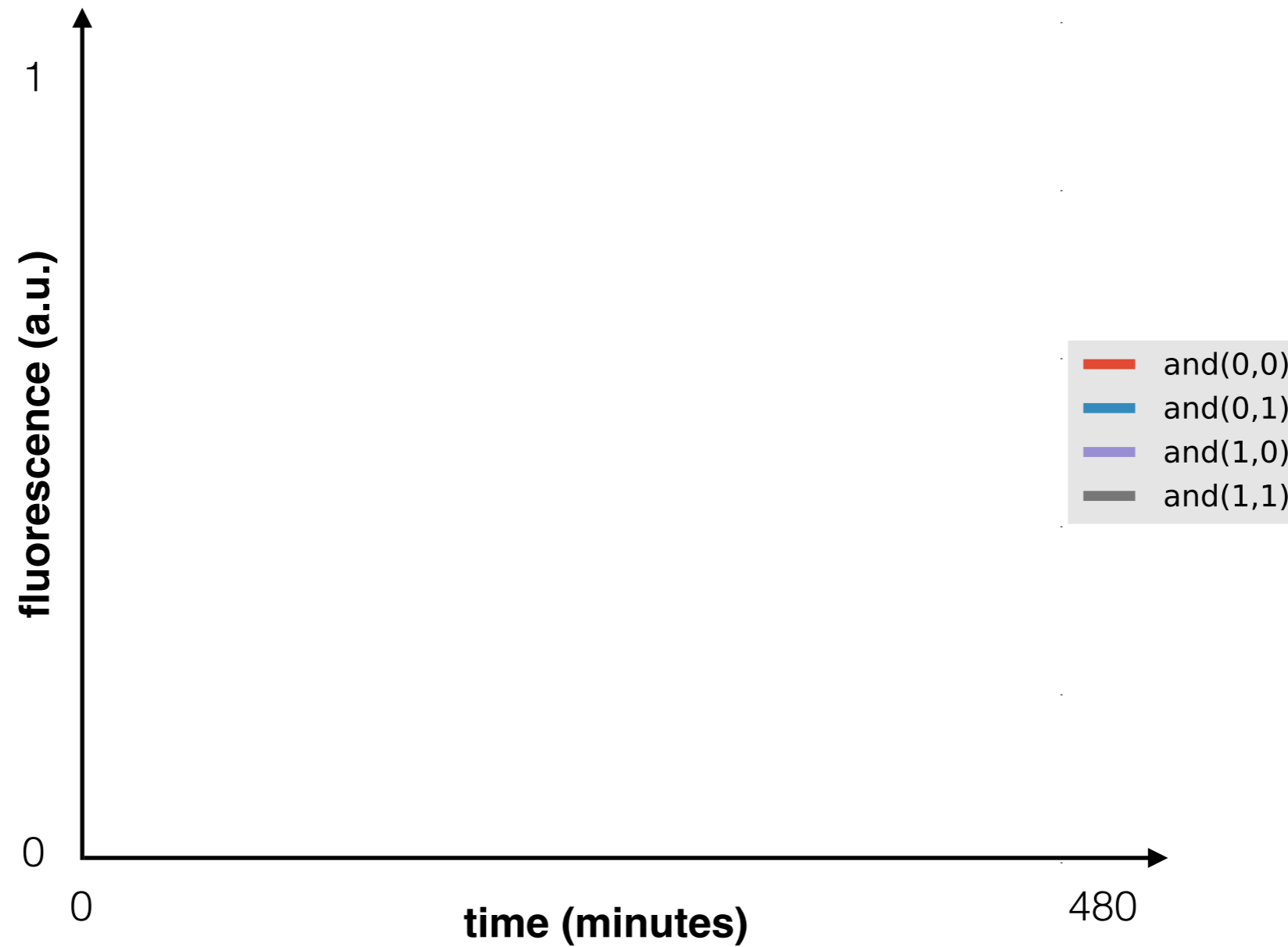
- ▶ Typical DSD circuits are 50nM - 200nM concentration  
(our circuits can operate at these concentrations)
- ▶ To demonstrate *robustness*, all experiments will be at 2uM  
(~20x higher than typical concentrations)

# AND gate

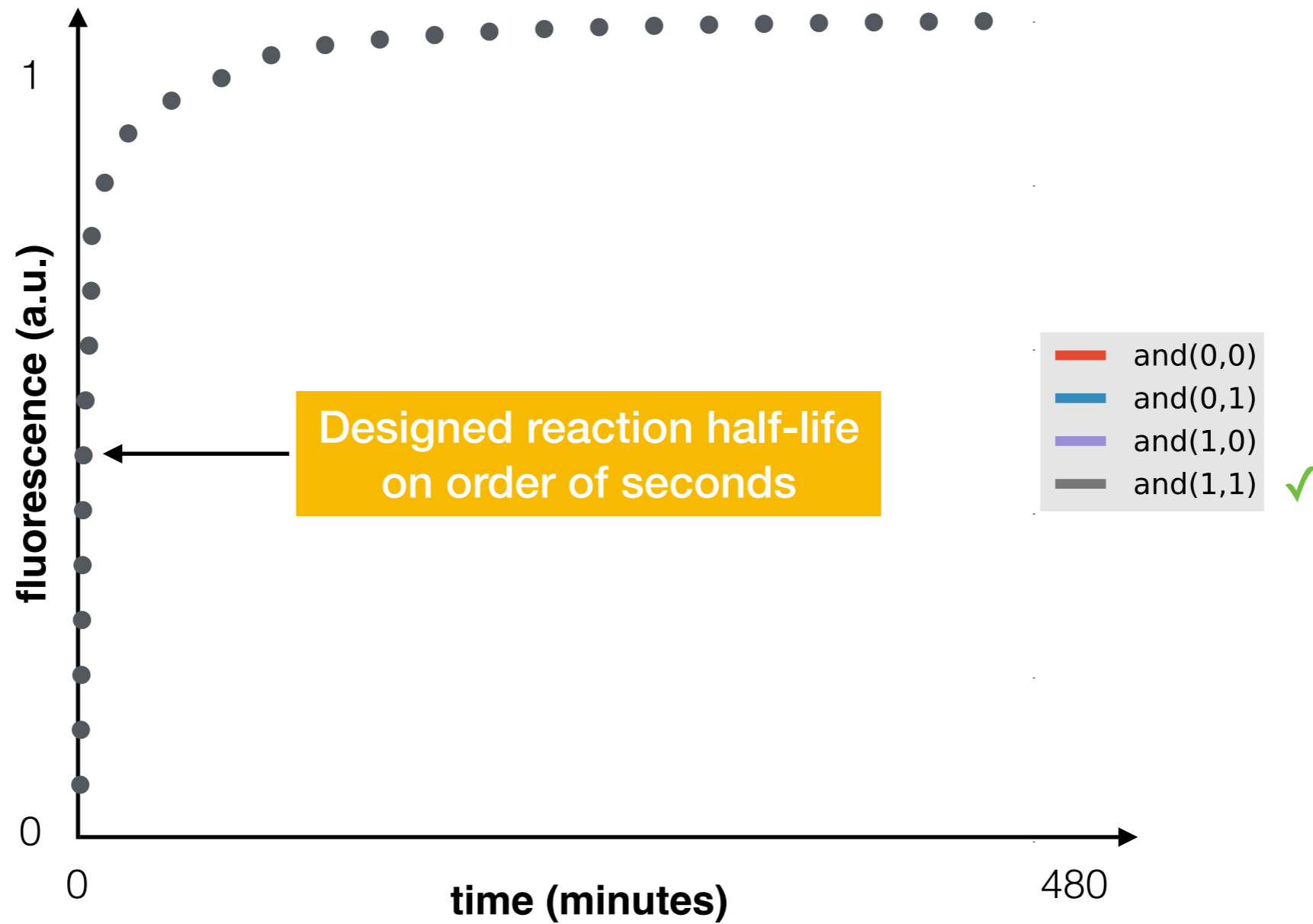




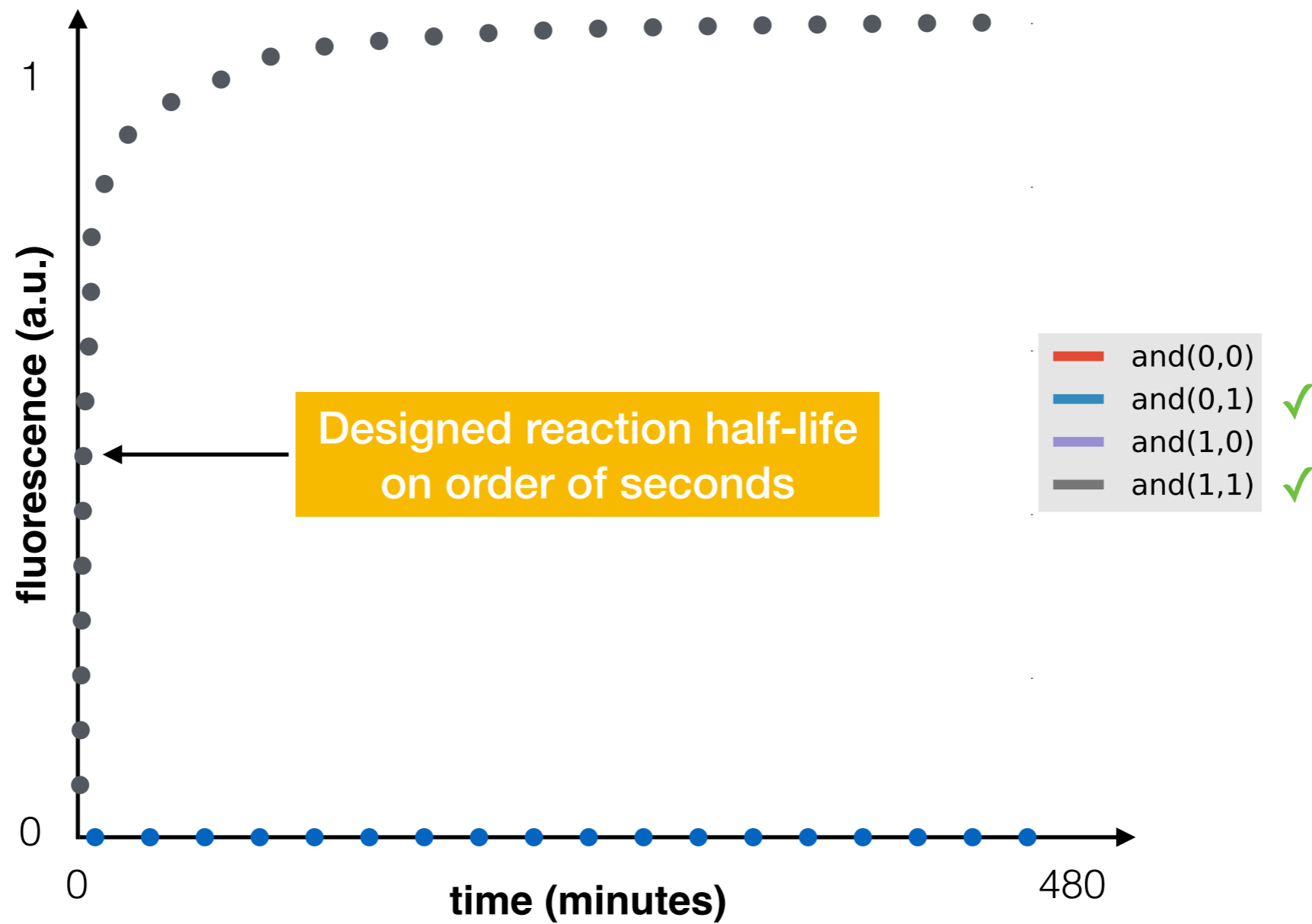
# *Ideal* AND gate simulation @ 2 $\mu$ M



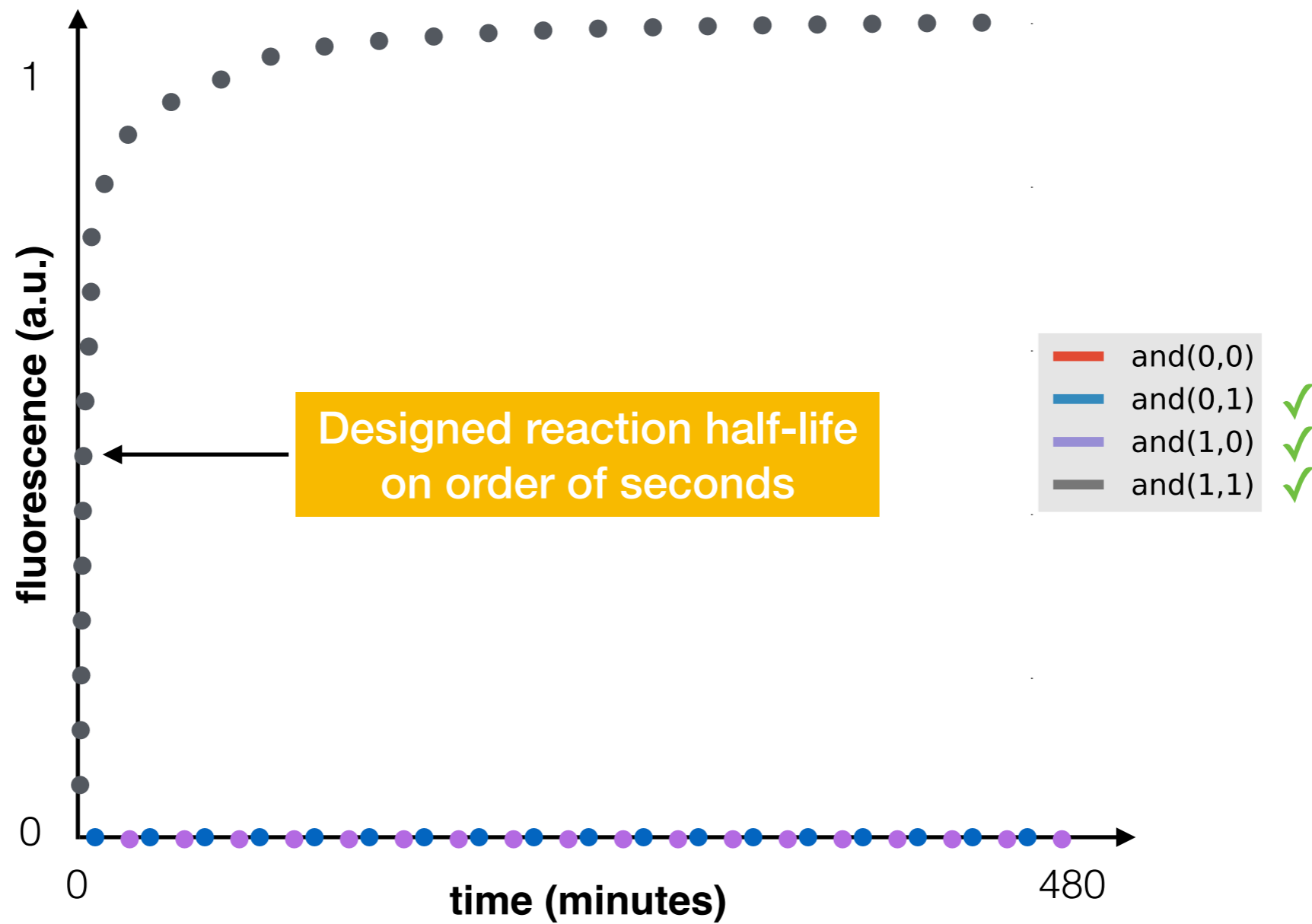
# Ideal AND gate simulation @ 2 $\mu\text{M}$



