

# Gene Regulatory Models I

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# Previous Lecture

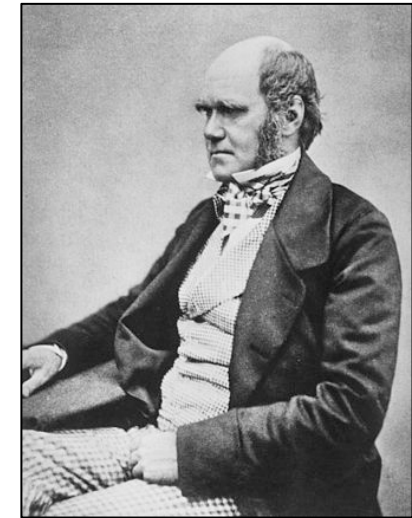
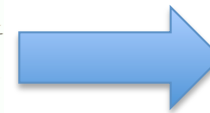
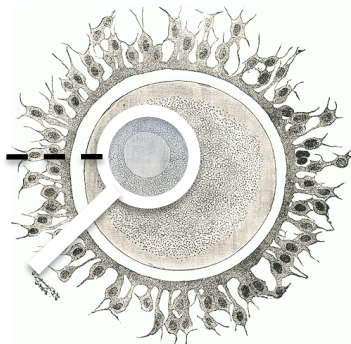
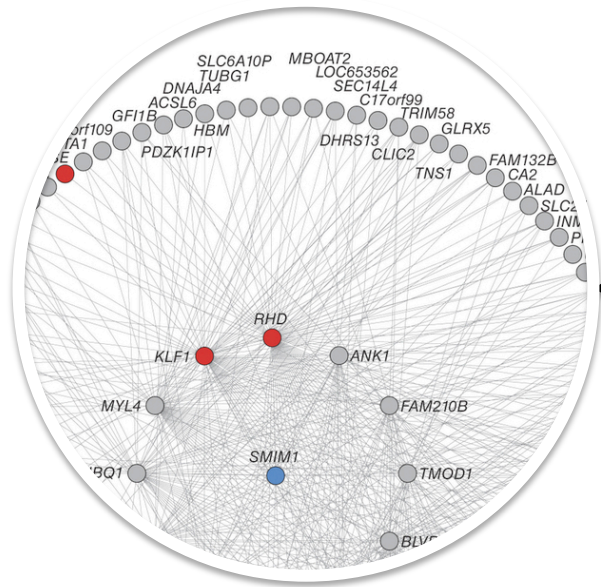
## ◇ Cellular automata

- ▷ Distributed, bottom-up, emergent behaviour
- ▷ Used to model natural systems
- ▷ Complexity from simple systems
- ▷ Can be used to compute



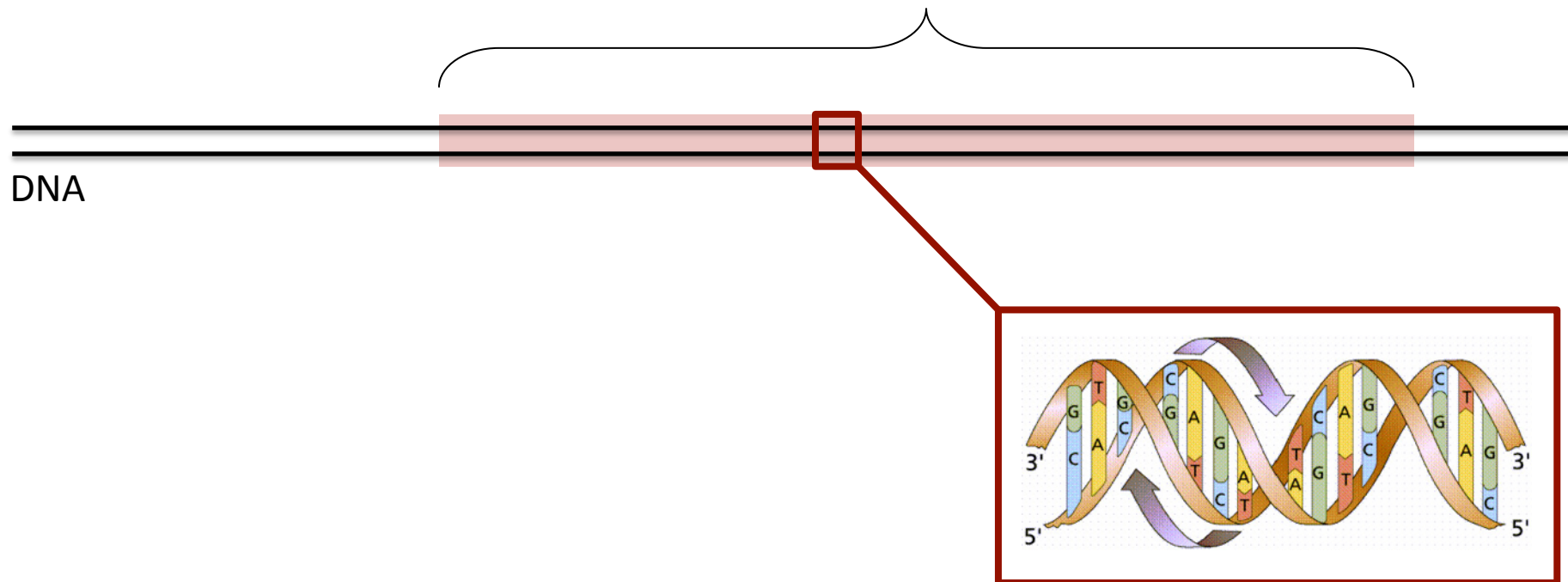
# Today's Lecture

- ◇ How biological cells actually “compute”
  - ▷ Gene regulatory networks (GRNs)
  - ▷ Computational models of GRNs
  - ▷ Artificial development using GRNs



# Gene Regulation in Biology

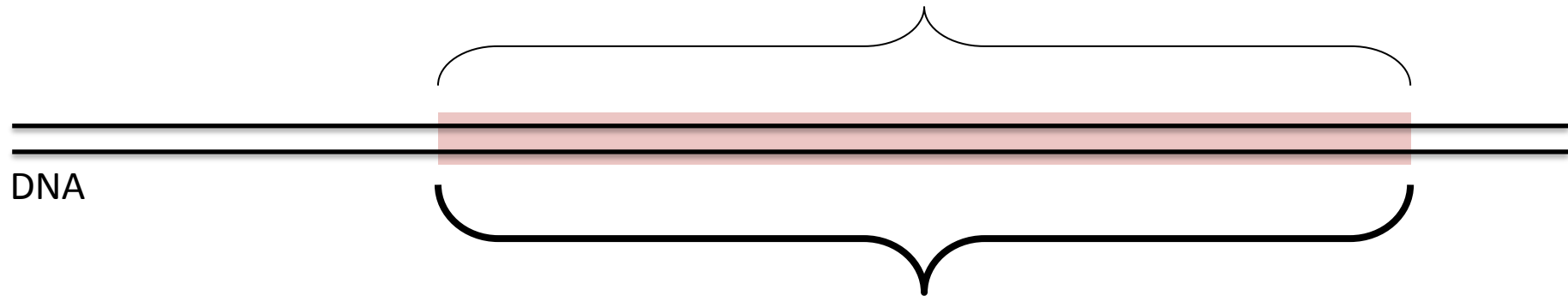
A **gene** is a contiguous region of DNA