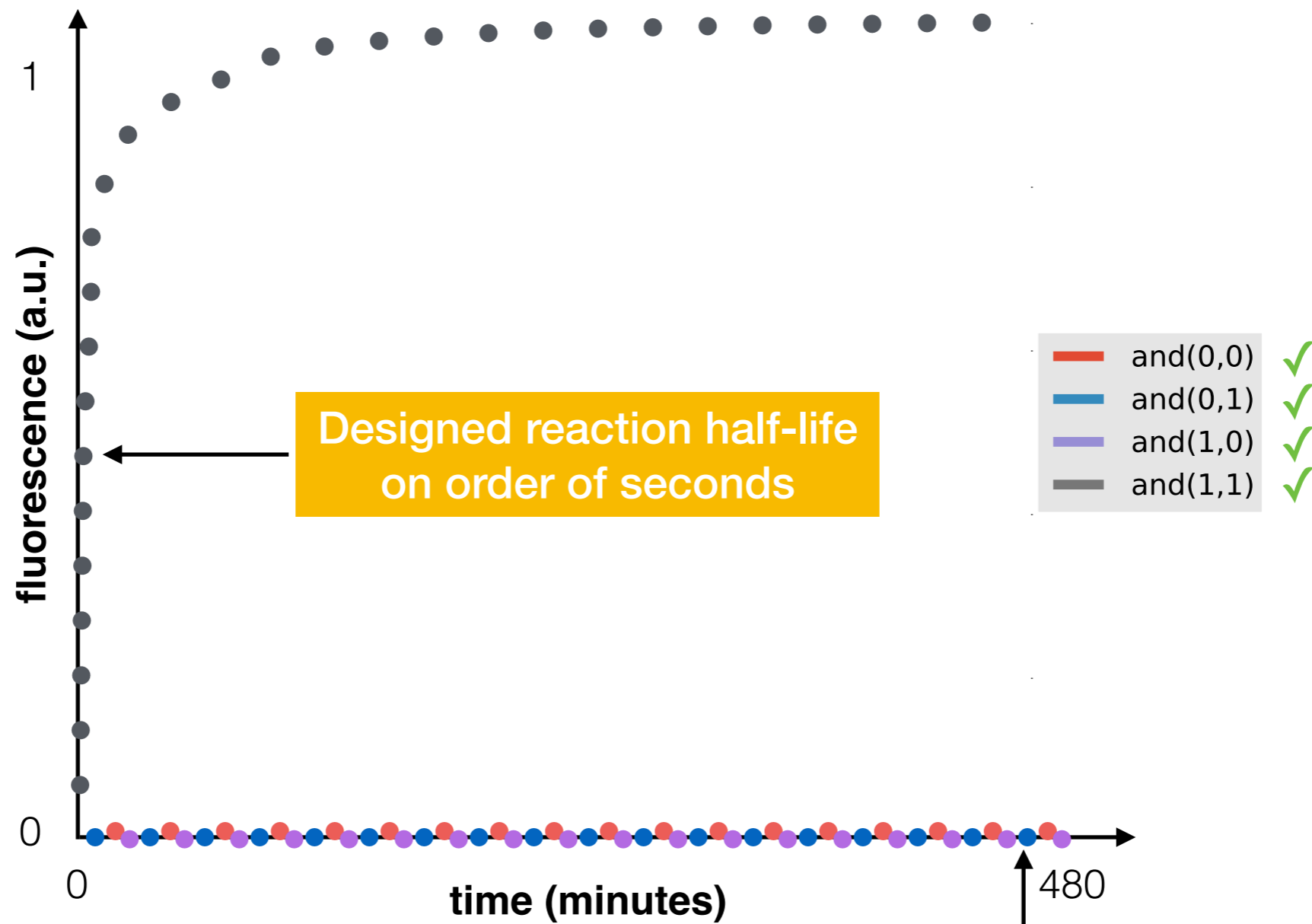
# Ideal AND gate simulation @ 2 $\mu\text{M}$



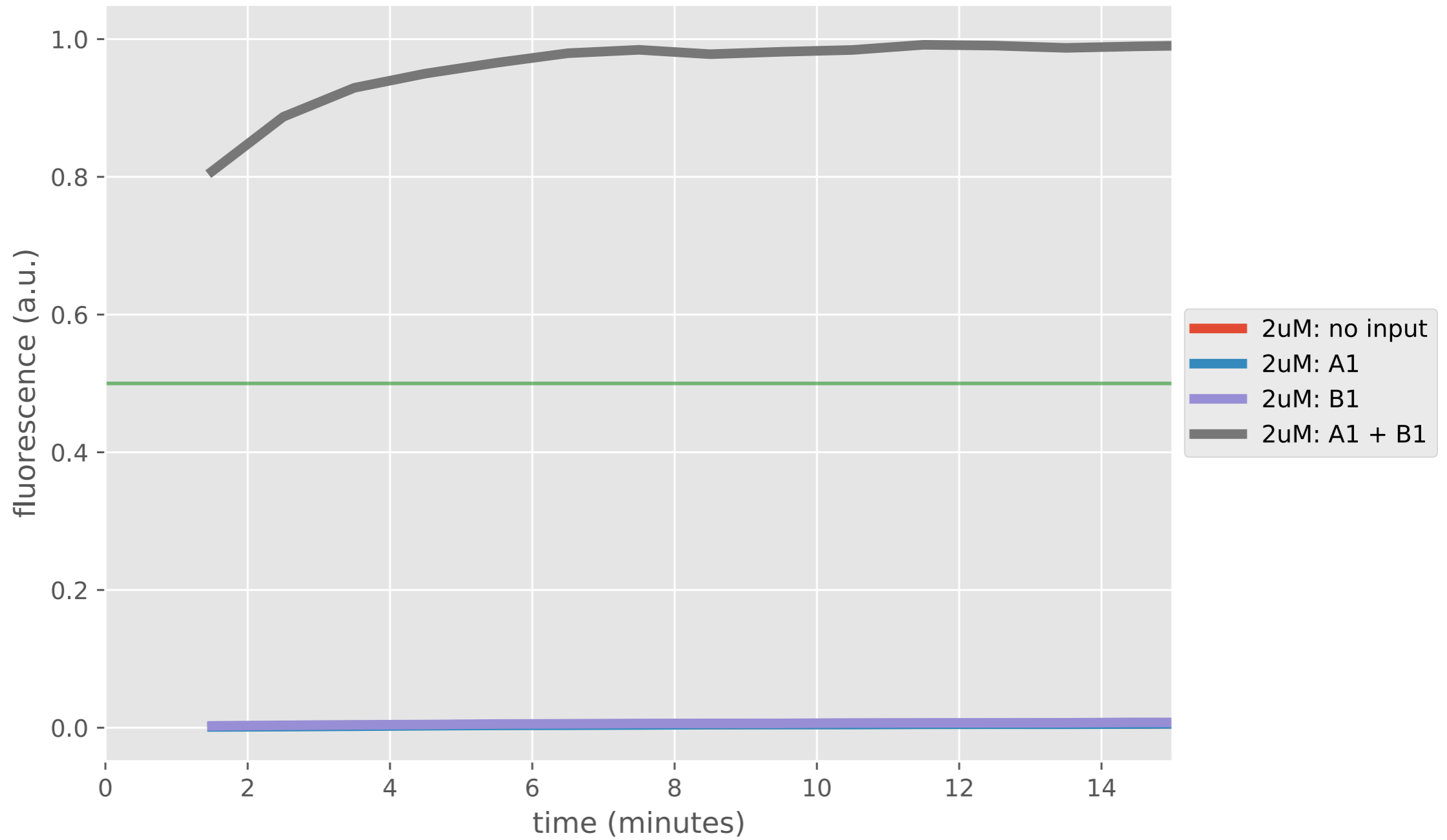
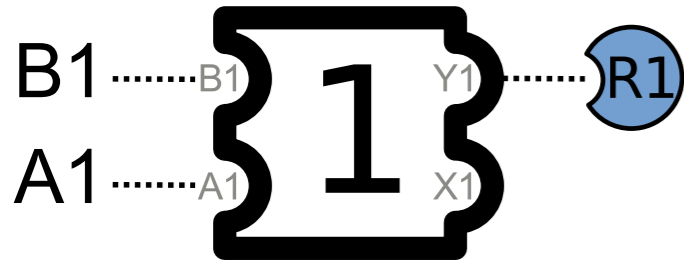
# Ideal AND gate simulation @ 2 $\mu\text{M}$



# Ideal AND gate simulation @ 2 $\mu\text{M}$

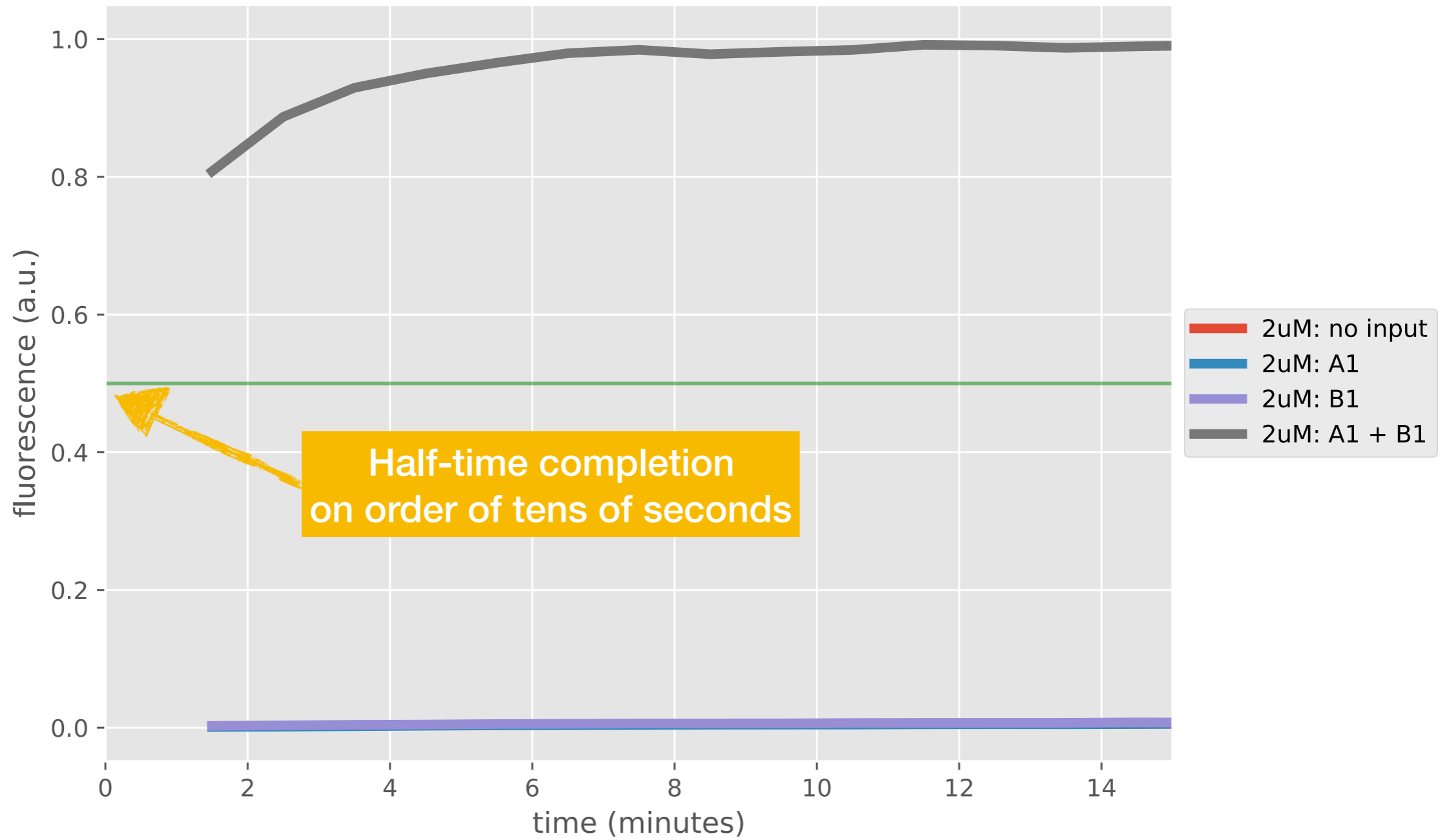
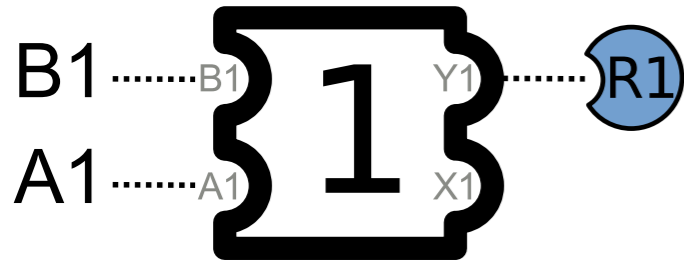


# AND gate @ 2 $\mu$ M



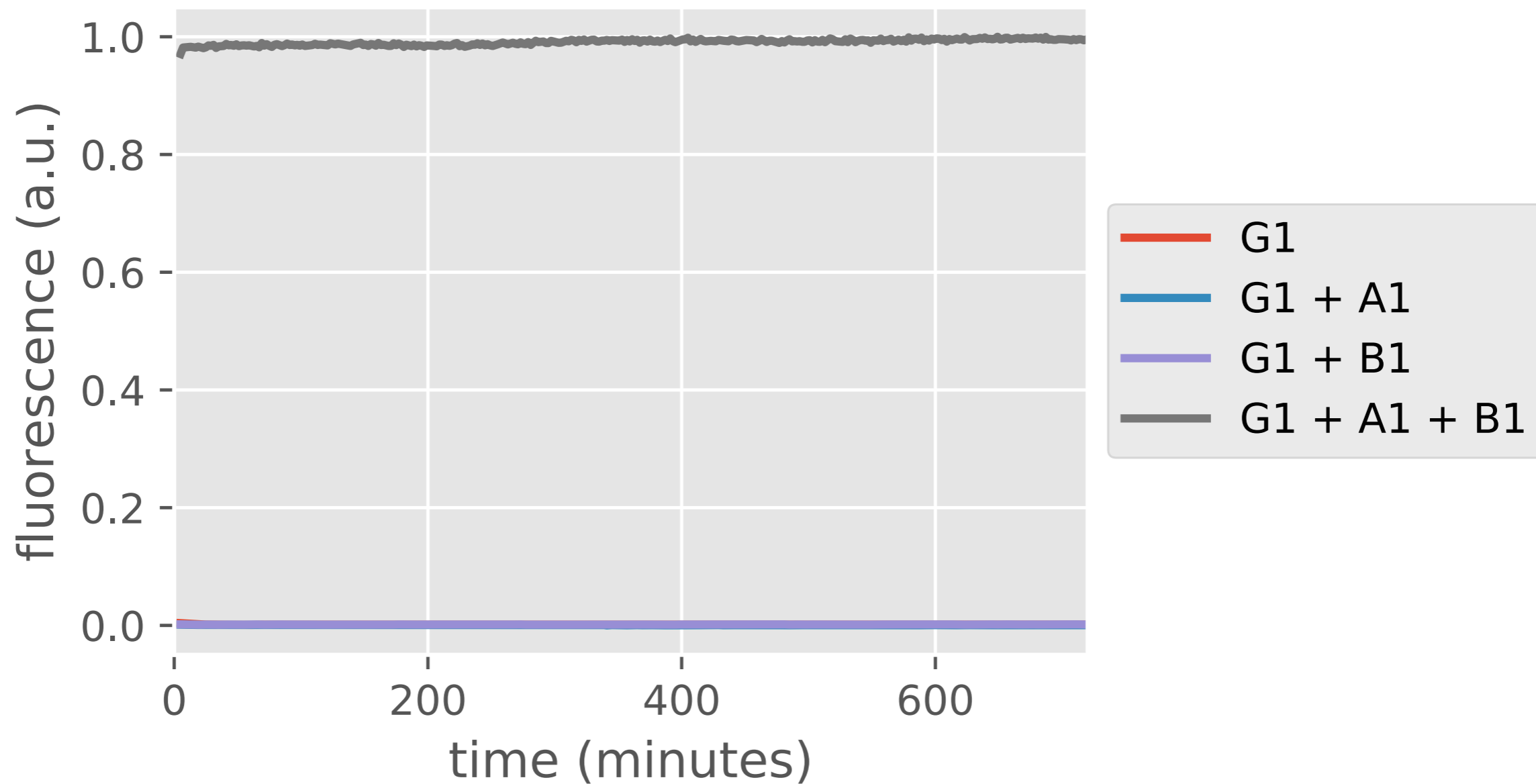
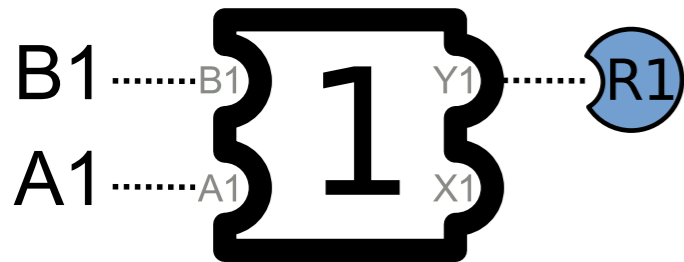
[fuel]=[input]=2uM, [reporter]=1uM

# AND gate @ 2 $\mu$ M



[fuel]=[input]=2uM, [reporter]=1uM

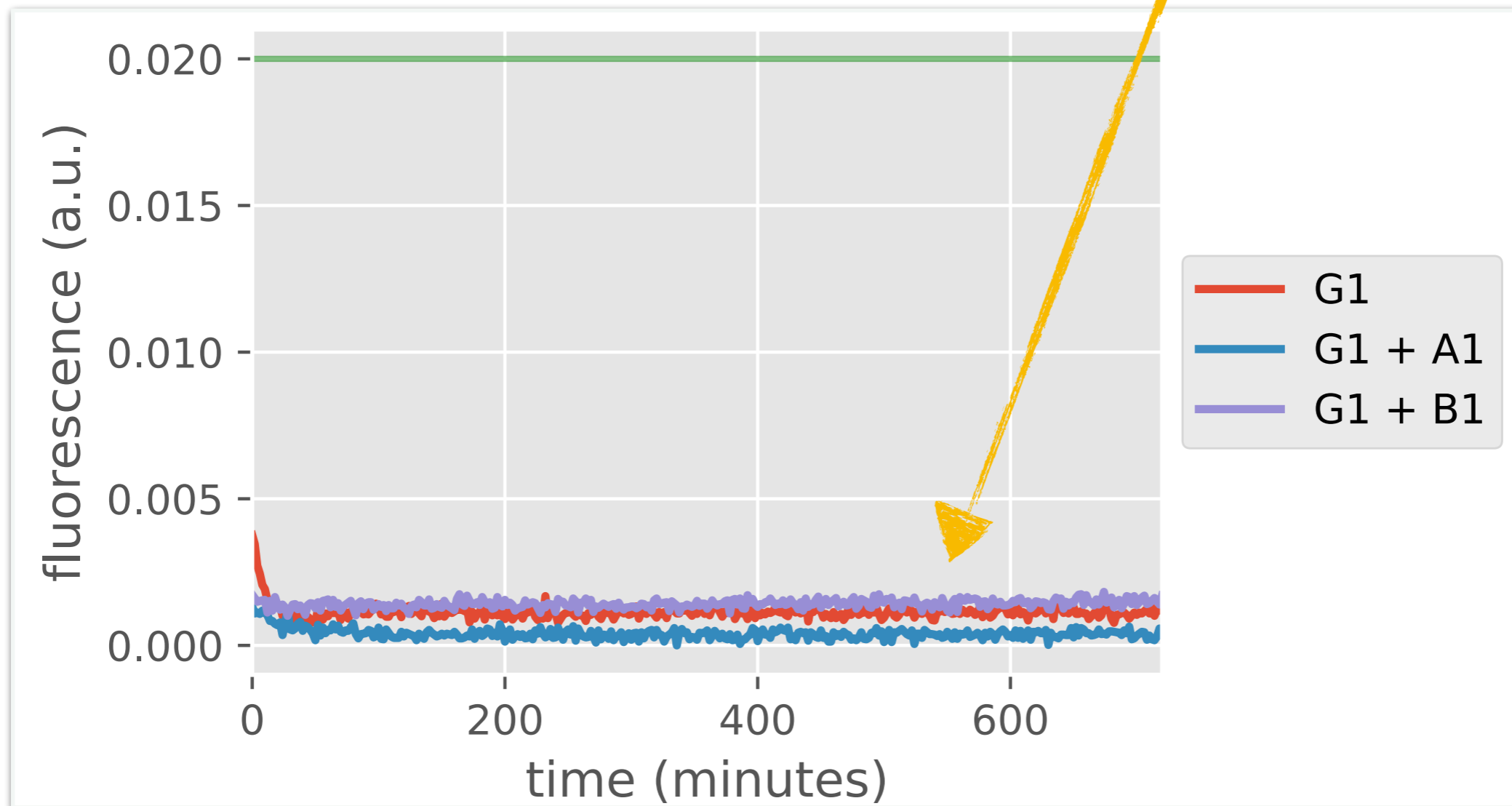
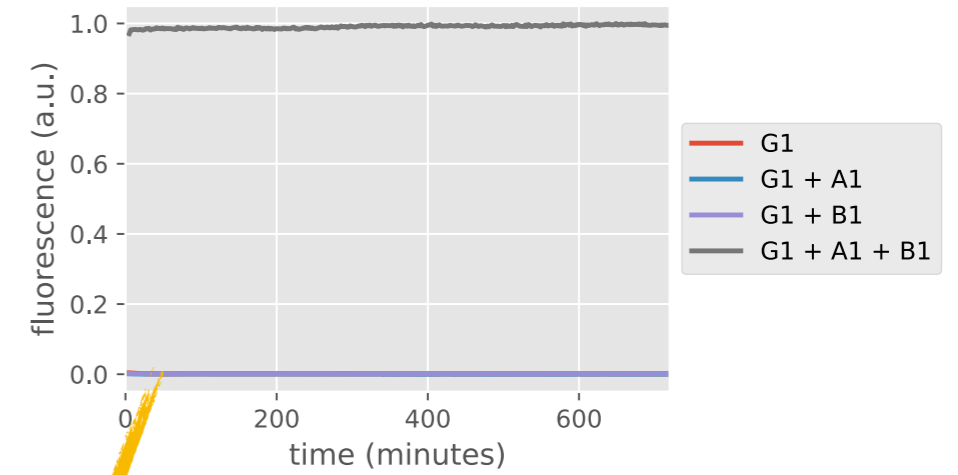
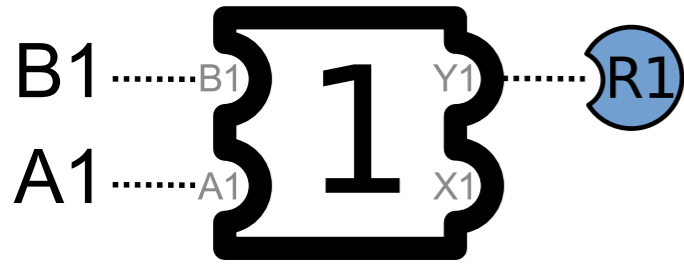
# AND gate @ 2 $\mu$ M (12 hours)



[fuel]=[input]=2 $\mu$ M, [reporter]=2.5 $\mu$ M

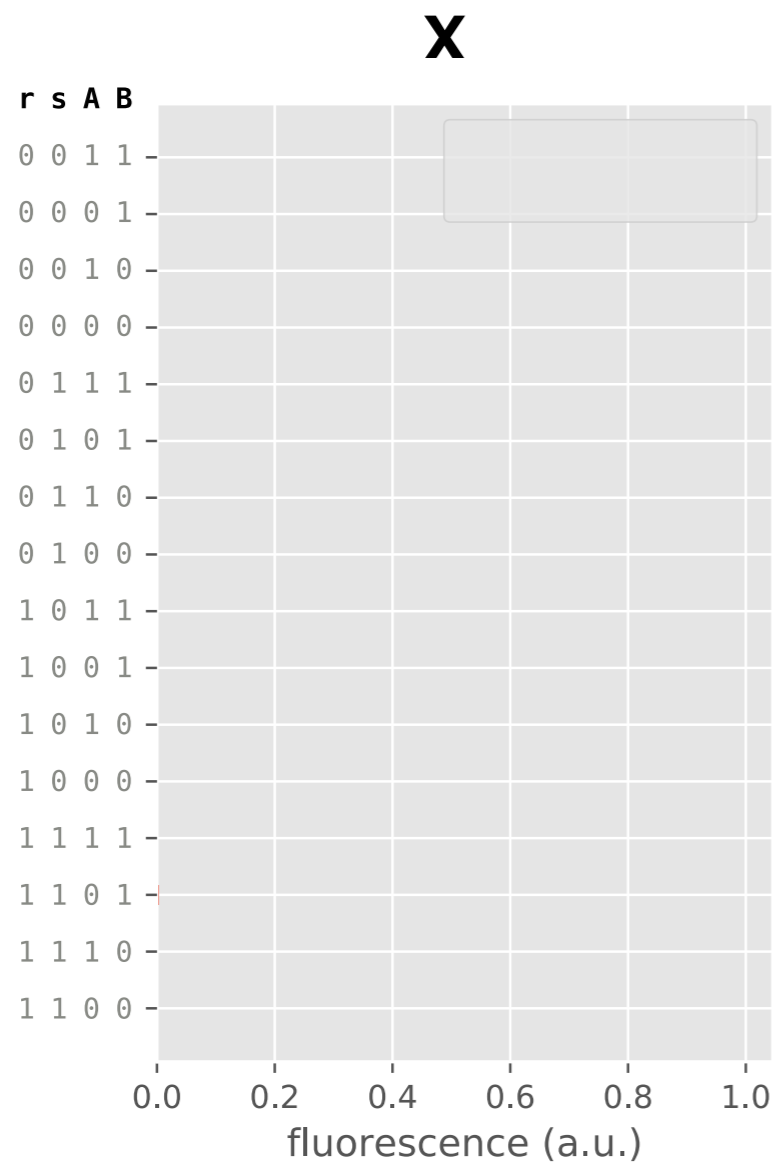
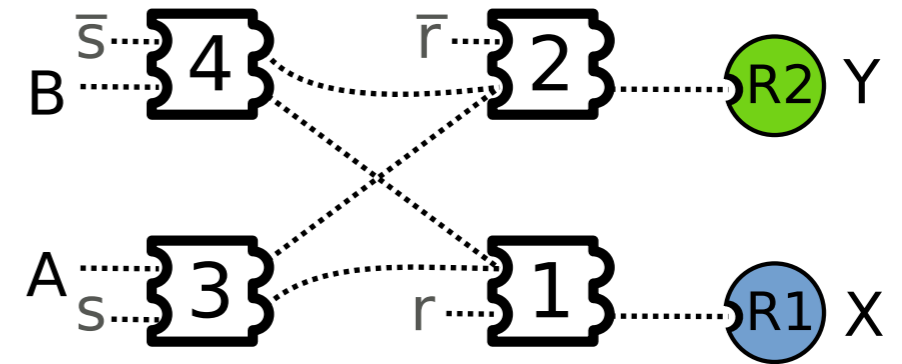
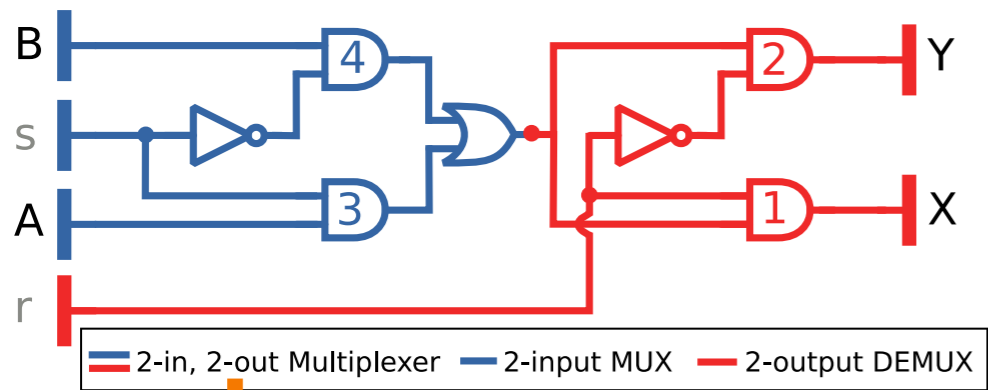


# AND gate @ 2 $\mu$ M (12 hours)

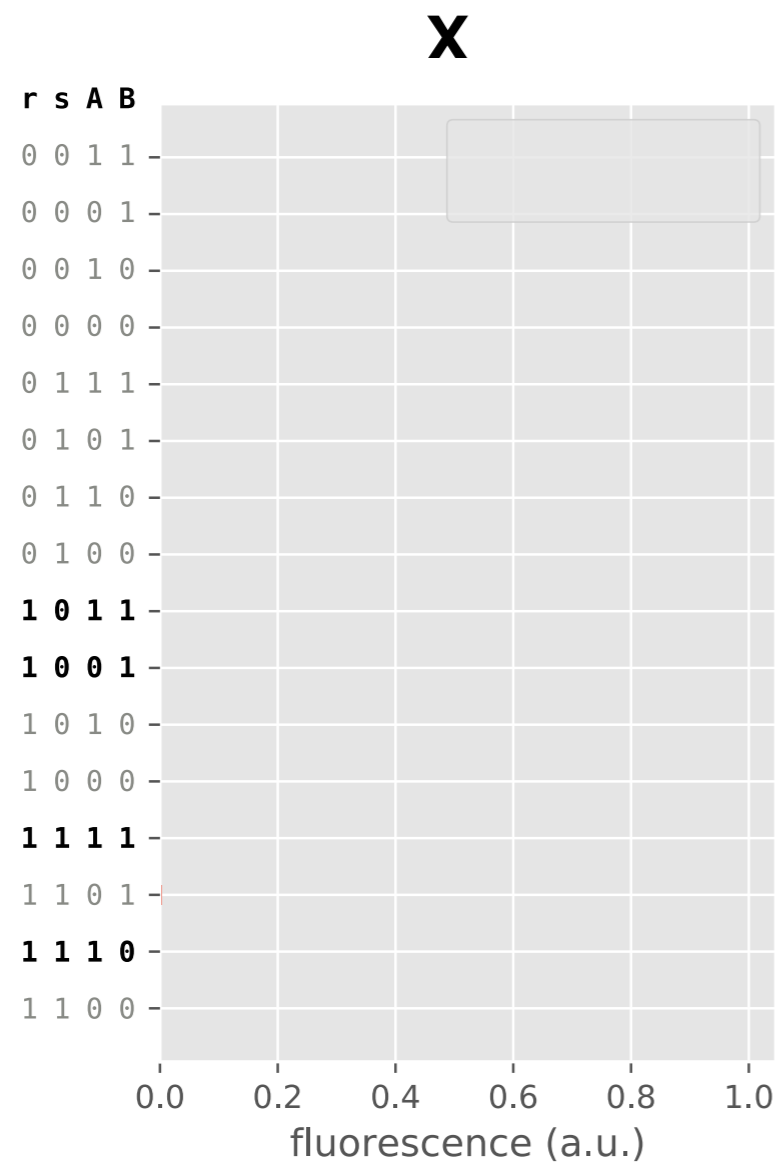
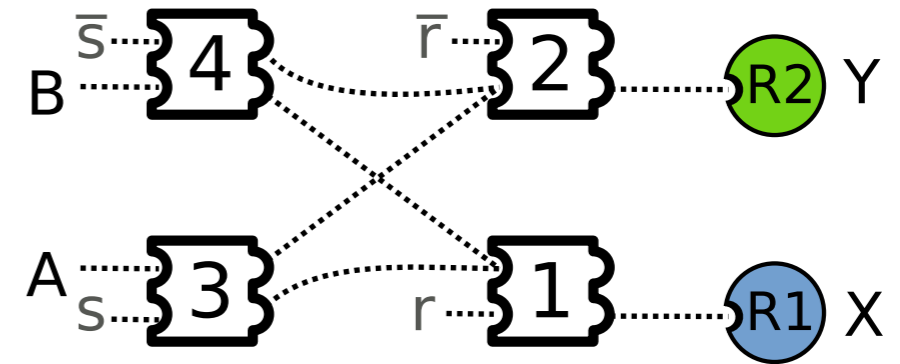
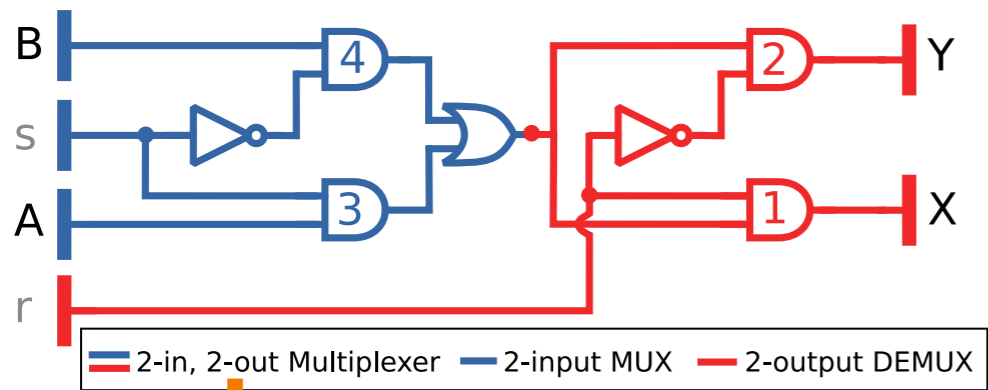