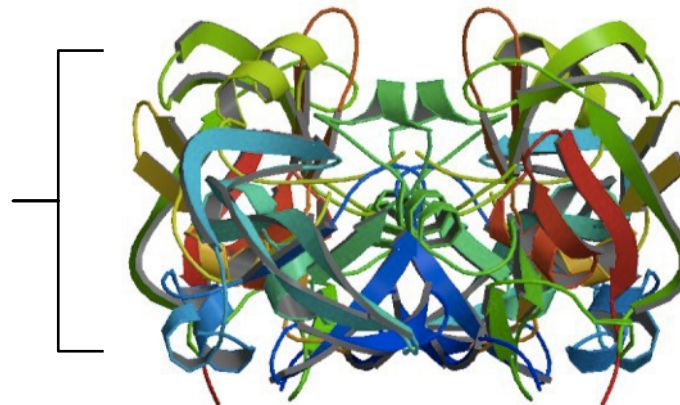


# Gene Regulation in Biology

A **gene** is a contiguous region of DNA

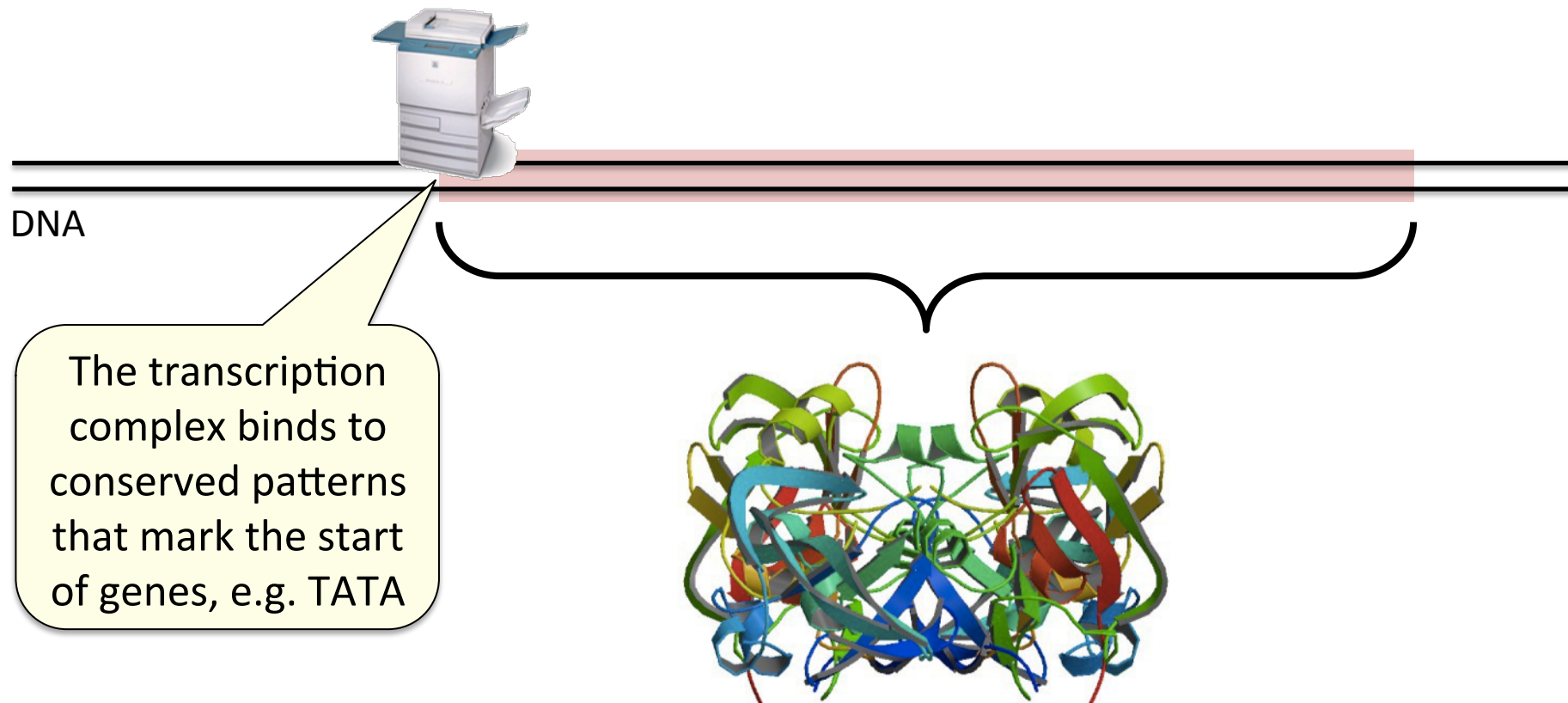


Each gene describes  
how to make a  
**protein**, which is a  
molecular machine



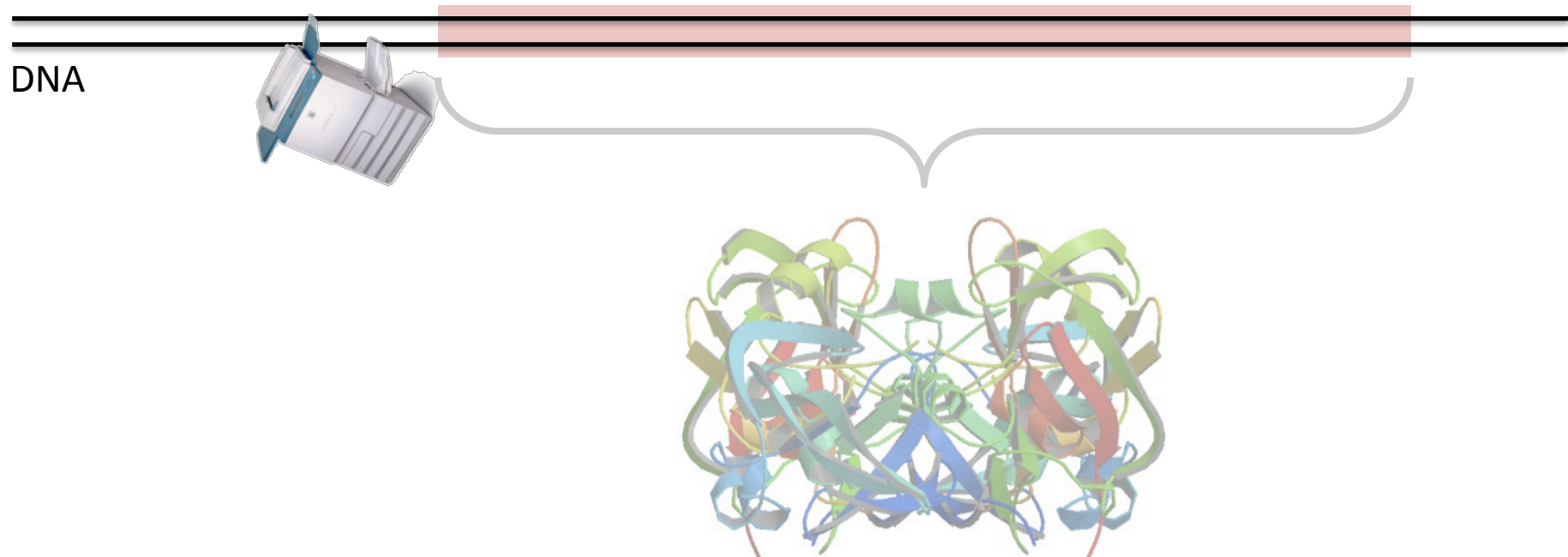
# Gene Regulation in Biology

Genes are expressed when a  
**transcription complex** forms  
– this is a bit like a photocopier



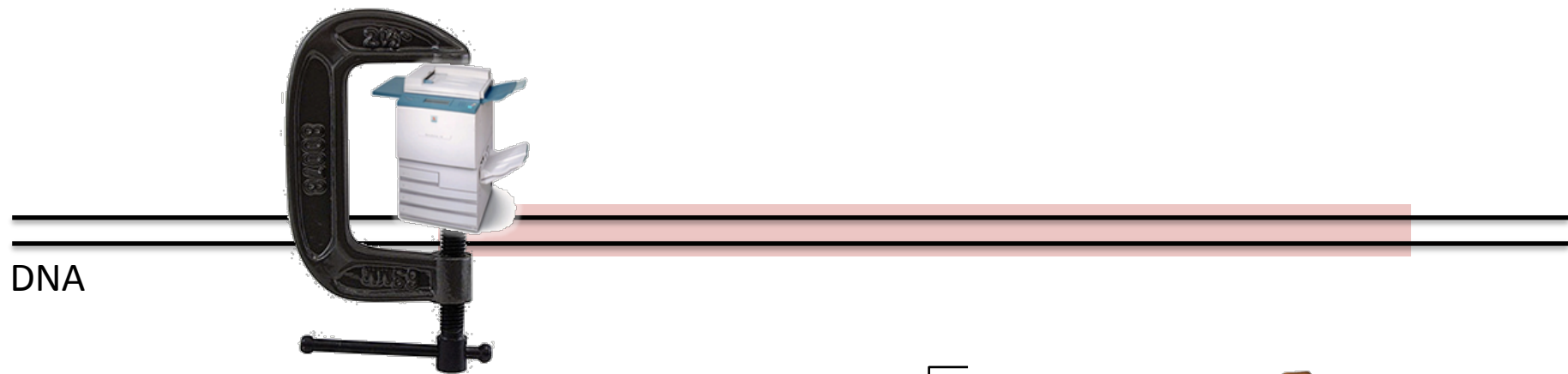
# Gene Regulation in Biology

However, the transcription complex is unstable, and rarely copies genes by itself

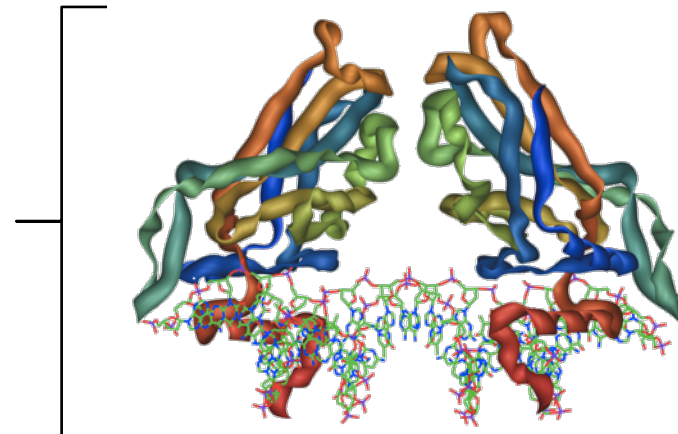


# Gene Regulation in Biology

Instead, it must be helped out by proteins called **transcription factors (TFs)**

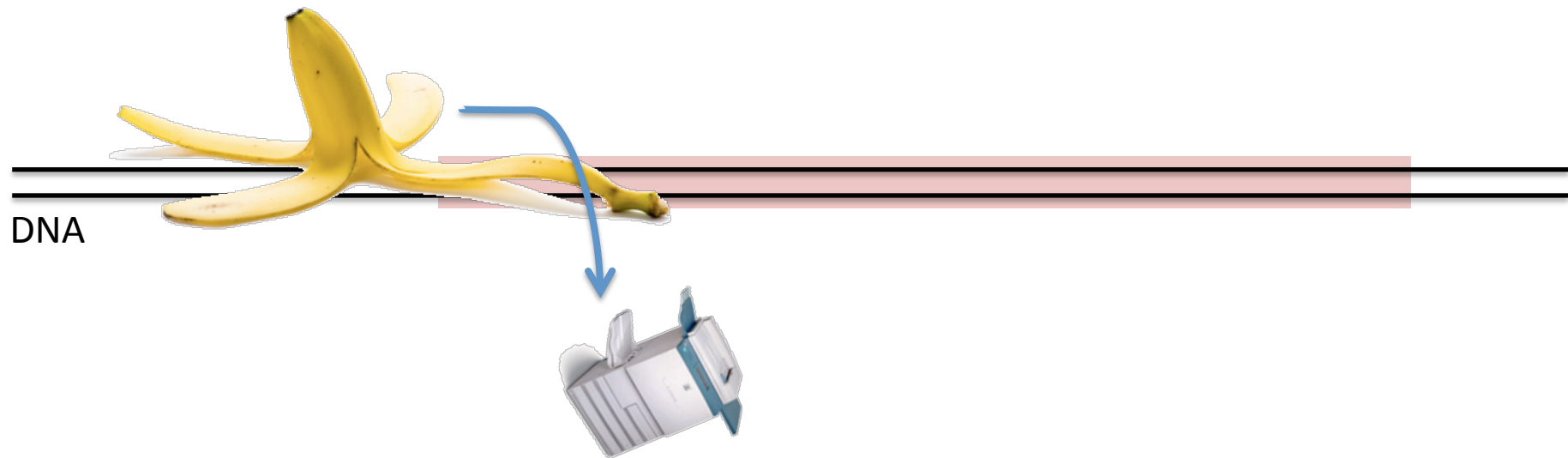


These bind to both the DNA and the transcription complex, holding everything in place – a bit like a clamp



# Gene Regulation in Biology

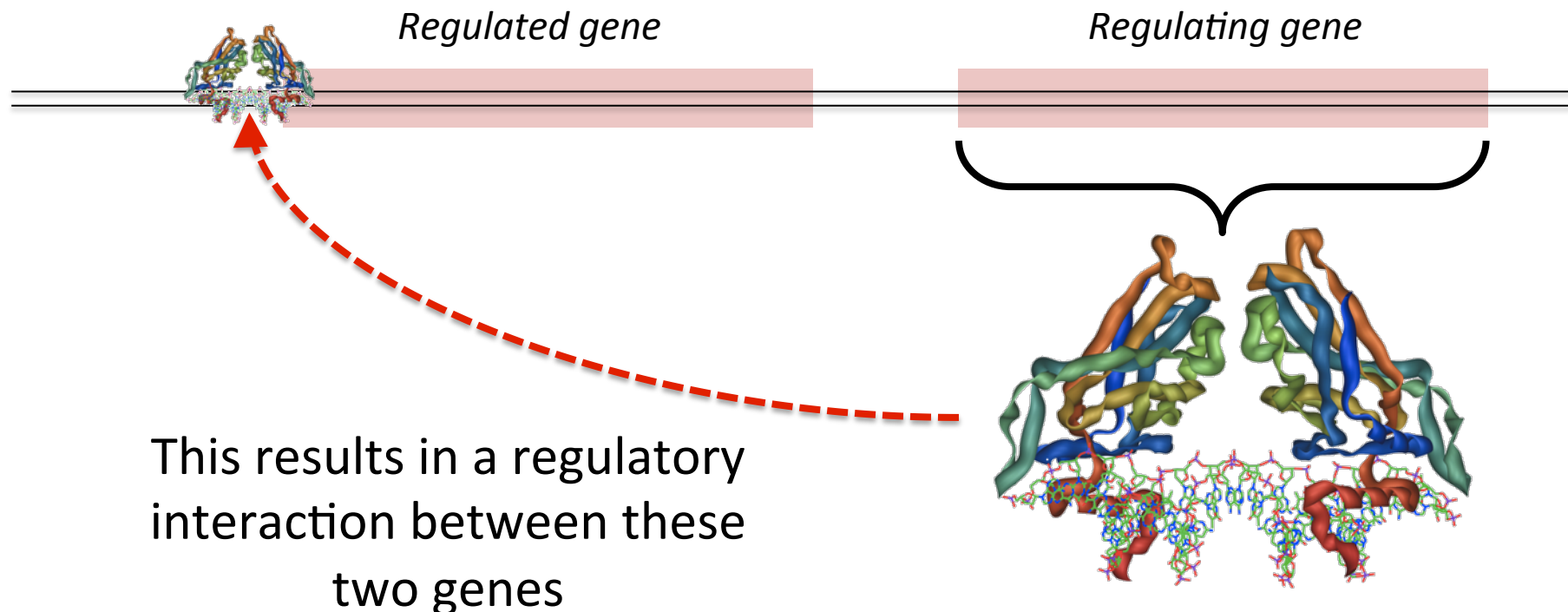
Some TFs are inhibitory and act to destabilise the transcription complex

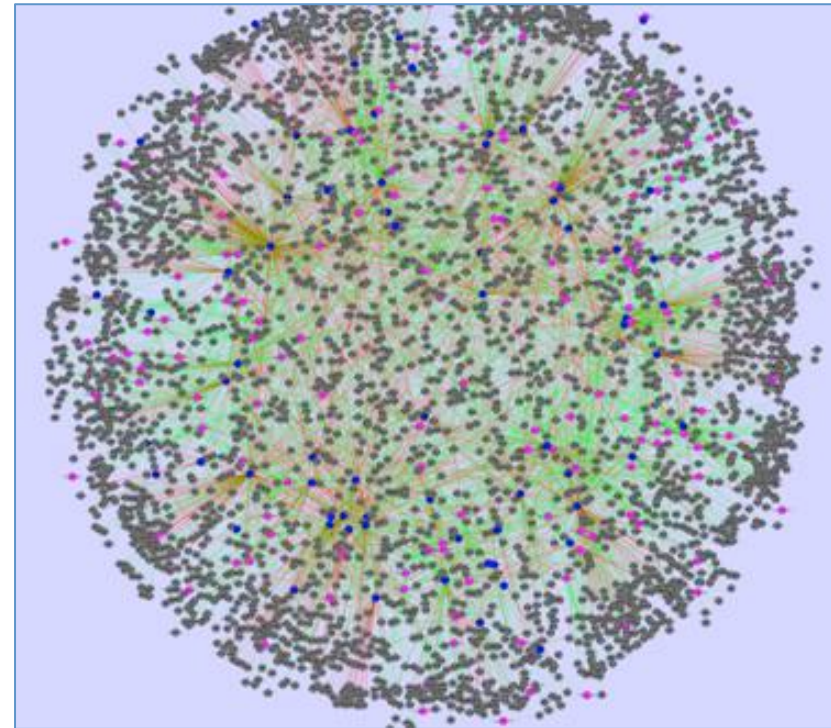




# Gene Regulation in Biology

Since transcription factors are proteins, they must be produced by other genes ...