[fuel]=[input]=2 $\mu$ M, [reporter]=2.5 $\mu$ M

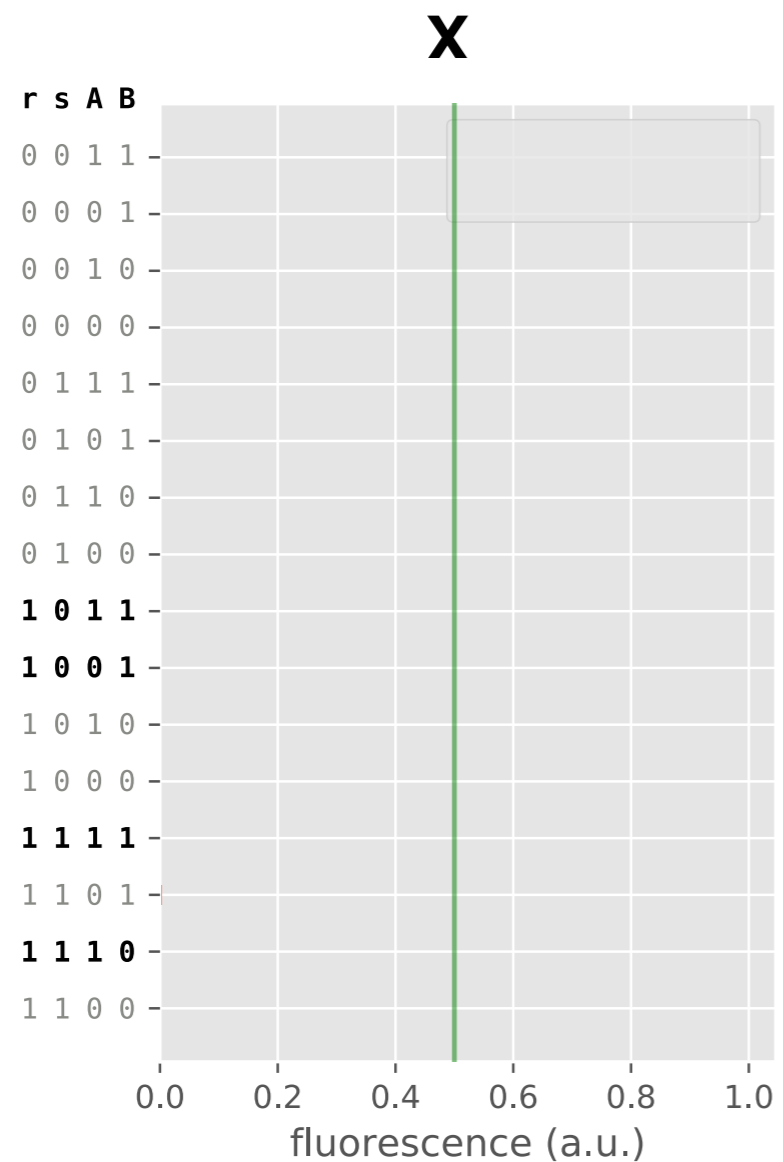
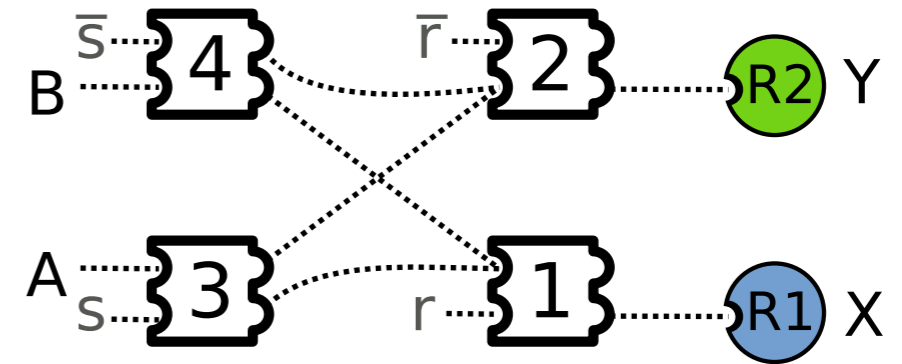
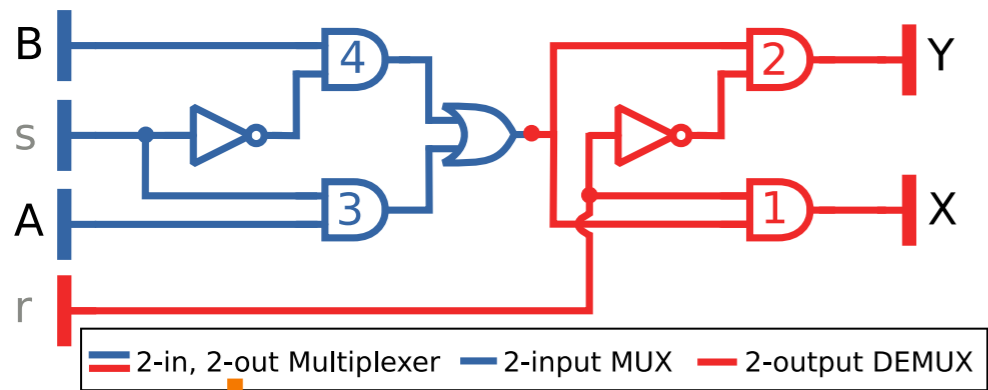
# Multiplexer-Demultiplexer



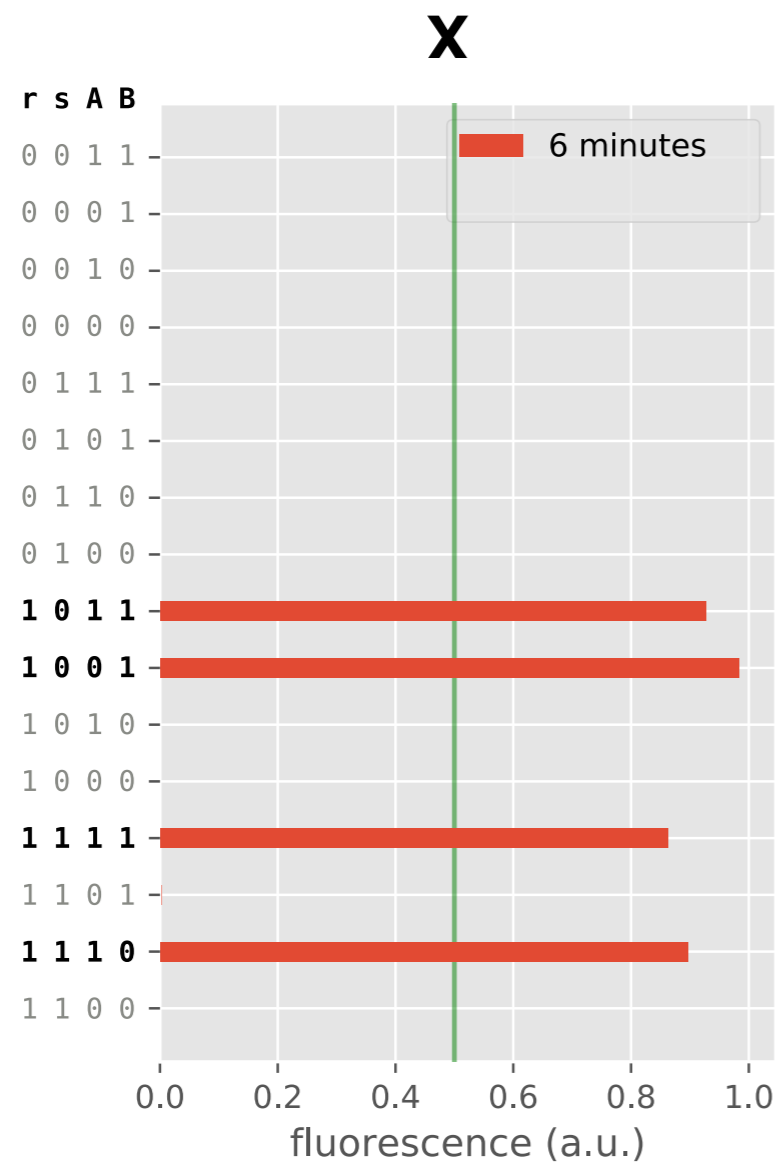
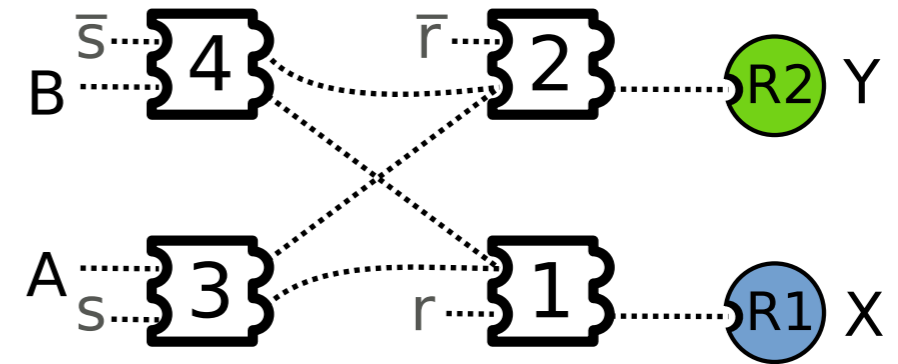
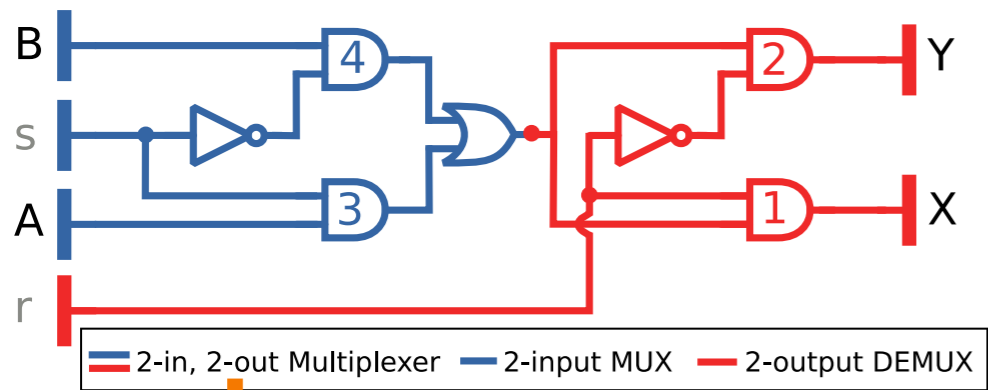
# Multiplexer-Demultiplexer



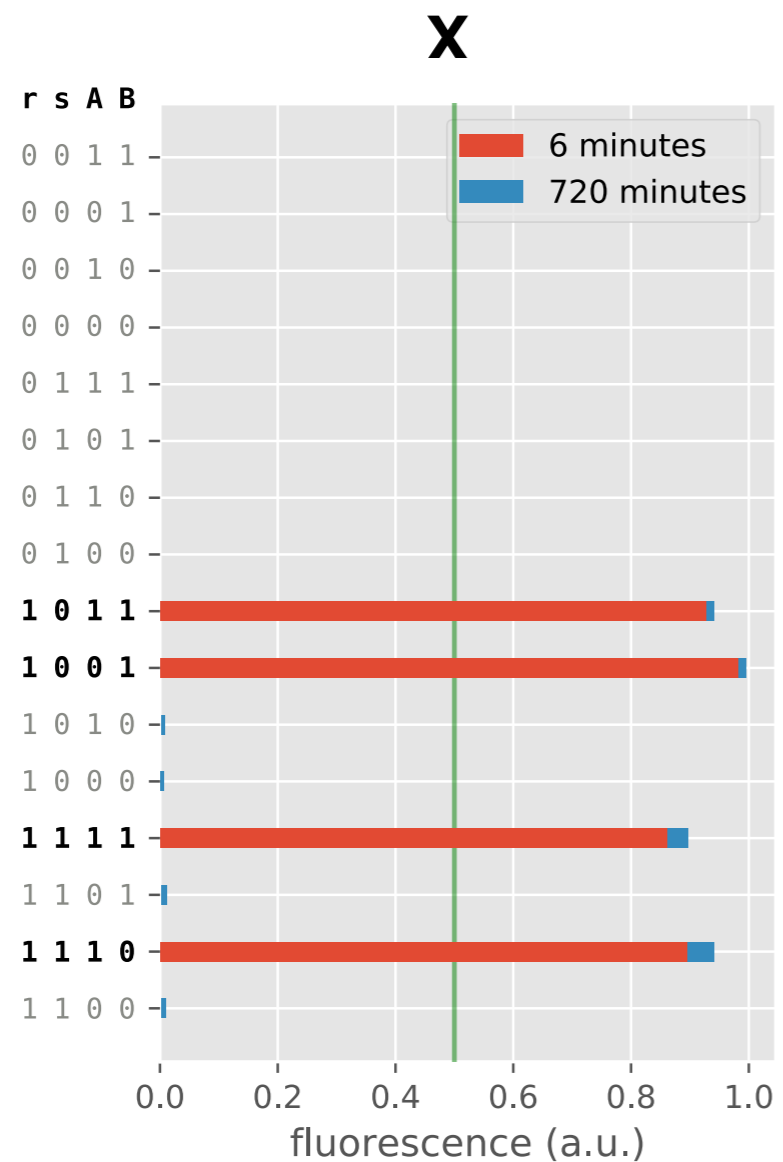
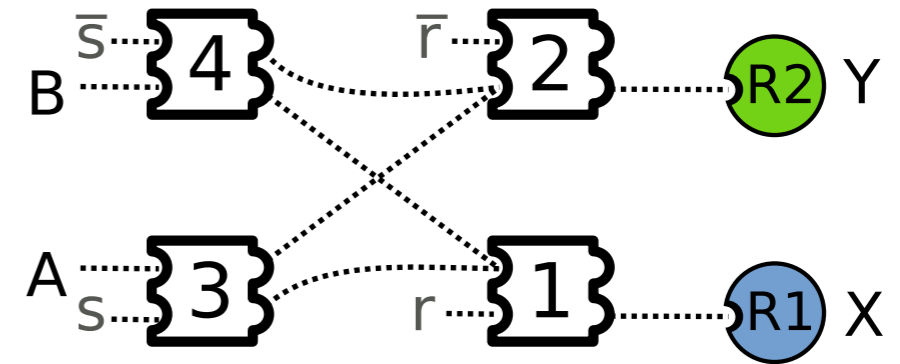
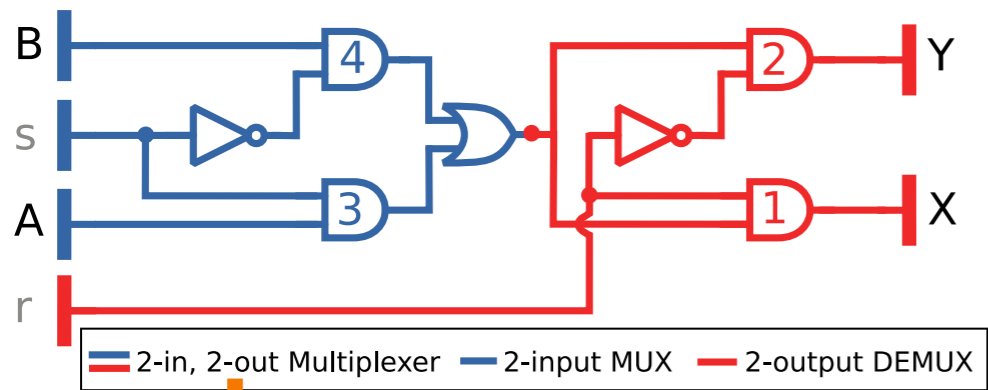
# Multiplexer-Demultiplexer



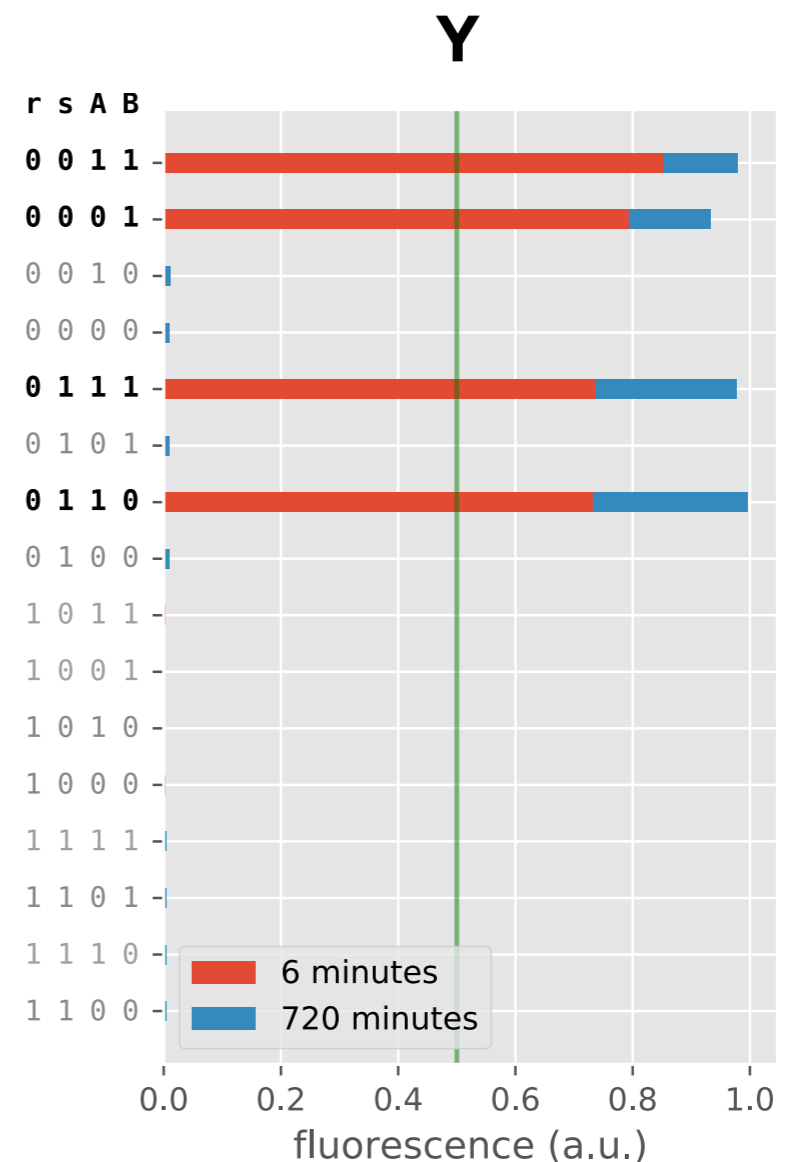
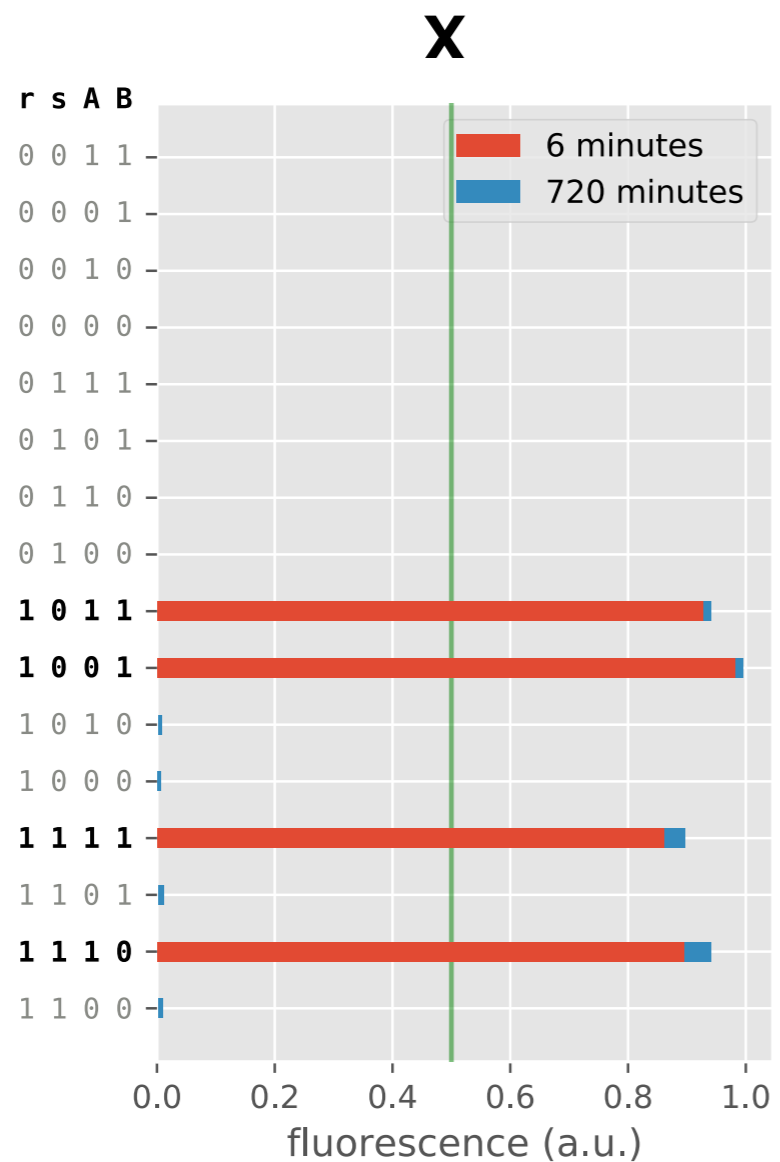
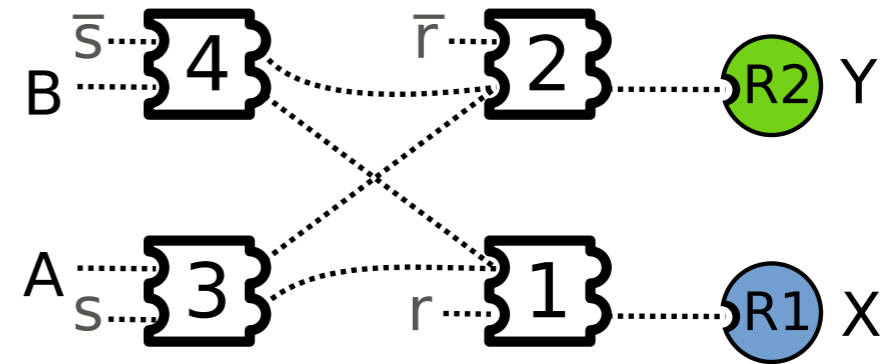
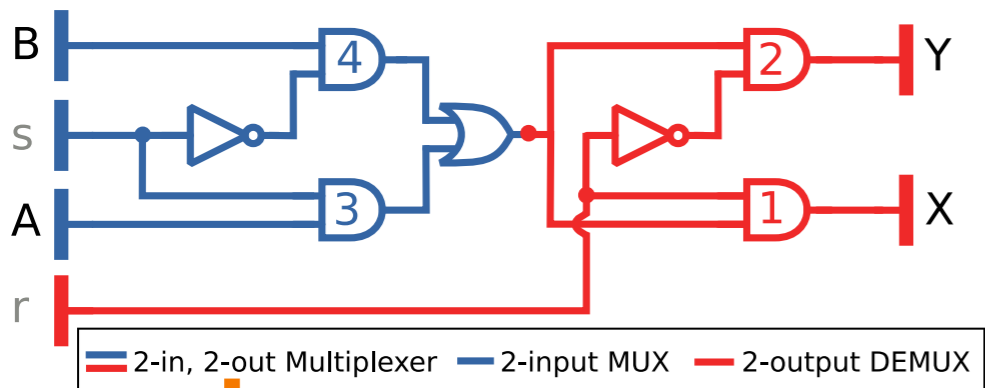
# Multiplexer-Demultiplexer



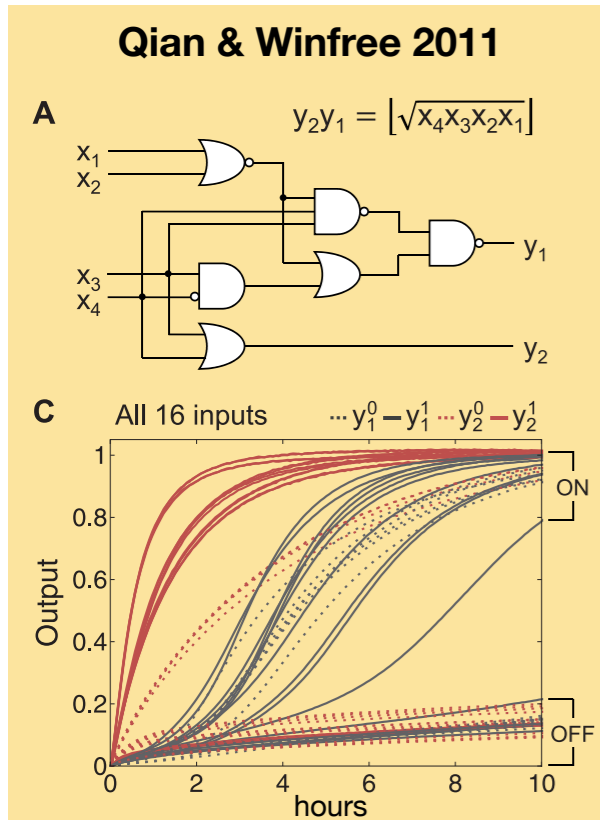
# Multiplexer-Demultiplexer



# Multiplexer-Demultiplexer

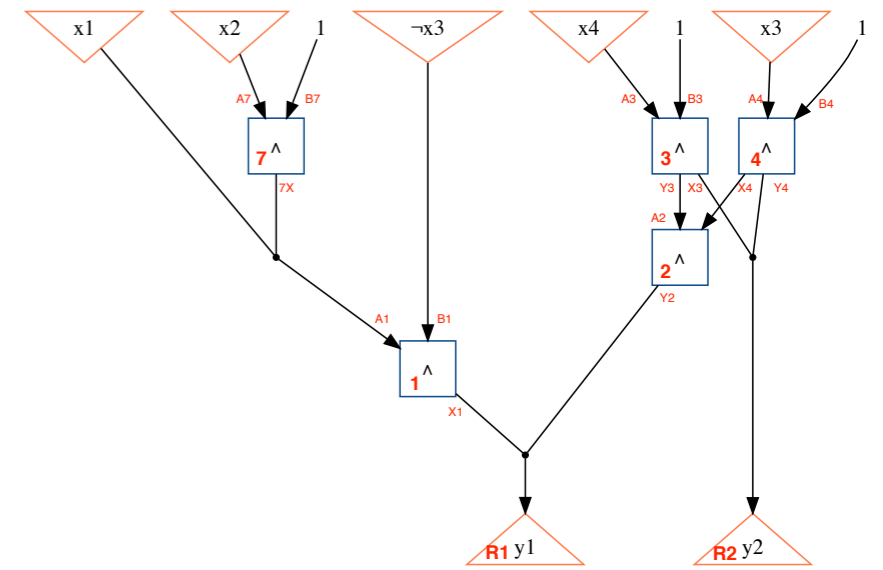
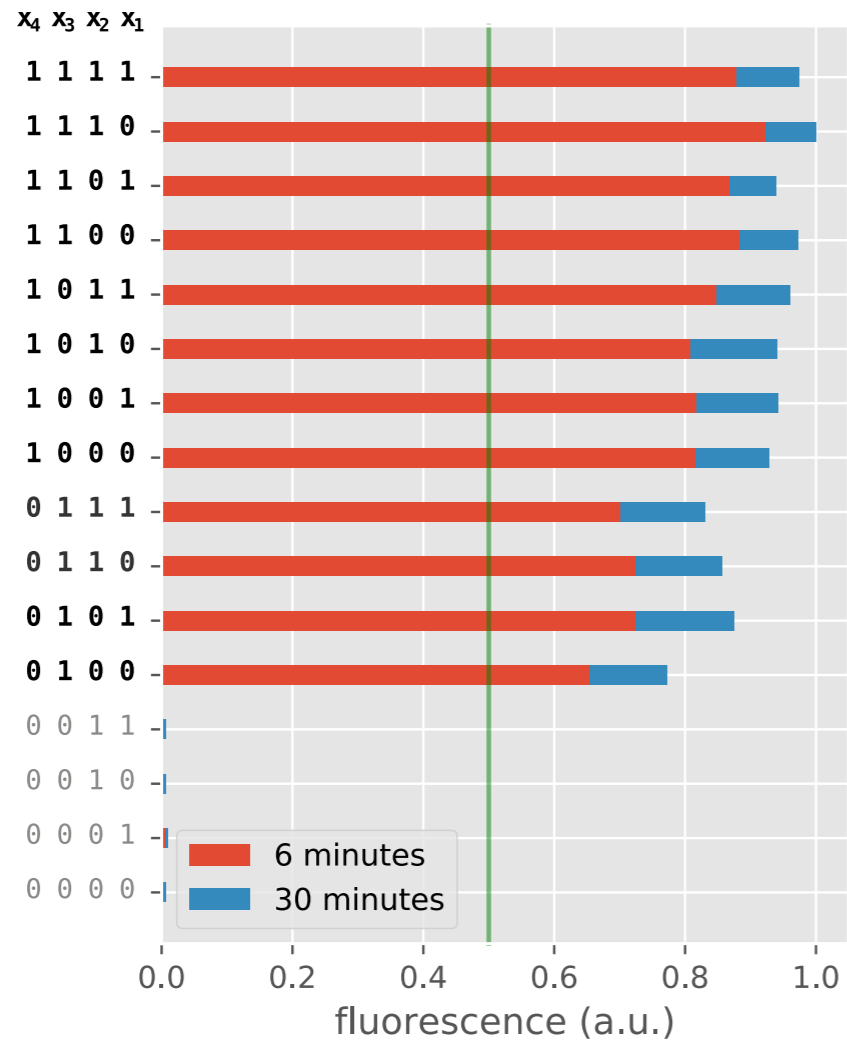