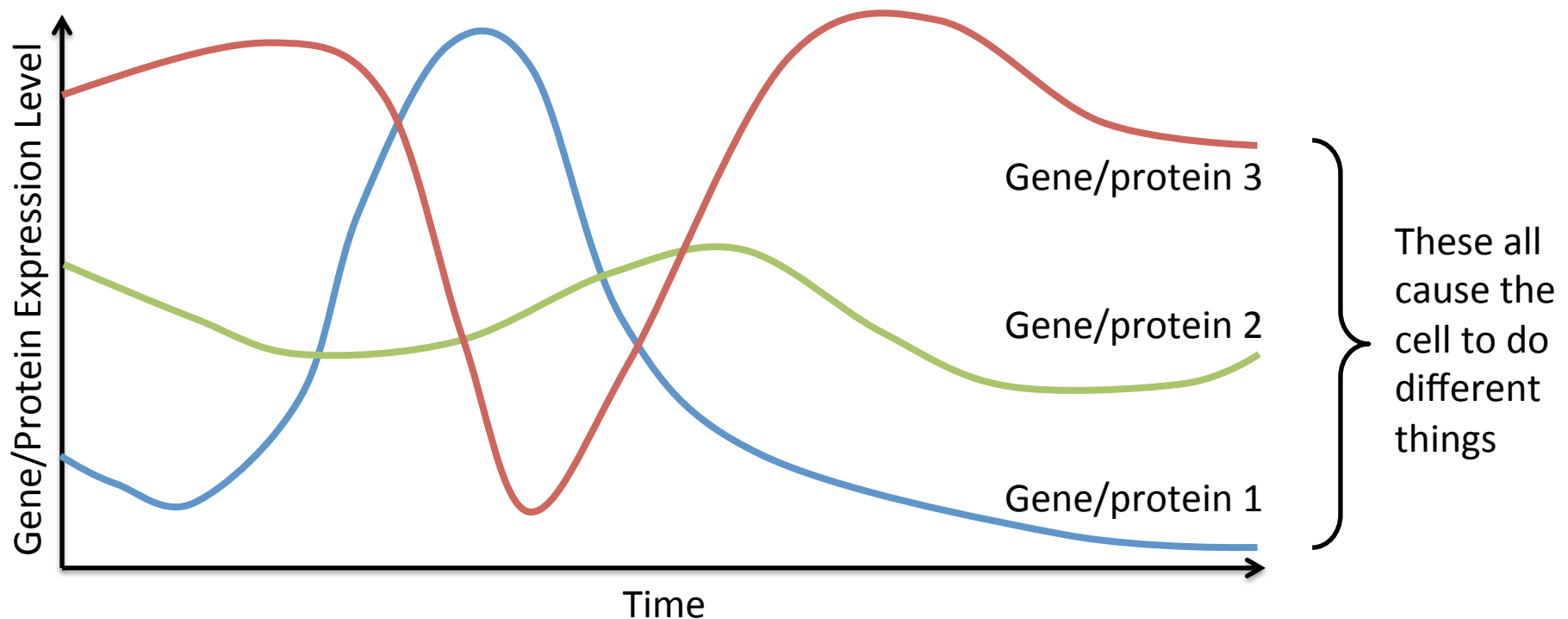




[http://www.nature.com/ng/journal/v45/n5/fig\\_tab/ng.2600\\_F2.html](http://www.nature.com/ng/journal/v45/n5/fig_tab/ng.2600_F2.html)  
<http://www.scbt.org/cgrnb/faq.htm>

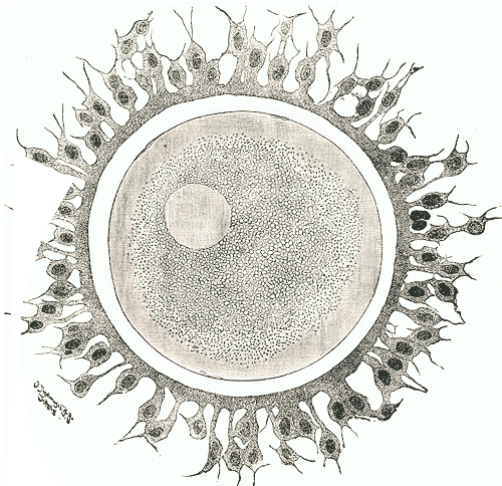
# Gene Regulation in Biology

- ◇ The GRN controls the expression of proteins, and hence the behaviour of the cell, over time
  - ▷ It is, basically, the cell's computer

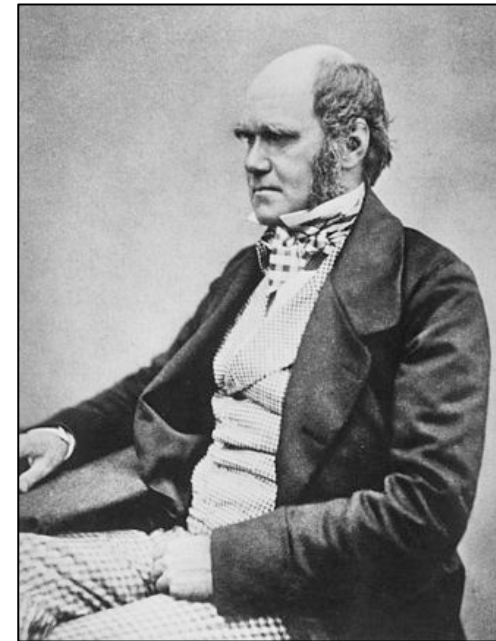


# Gene Regulation in Biology

- ◆ The GRN also determines when cells divide and the kind of cells they will become
  - ▷ i.e. an organism's developmental process



Development





# Gene Regulation in Biology

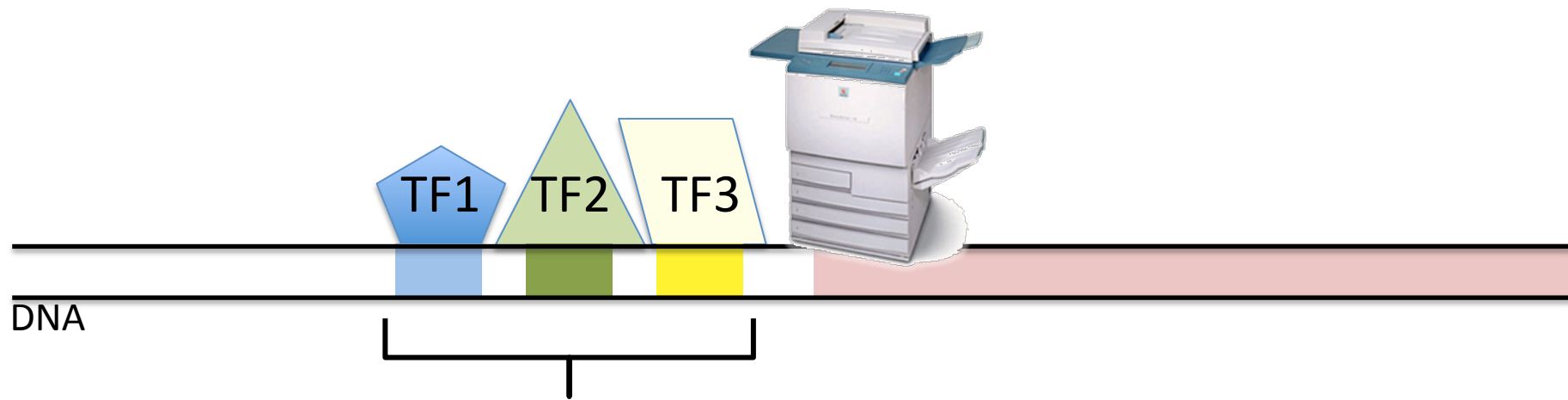
- ◇ Why is gene regulation of computational interest?
  - ▷ GRNs underlie the complexity of biological systems, such as ourselves
- ◇ Biological systems are **structurally complex**
  - ▷ This has led to an interest in how computational models of GRNs can be used to generate intricate structures
- ◇ Biological systems are **dynamically complex**
  - ▷ GRNs produce robust and intelligent responses, leading to interest in whether computational models can do the same, e.g. for controlling robots



# Gene Regulation in Biology

- ◇ Also theoretical interest in **computability**
  - ▷ How do biological systems process information?
  - ▷ How does this differ from conventional computers?
  - ▷ Is it in some ways better? e.g. more compact and robust
  
- ◇ And from an EA perspective **evolvability**
  - ▷ GRNs are known to be evolvable, i.e. able to respond robustly to mutation and crossover
  - ▷ Especially in comparison to computer programs
  - ▷ Potentially an evolvable representation for GP