# Large circuits that are fast

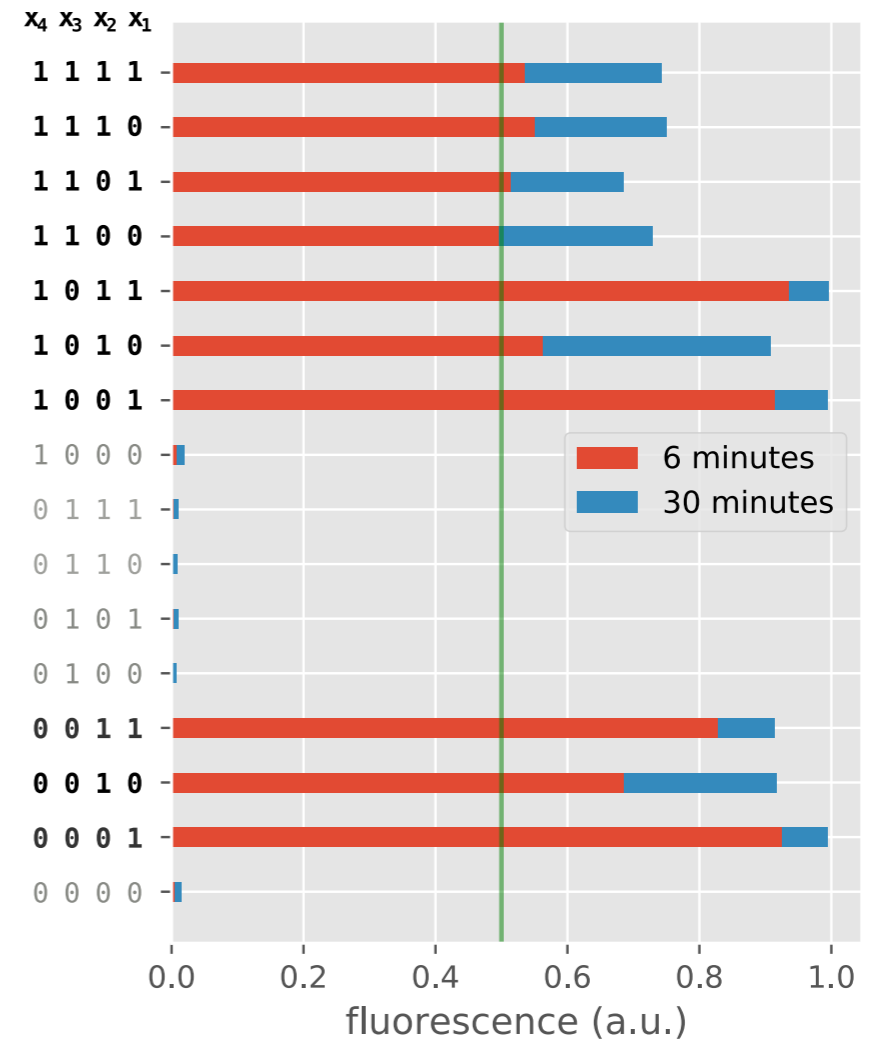


Reaction half-time improved from ~6 hours to < 6 minutes

**Y2**



**Y1**



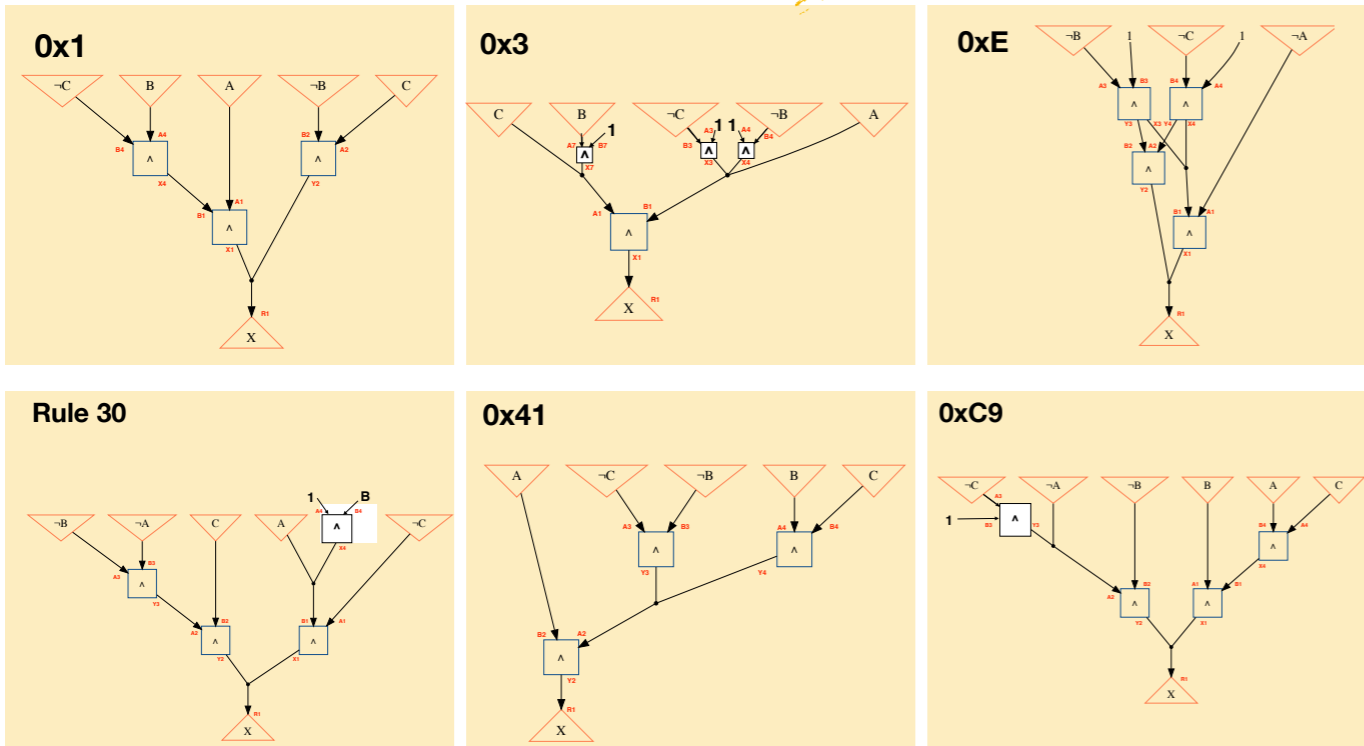


Breadboard plate

Acoustic Liquid Handler

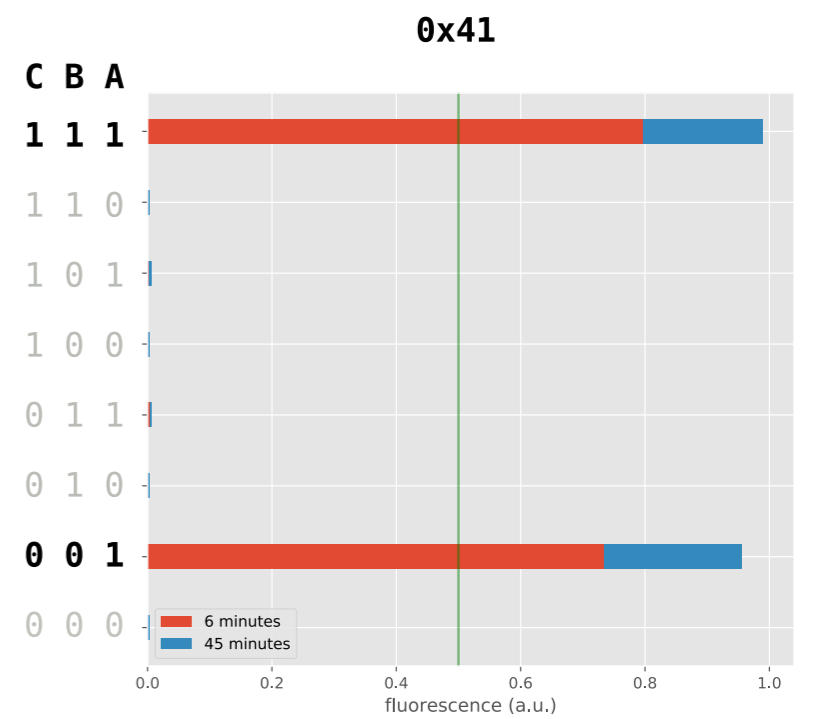
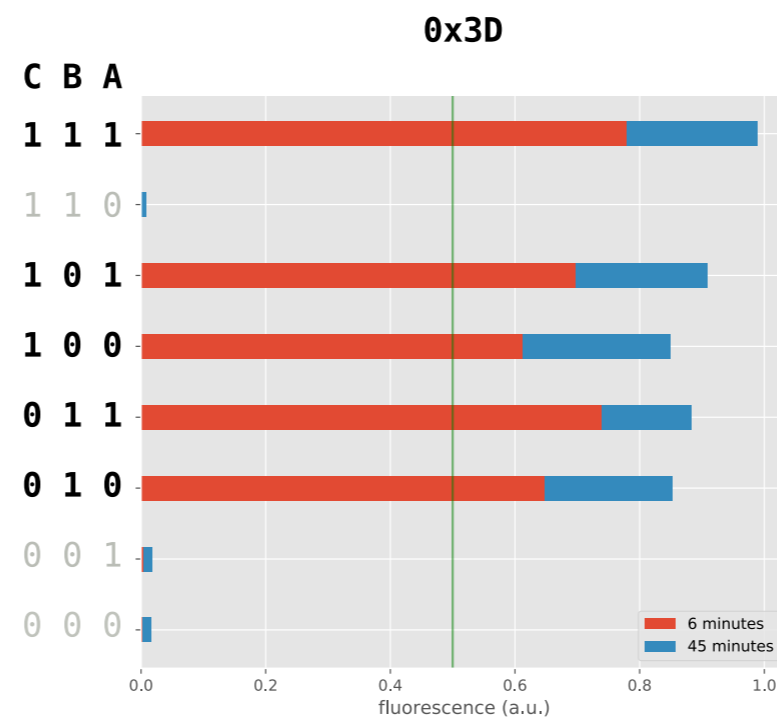
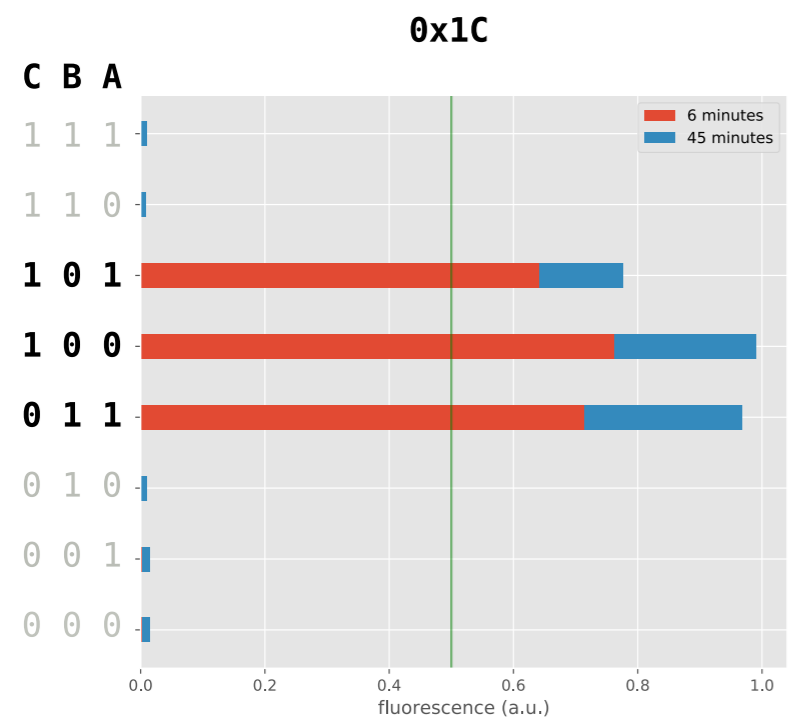
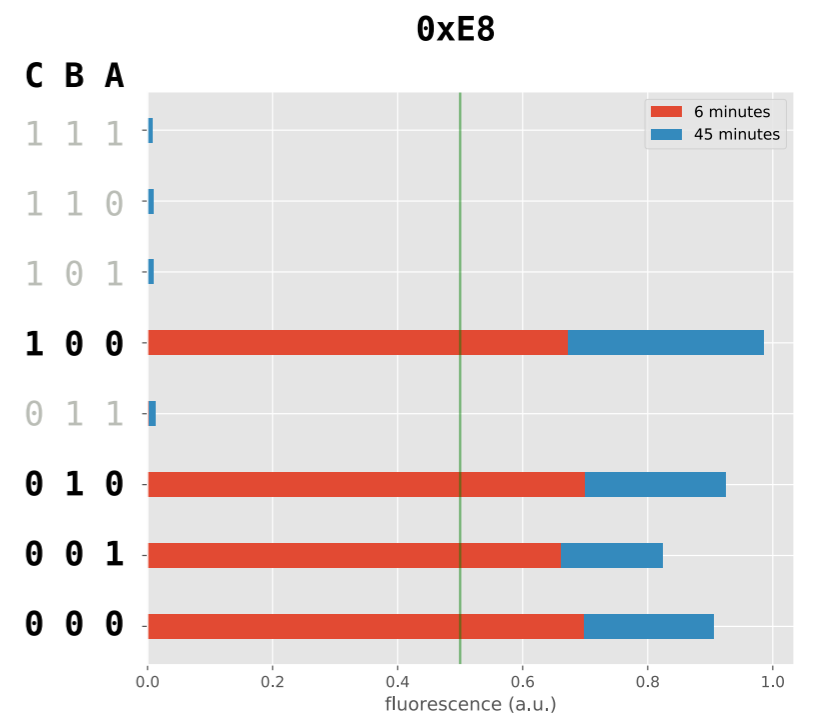
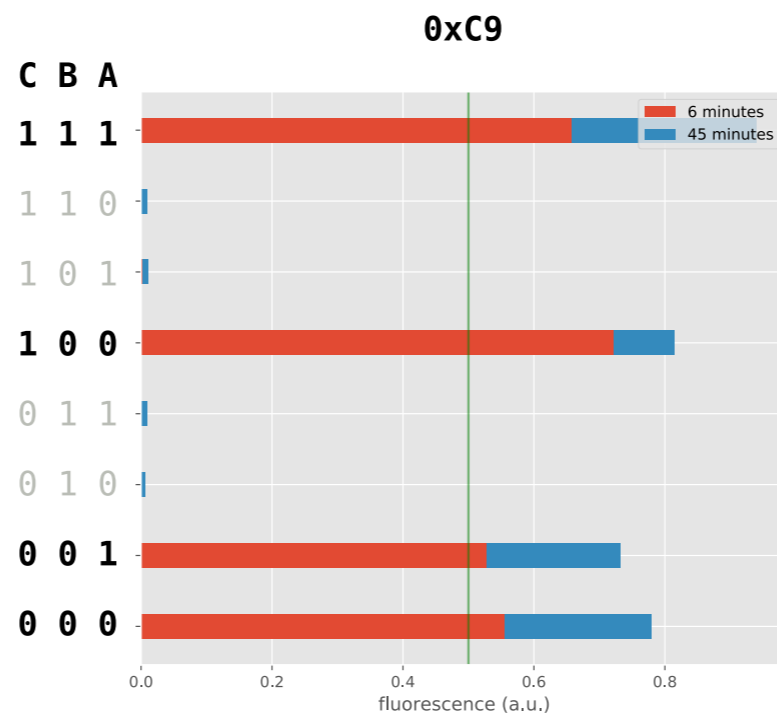
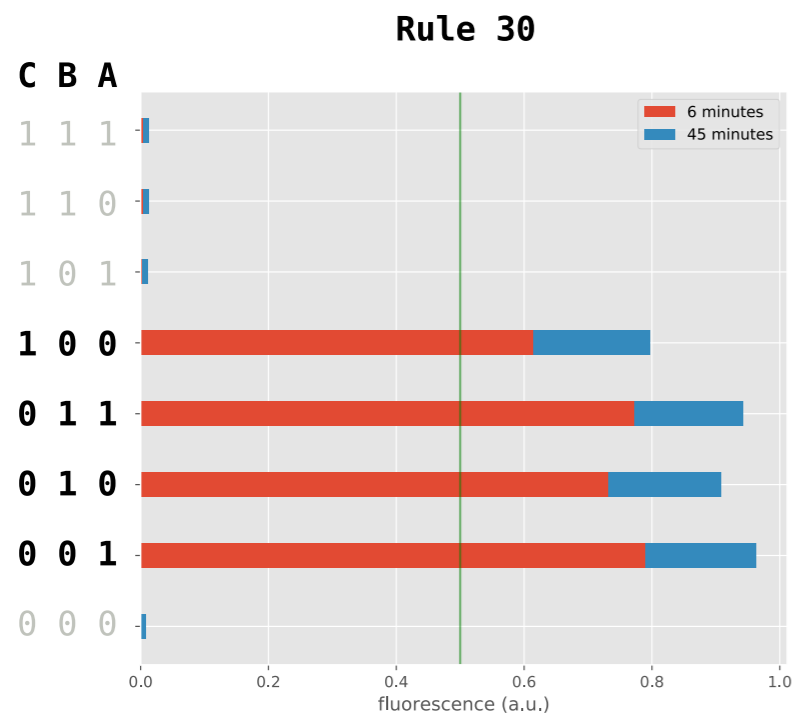
Breadboard compiler produces a mixing protocol

All 8 input combinations for 6 circuits



Destination plate

# First measurement 6 minutes after mixing start time



# Molecular Circuit Breadboard

## Roadmap

# Molecular Breadboard 2.0:

More components

input signals

A1 B1  
A2 B2  
A3 B3  
A4 B4  
A5 B5  
⋮  
⋮  
A25 B25

reaction gates

1 2  
3 4  
5 6  
⋮  
⋮  
24 25

wires

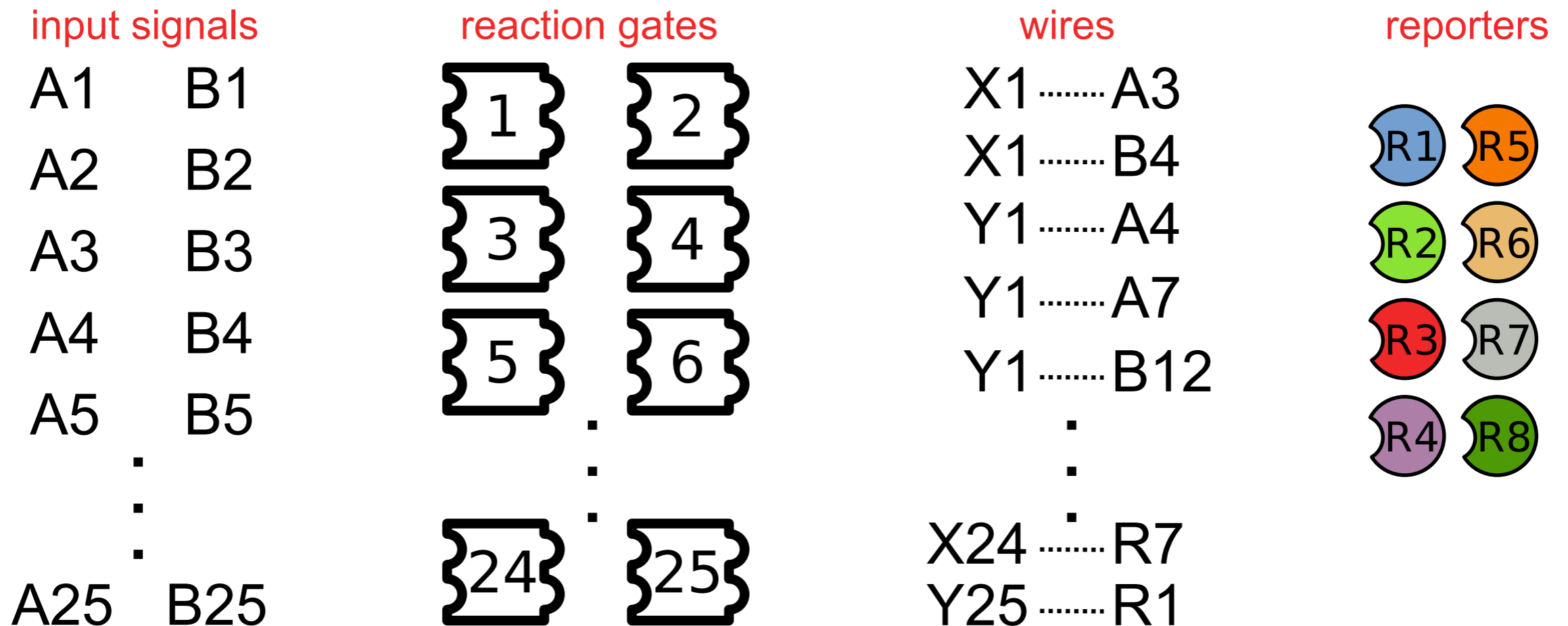
X1 ..... A3  
X1 ..... B4  
Y1 ..... A4  
Y1 ..... A7  
Y1 ..... B12  
⋮  
⋮  
X24 ..... R7  
Y25 ..... R1