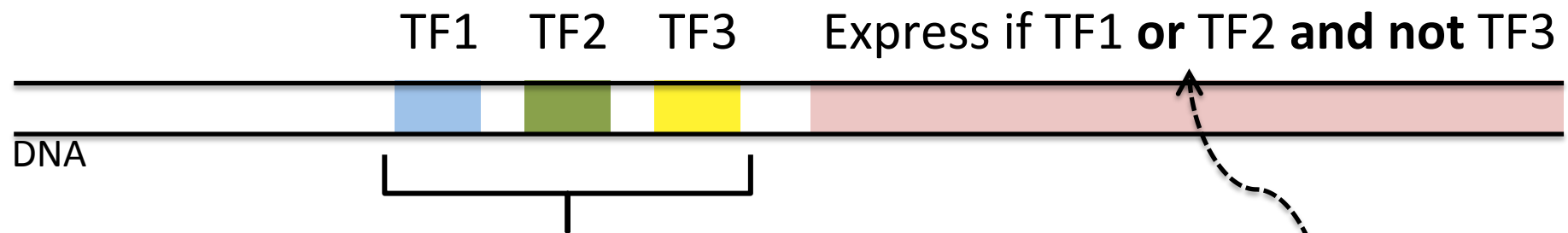
# Gene Regulation in Biology



A number of different TFs are often involved in regulation, binding to different patterns in the **regulatory region** upstream of the gene

*This pattern is different for every gene*

# Gene Regulation in Biology

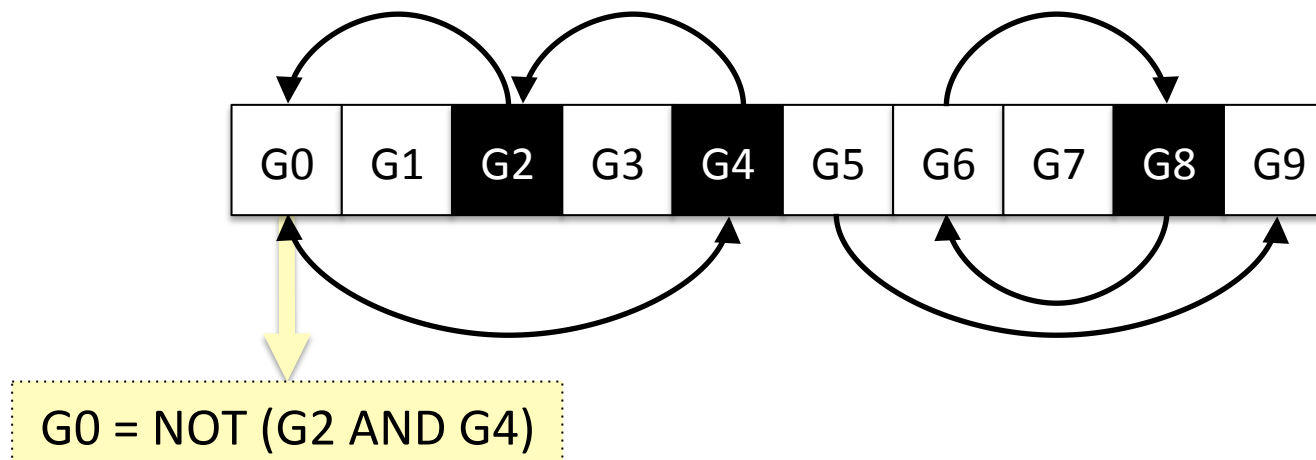


So, whether a gene is expressed depends on whether some other genes are expressed and whether some other genes are not expressed – this is the gene's **regulatory function**

*Often this can be captured by a Boolean function*

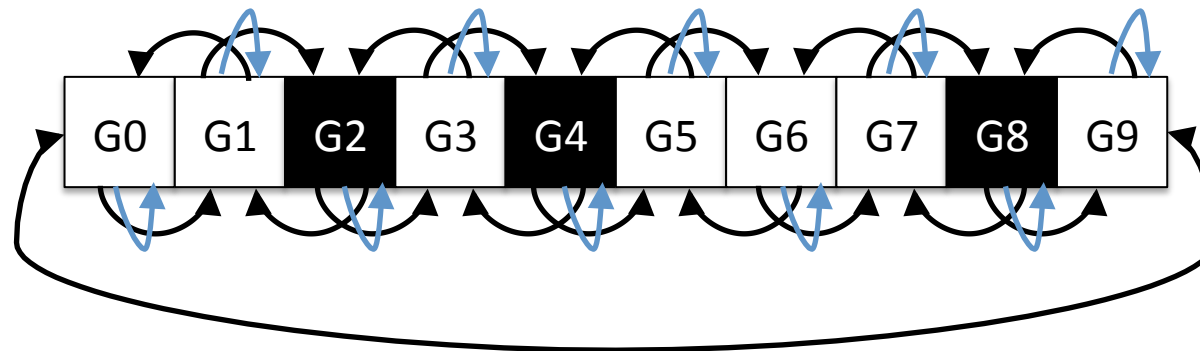
# Boolean Network

- ◇ This idea can be modelled as a Boolean Network
  - ▷ A set of nodes (representing genes)
  - ▷ Each with a binary state (expressed or not expressed),
  - ▷ a set of input nodes (their regulating genes),
  - ▷ and a Boolean function (their regulatory function)
  - ▷ These are executed synchronously at each time step



# Boolean Network

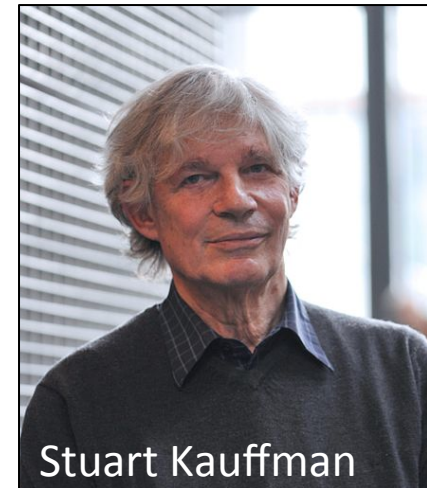
- ◆ Looks a bit like an elementary cellular automata
  - ◆ But without a fixed neighbourhood
  - ◆ And with a different update rule in each cell
  - ◆ In fact, a Boolean network is a generalisation of a CA
  - ◆ (i.e. a Boolean network can implement a CA ↓)
  - ◆ Therefore must be capable of universal computation





# Random Boolean Networks

- ◇ Their behaviour can be studied statistically
  - ▷ By sampling and executing networks with particular sizes, connectivities and function sets
  - ▷ These are termed **Random Boolean Networks** (RBNs)
  
- ◇ Stuart Kauffman is known for this
  - ▷ He studied **NK networks**:
    - RBNs with  $N$  nodes
    - $K$  inputs per node
    - A random function for each node
    - Also called Kauffman networks



Stuart Kauffman  
[http://en.wikipedia.org/wiki/  
File:Stuart\\_Kauffman.jpg](http://en.wikipedia.org/wiki/File:Stuart_Kauffman.jpg)

# Boolean Functions

- ◇ For a particular value of  $K$ , there are  $2^{(2^K)}$  functions
  - ▷ E.g. for  $K=2$ , there are 16 possible functions:

A	B	False	AND	A AND NOT B	A	NOT A AND B	B	XOR	OR
0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	1	1	1	1
1	0	0	0	1	1	0	0	1	1
1	1	0	1	0	1	0	1	0	1

A	B	NOR	XNOR	NOT B	A OR NOT B	NOT A	NOT A OR B	NAND	True
0	0	1	1	1	1	0	1	1	1
0	1	0	0	0	0	1	1	1	1
1	0	0	0	1	1	0	0	1	1
1	1	0	1	0	1	0	1	0	1

# Kauffman's NK Networks

◇ There are *very* many networks for each NK

▷ In fact, there are  $\left( \frac{2^{2^K} N!}{(N-K)!} \right)^N$

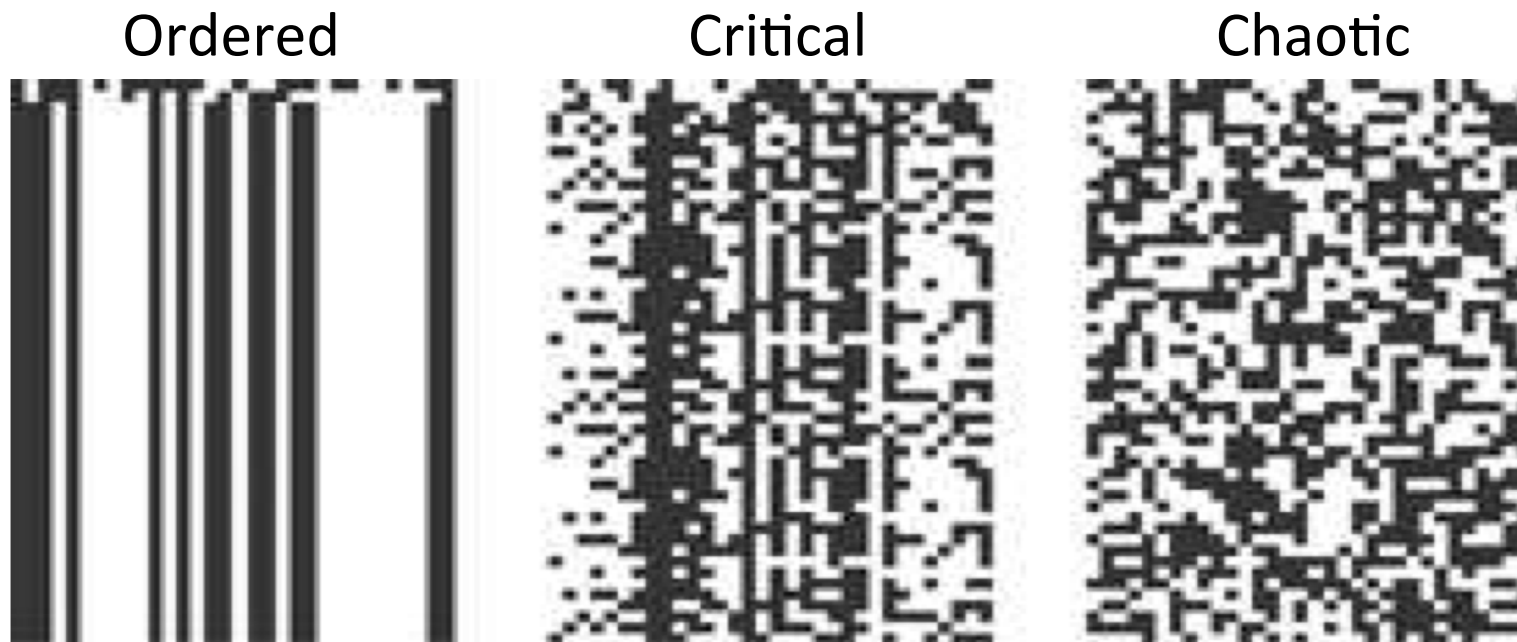
- for  $K=2$ ,  $N=10$ , there are ~2 million
- for  $K=3$ ,  $N=10$ , there are  $\sim 6 \times 10^{15}$ , which is *a lot*

▷ This is why they are studied statistically

- Too many to study them exhaustively, as Wolfram did with elementary CAs

# Kauffman's NK Networks

- ◆ The behaviour of an RBN falls into 3 categories:



From [Gershenson, 2004] Introduction to Random Boolean Networks  
<http://uk.arxiv.org/abs/nlin.AO/0408006>

# Kauffman's NK Networks

◇ Kauffman observed that, *on average*\*

Ordered when  $K < 2$



Critical when  $K = 2$



Chaotic when  $K > 2$

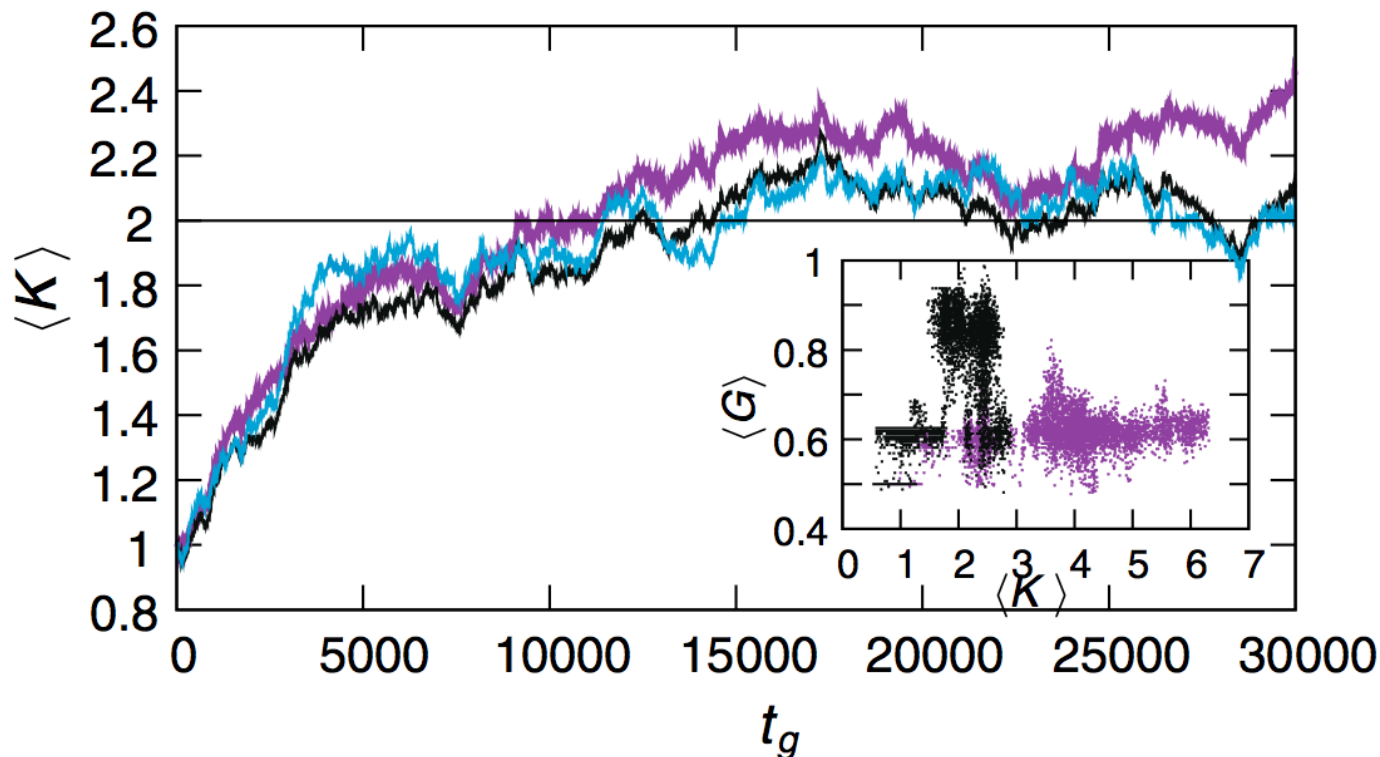


\*But note this doesn't mean that **all**  $K = 2$  networks are critical, or that critical networks can't be found for  $K > 2$



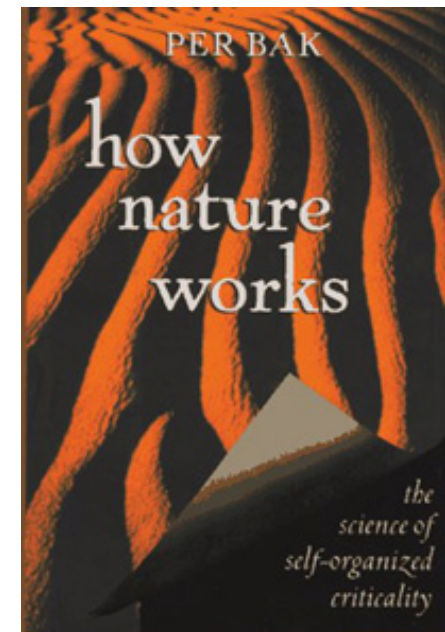
# Evolved Criticality

- ◇ Evolved Boolean networks appear to favour criticality
  - ▷ Several studies have shown this, with  $K$  tending to 2
  - ▷  $K=2$  also promotes learning and generality [Goudarzi'12]:



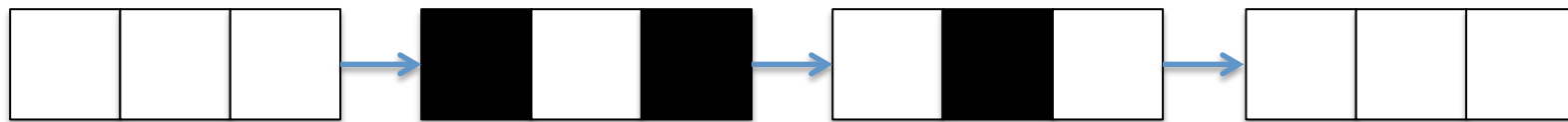
# Edge of Chaos

- ◇ Criticality is also known as the ‘edge of chaos’
  - ▷ Dynamics are neither ordered nor chaotic, but complex
  - ▷ Hypothesised to be the sweet spot for computation
  - ▷ This is where CA Rule 110 (universality) is found
  