reporters

R1 R5  
R2 R6  
R3 R7  
R4 R8

# Molecular Breadboard 2.0:

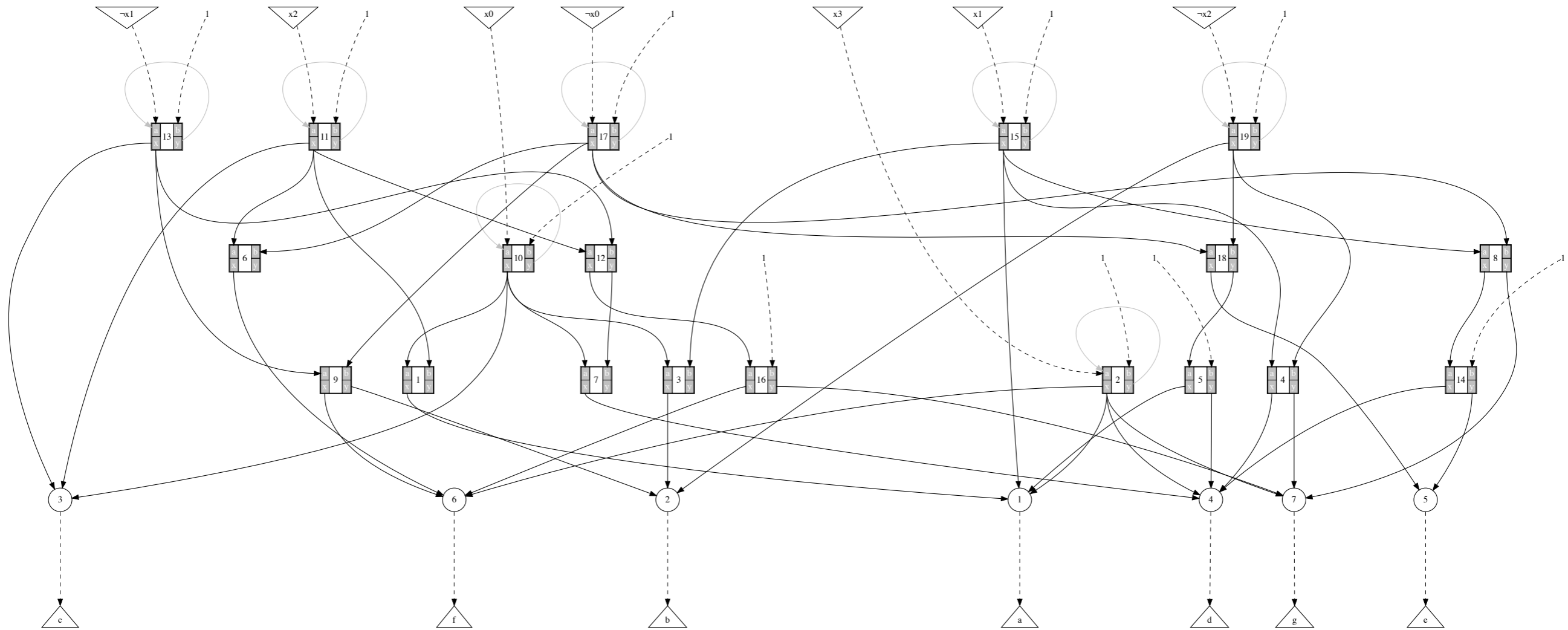
More circuits



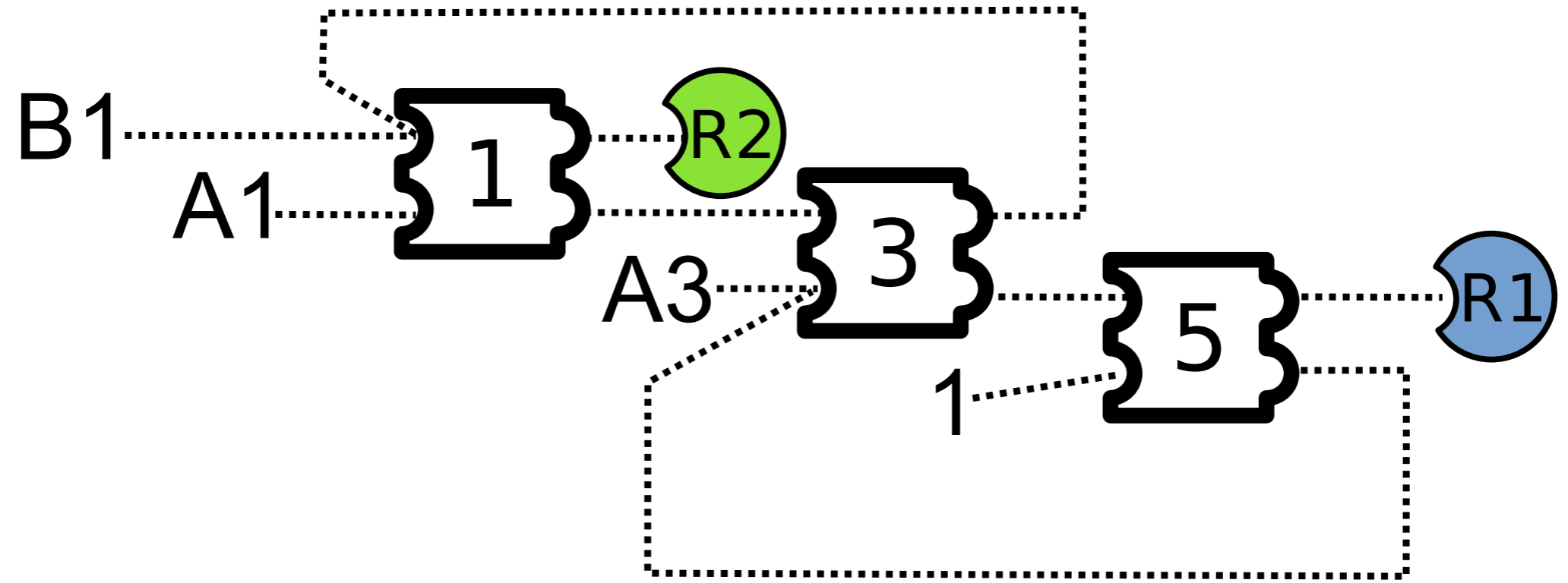
Breadboard 2.0 can  
realize > 130 K circuits

# Molecular Breadboard 2.0:

Larger circuits



# Building circuits with feedback loops

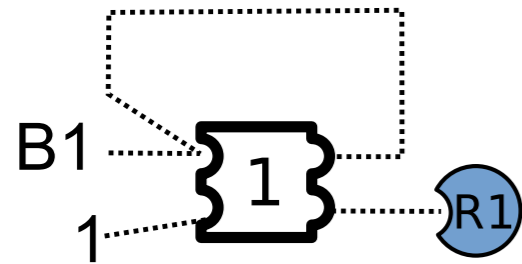


## Chemical Reaction Networks

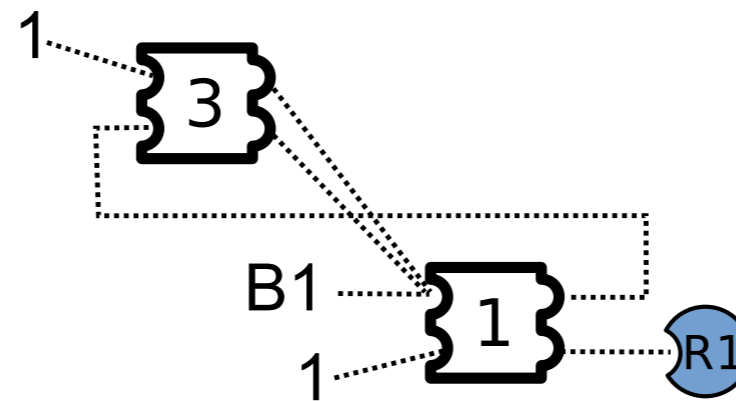
**Asynchronous Sequential Logic Circuits**



# Providing input amplifiers & output signal restoration



**Linear input amplifier**



**Exponential input amplifier**



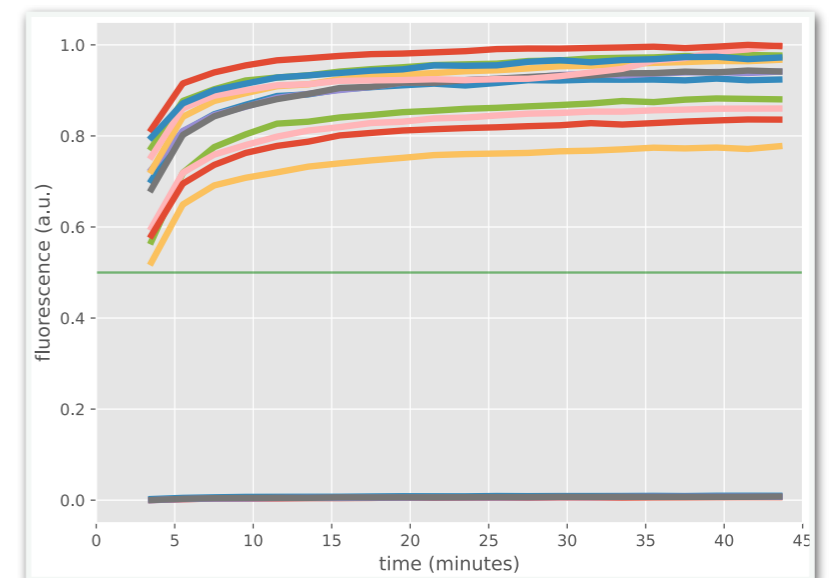
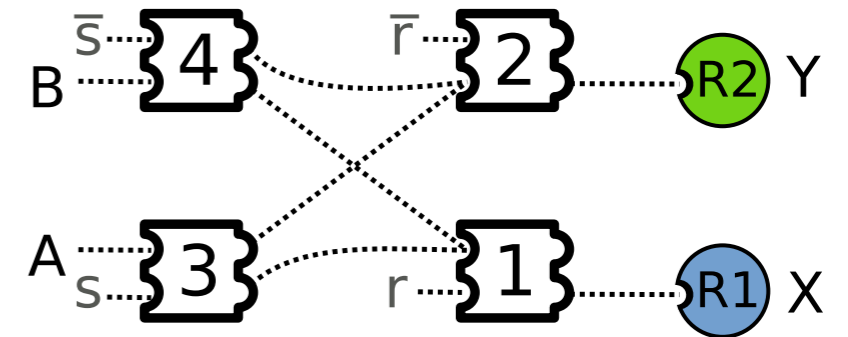
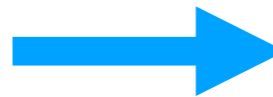
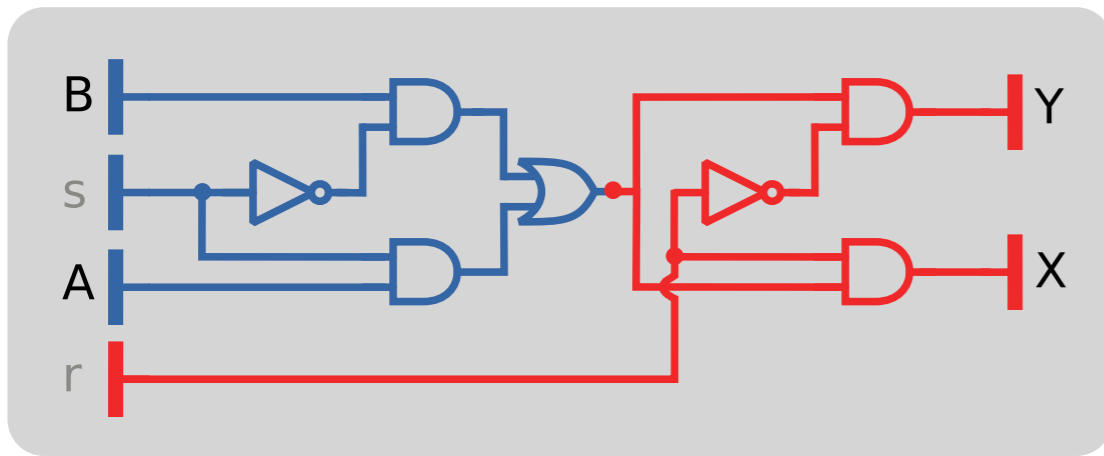
**Output signal restoration**



Increased speed

Robustness to error

Automation



# Related talks & posters @ DNA 24

Dominic Scalise, Nisita Dutta and [Rebecca Schulman](#)  
DNA strand-displacement buffers

Si-Ping Han, Lisa Scherer, Matt Gethers, Marwa Ben Hadj Salah, Rebecca Mancusi, Sahil Sagar, Robin Hu, Julia Derogatis, Ya-Huei Kuo, Guido Marcucci, John Rossi and William A. Goddard III  
Development and optimization of strand displacement based conditional small interfering RNAs for operation inside mammalian cells

[Eyal Nir](#), Yaron Berger and Miran Liber  
Computer Controlled DNA Bipedal Walker that Perform Several Steps a Minute

Abhinav Singh and [Manoj Gopalkrishnan](#)  
EM Algorithm with DNA Molecules

Wooli Bae, [Thomas Ouldridge](#) and [Guy-Bart Stan](#)  
Autonomous generation of multi-stranded RNA complexes for synthetic molecular circuits

Yan Shan Ang and Lin-Yue Lanry Yung  
Design of Split Proximity Circuit as a Plug-and-Play Translator for Discriminating Single Nucleotide Mutation

Yan Shan Ang and Lin-Yue Lanry Yung  
Dynamically Elongated Association Toehold for Tuning Circuit Kinetics and Thermodynamics

Patrick Irmisch and Ralf Seidel  
Modelling DNA-strand displacement reactions in the presence of base-pair mismatches

Boya Wang and [David Soloveichik](#)  
Experimentally characterizing the design space of strand displacement translators with toehold-size clamps

Allison Tai and Anne Condon  
Error-free stable computation with stack-supplemented chemical reaction networks

Kevin Cherry, Gokul Gowri and Lulu Qian  
DNA-based neural networks that learn from their molecular environment

Robert F. Johnson and [Erik Winfree](#)  
Using Bisimulation for Verification of Polymer Reaction Networks

# Acknowledgments

- **Winfrey lab** (Caltech)
- **Soloveichik lab** (University of Texas at Austin)
- **Qian lab** (Caltech)
- **Murray lab** (Caltech)
- Thanks to DNA 24 organizers for the invitation



# Tools discussed in tutorial

## **ABC: logic synthesis and verification**

<https://people.eecs.berkeley.edu/~alanmi/abc>

## **VisualDSD**

<https://lepton.research.microsoft.com/webdna>

## **Nuskell compiler framework**

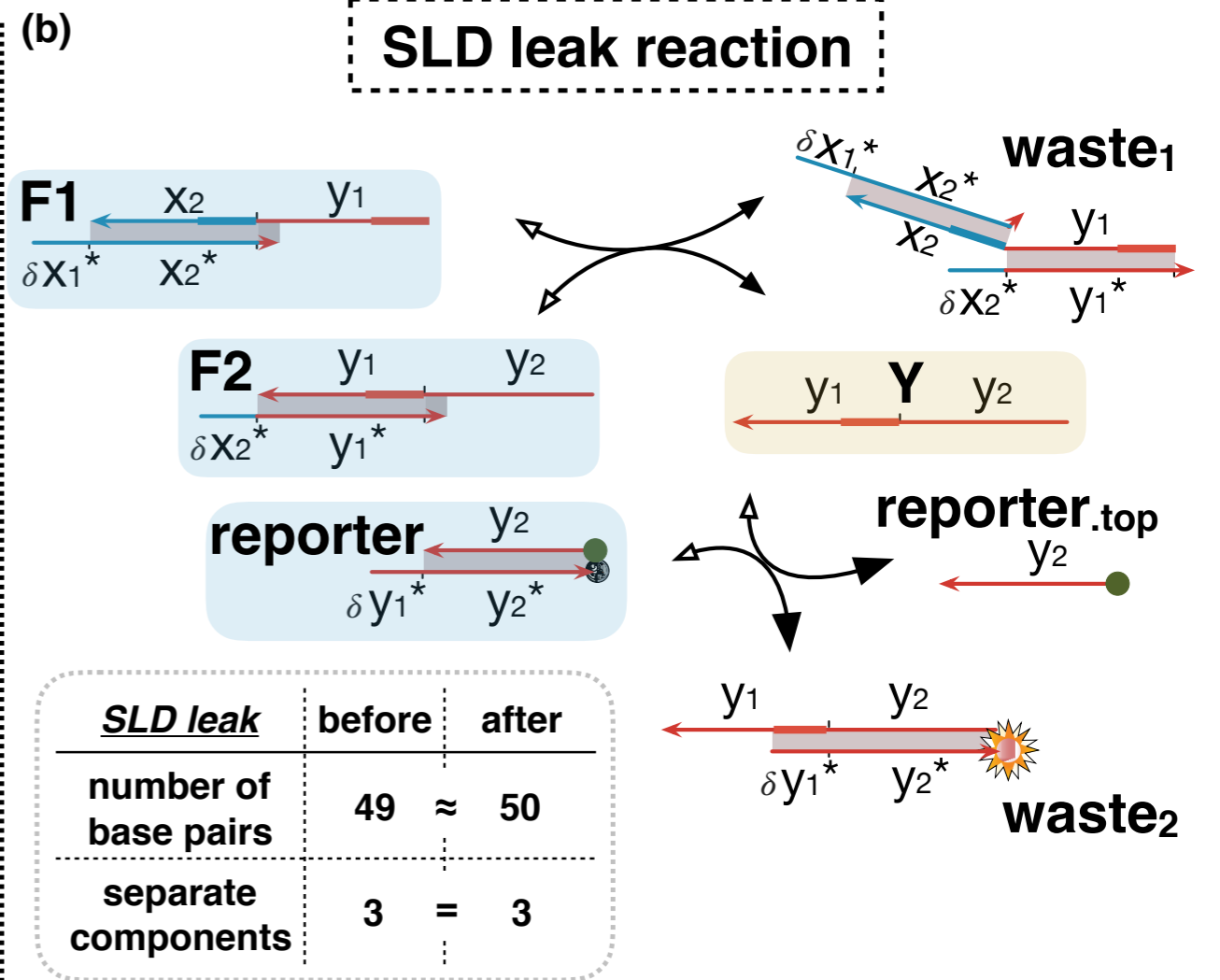
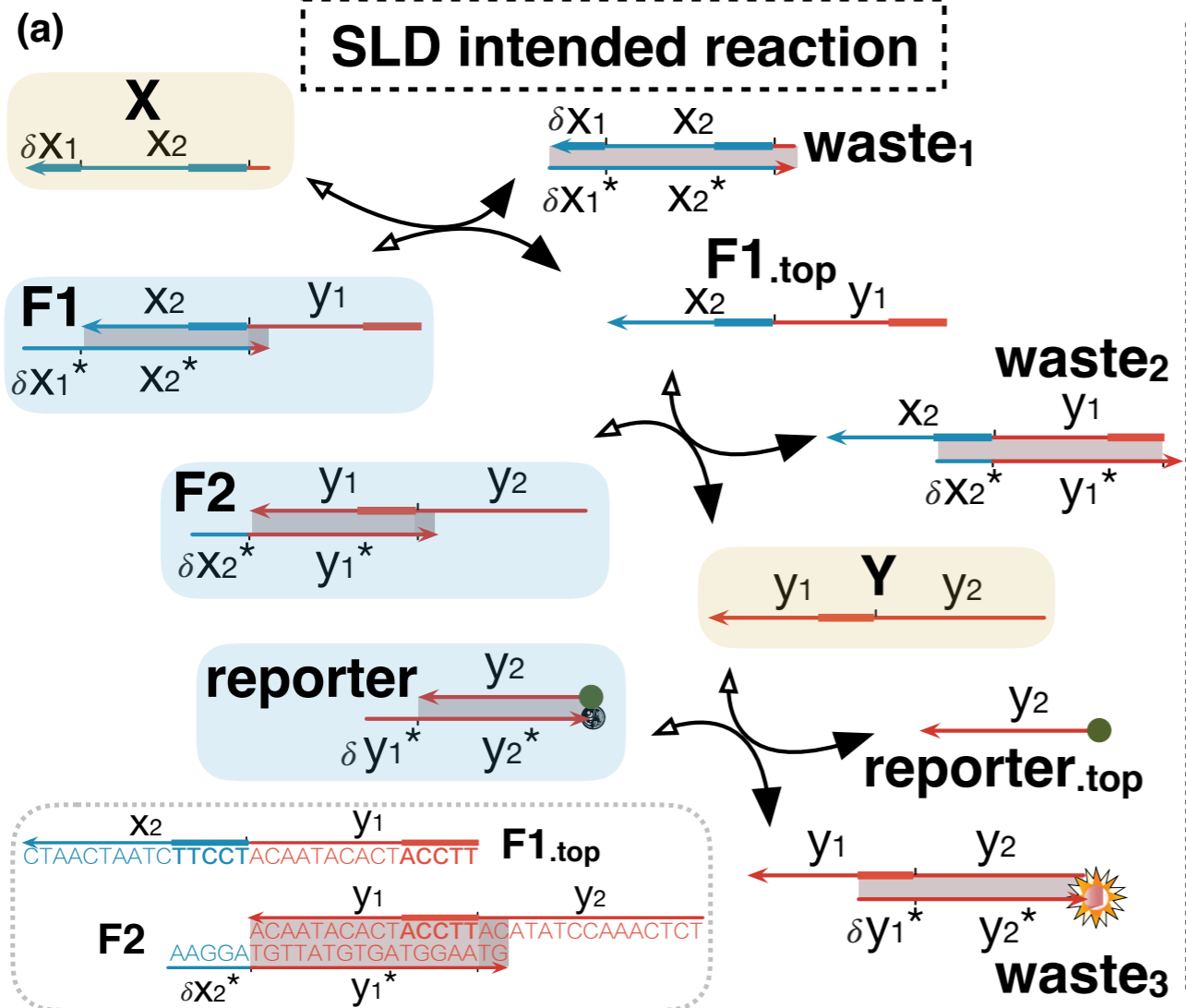
<https://github.com/DNA-and-Natural-Algorithms-Group>