- ◇ Appears frequently in natural systems
  - ▷ Genes, brains, proteins, flocks ...
  - ▷ Evolution may select for criticality
  - ▷ Per Bak, “How Nature Works” →
  - ▷ “Are biological systems poised at criticality?”  
[<http://arxiv.org/pdf/1012.2242v1.pdf>]



# Attractors

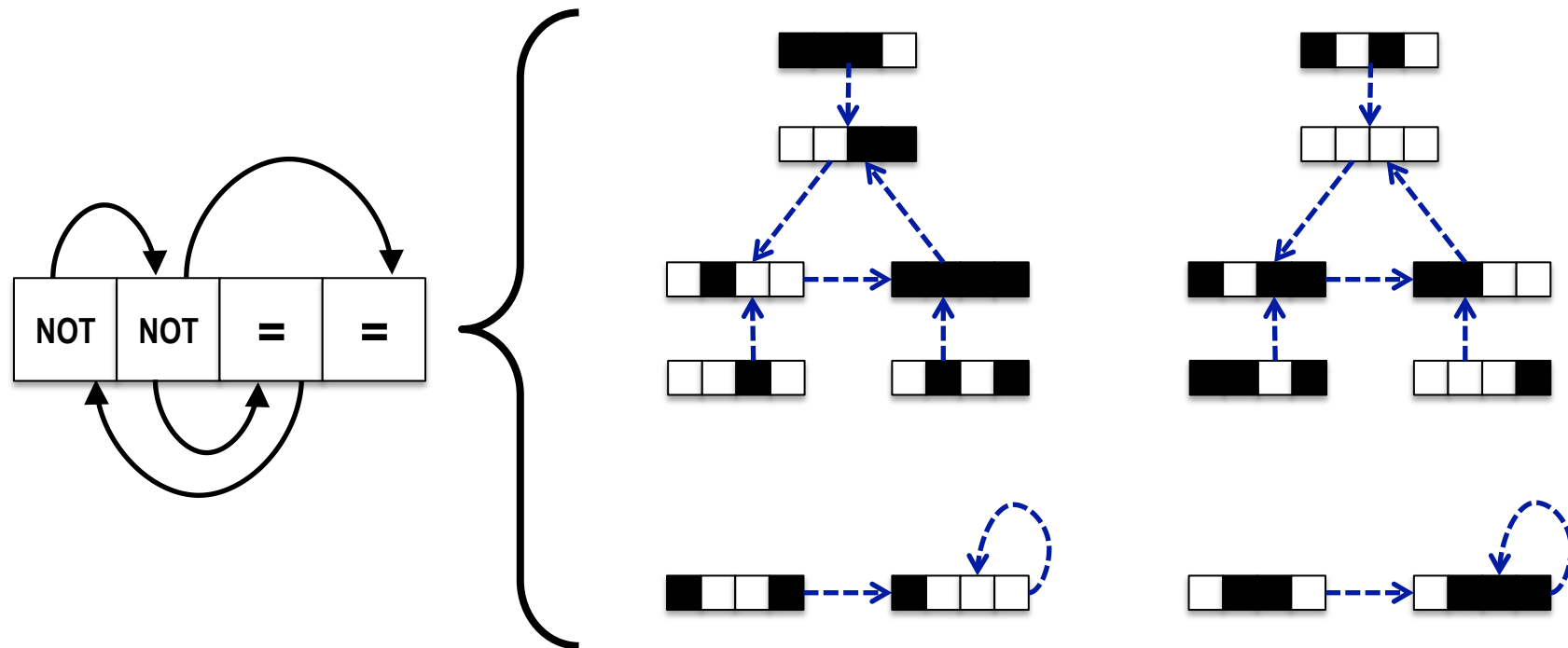
- ◇ Attractors are an important concept for RBNs
  - ▷ A finite number of nodes means that states must repeat
  - ▷ An attractor of length  $L$  repeats every  $L$  steps
  - ▷ e.g.  $L=3$ :



- ▷ An attractor of length 1 is termed a point attractor
- ◇ Transients occur before an attractor is reached
  - ▷ e.g. “Acorn” is a transient leading to a stable attractor

# Attractors

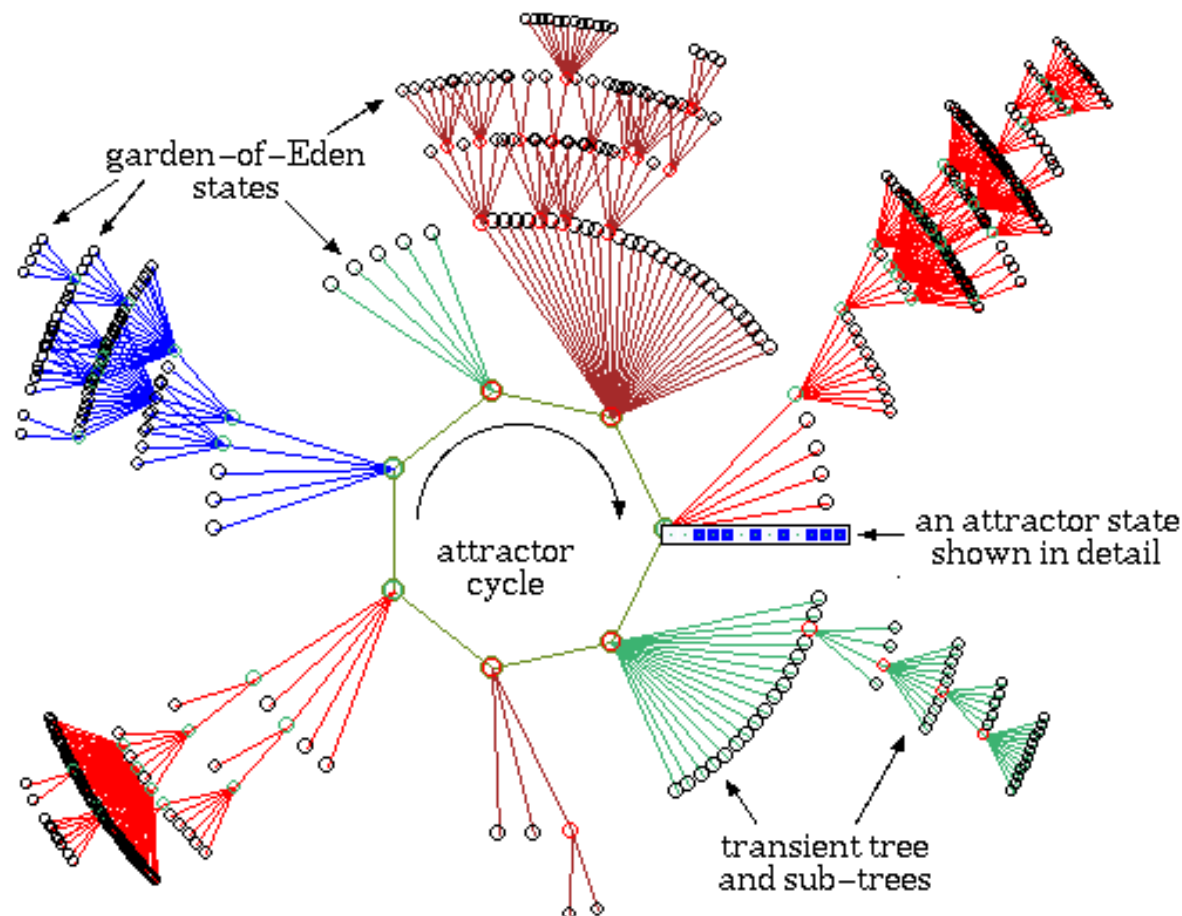
## ◇ Complete attractor map for a small network