## **DSD breadboard**

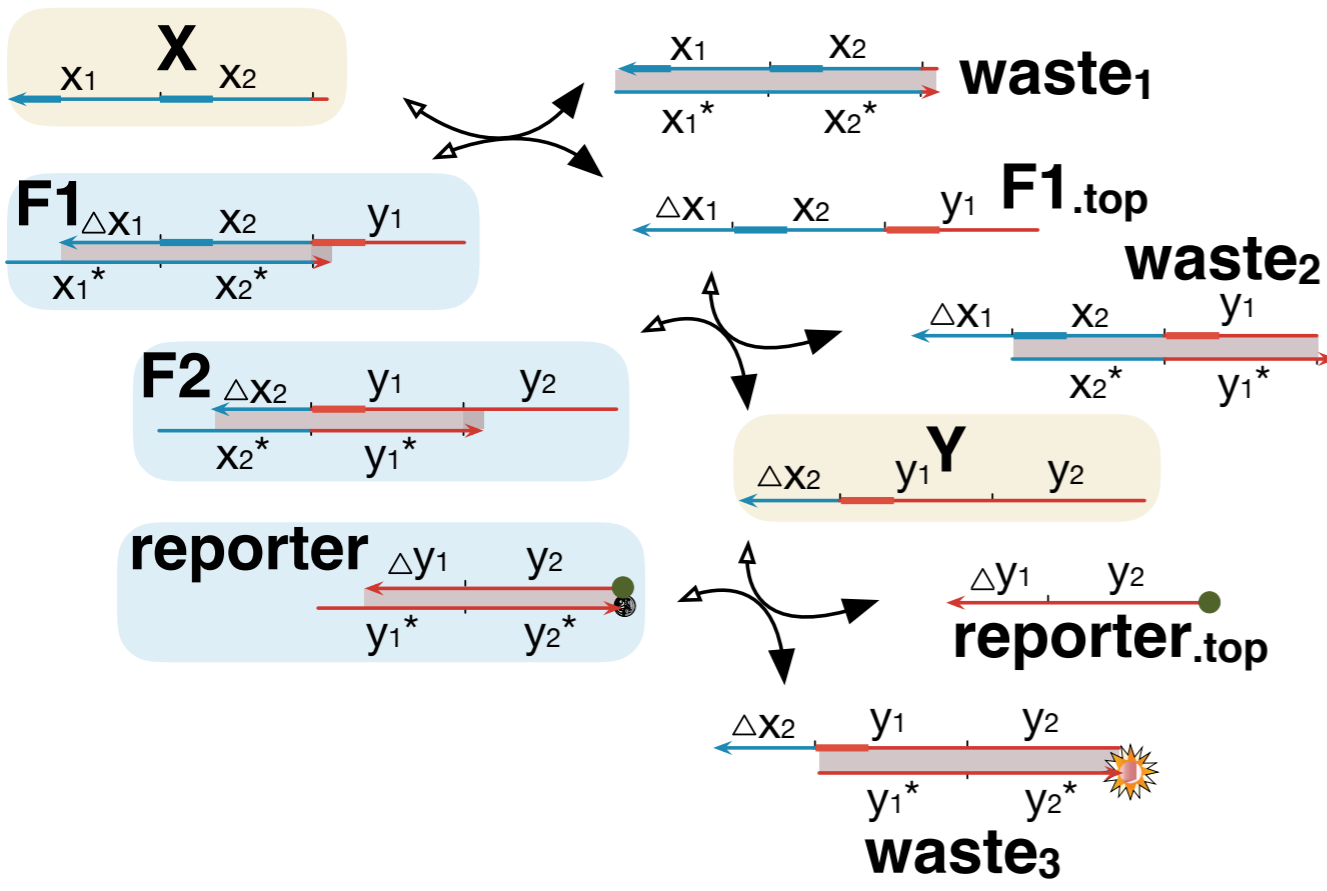
<http://dsdbreadboard.org> *(online later this year)*



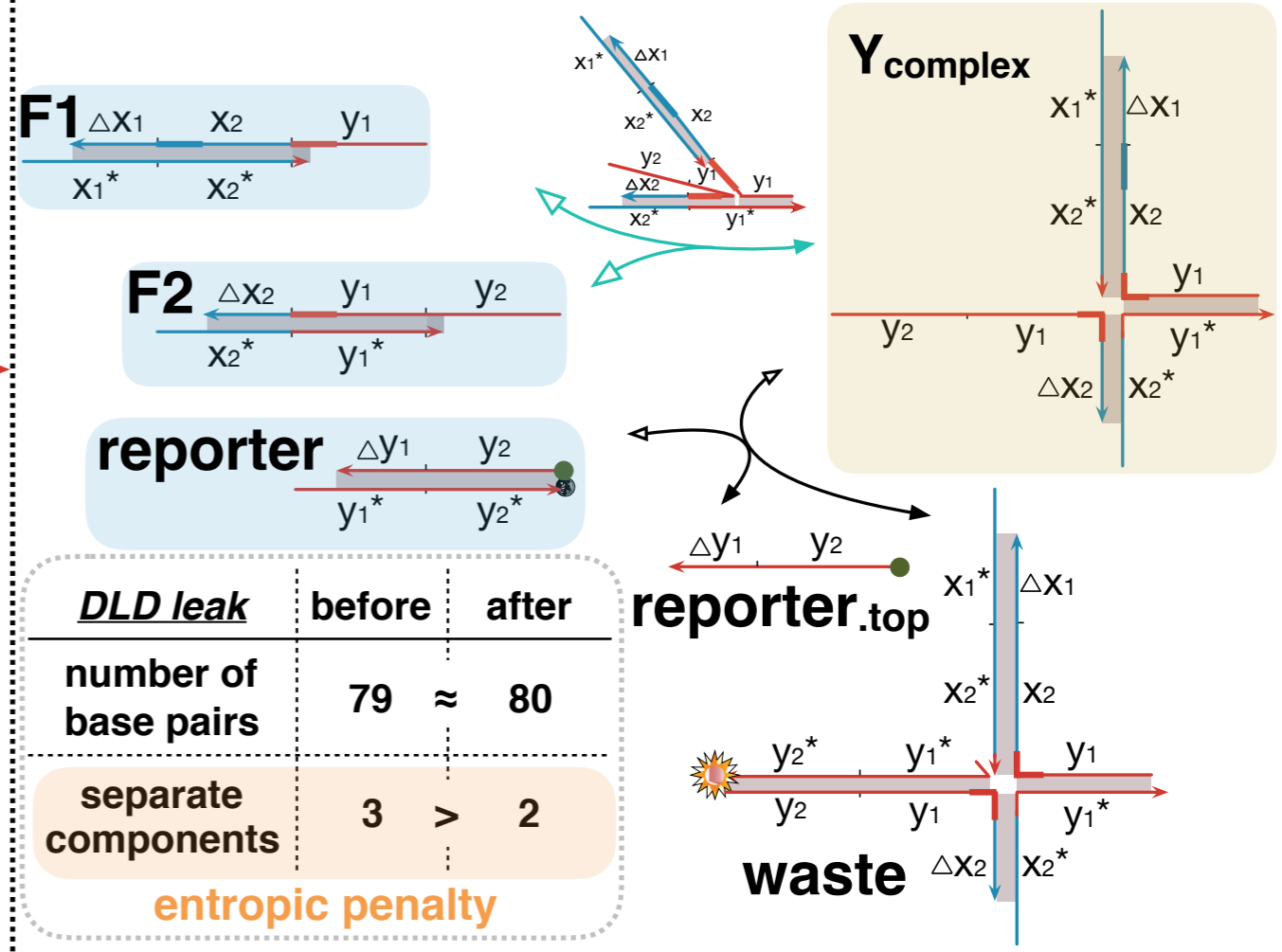




(a) **DLD intended reaction**

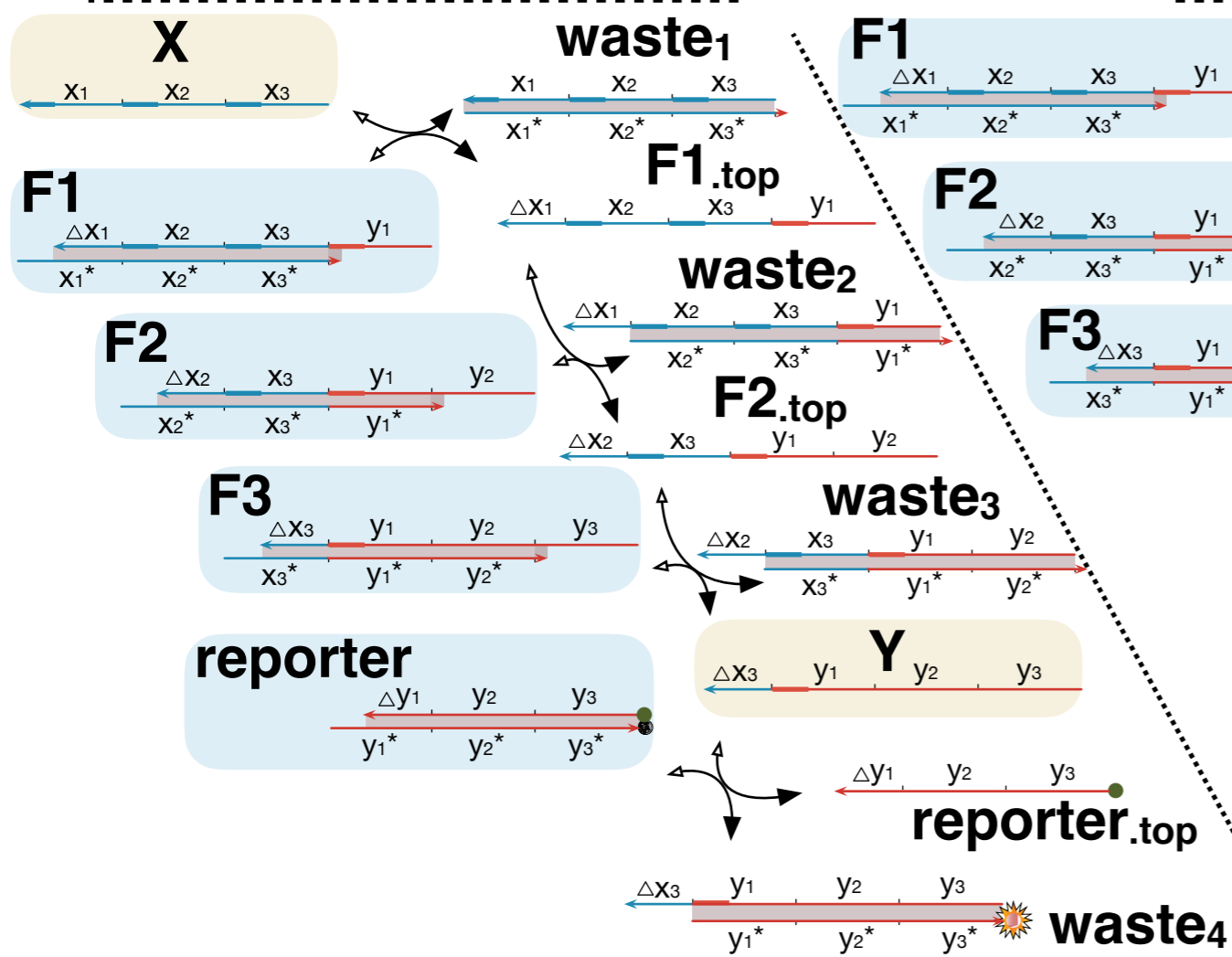


(b) **DLD leak reaction**

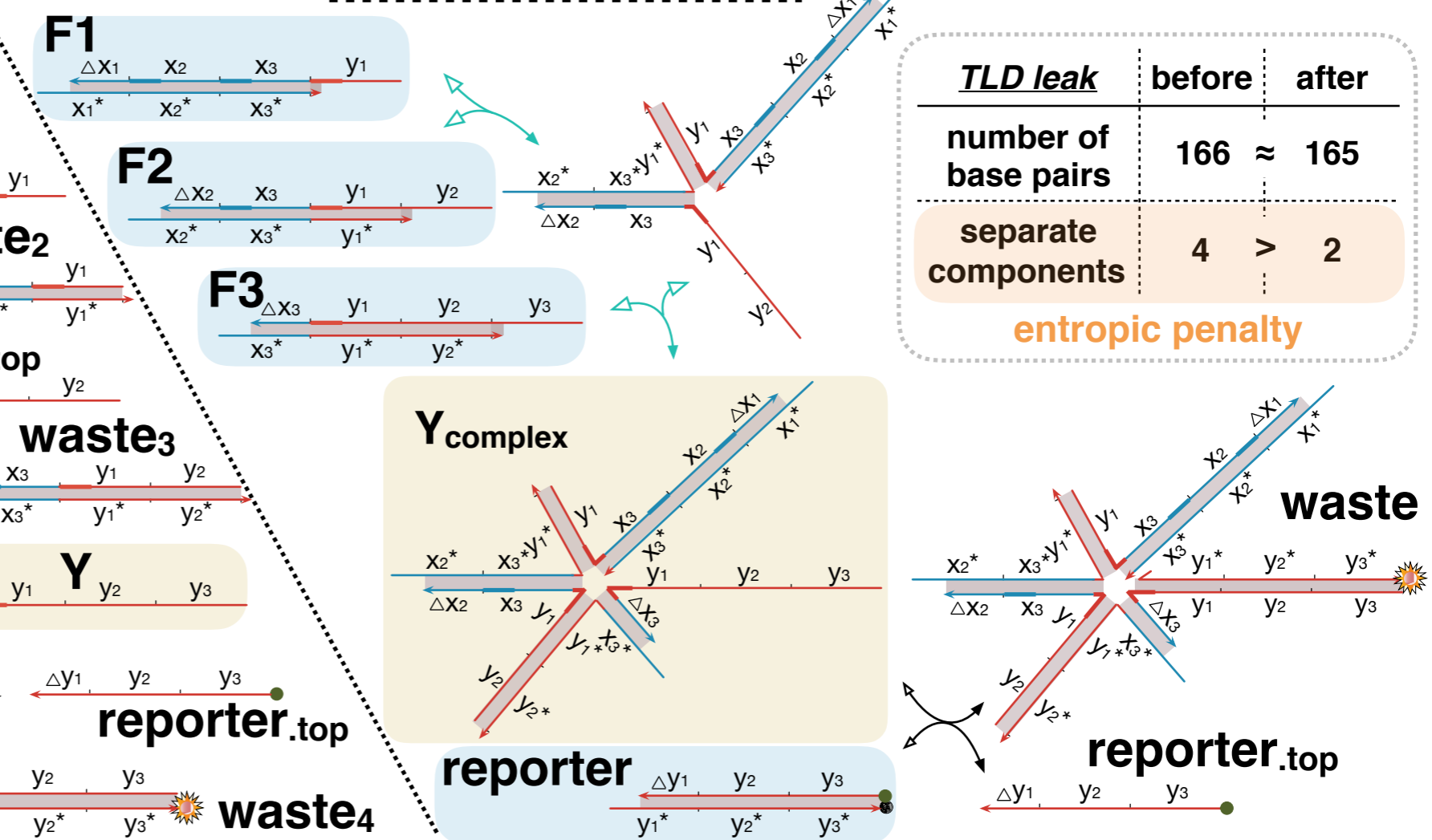




**(a) TLD intended reaction**



**(b) TLD leak reaction**



<i>TLD leak</i>	before	after
number of base pairs	166	≈ 165
separate components	4	> 2

**entropic penalty**