- ▷ 2 attractors of length 3, and 2 point attractors

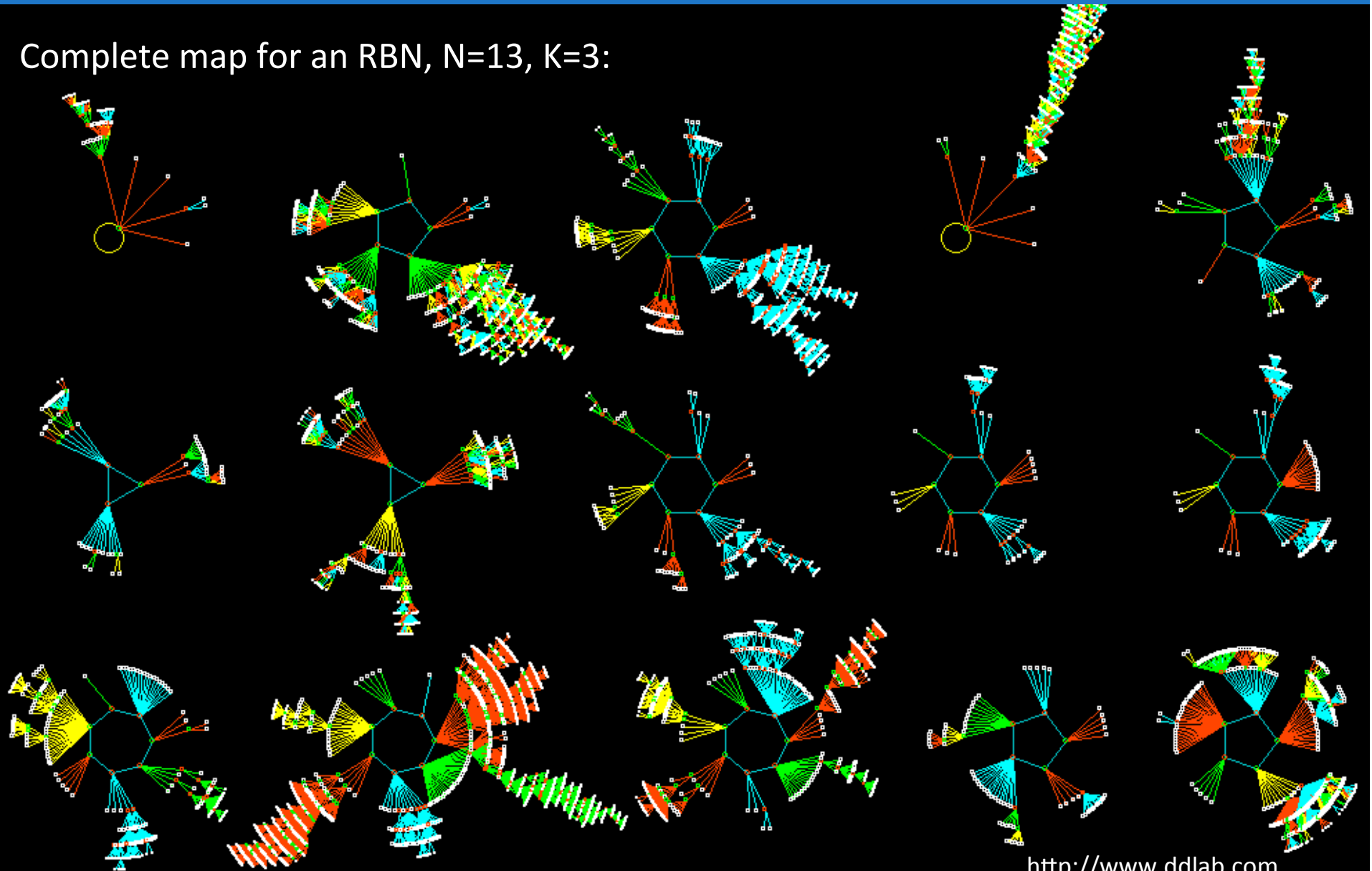
# Attractors

- ◆ Attractors often have large **basins of attraction**



# Attractors

Complete map for an RBN,  $N=13$ ,  $K=3$ :

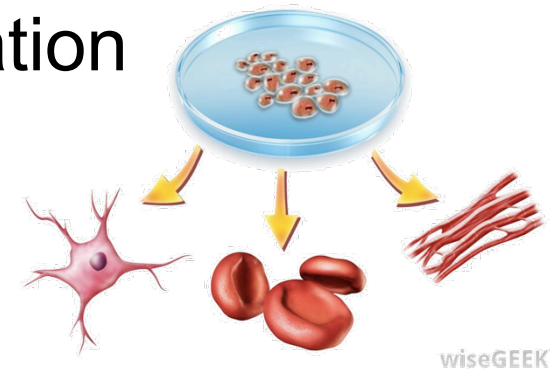




# Attractors

## ◇ Attractors have a biological interpretation

- ▷ Stable states for a cell  
e.g. cell types: neuron, liver, skin, ...
- ▷ Cancer can also be seen as an attractor



## ◇ Boolean networks are used to study bio GRNs

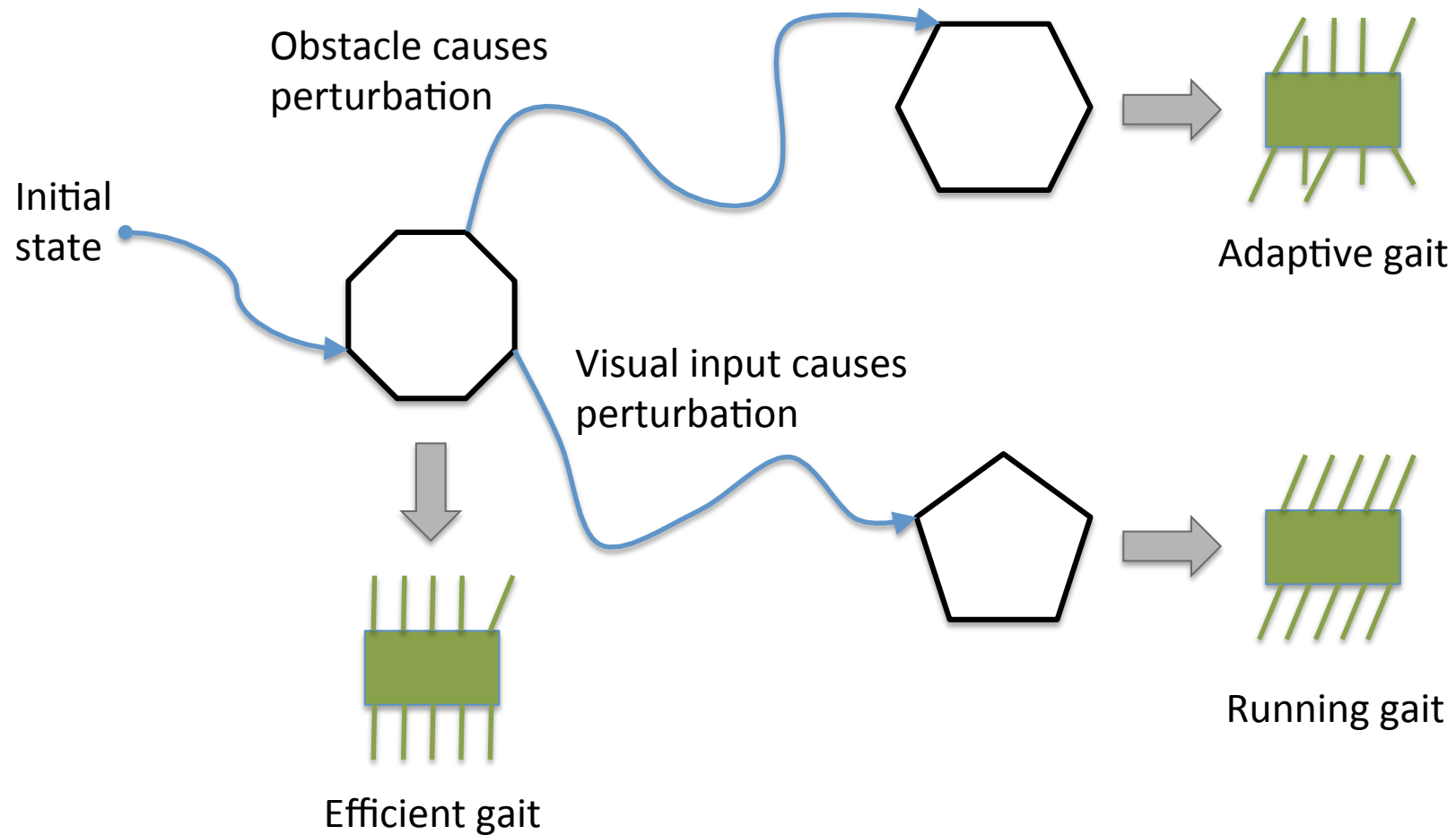
- ▷ Captures their qualitative dynamics
- ▷ Usually using NOT, OR and AND functions
- ▷ See “Boolean modeling of biological regulatory networks: A methodology tutorial”:

<http://www.sciencedirect.com/science/article/pii/S1046202312002770>

# Attractors

- ◇ And a computational interpretation?
  - ▷ An attractor can be seen as a computational state
  - ▷ e.g. a point attractor represents a particular 'output'
  
- ◇ A cyclic attractor generates a repeating sequence
  - ▷ Which can be interpreted as a sequence of actions
  - ▷ e.g. robot actuator movements
  
- ◇ Transients can be seen as computing the attractor
  - ▷ Either from the initial state
  - ▷ Or between attractors (especially if inputs are allowed)

# Illustrative Example

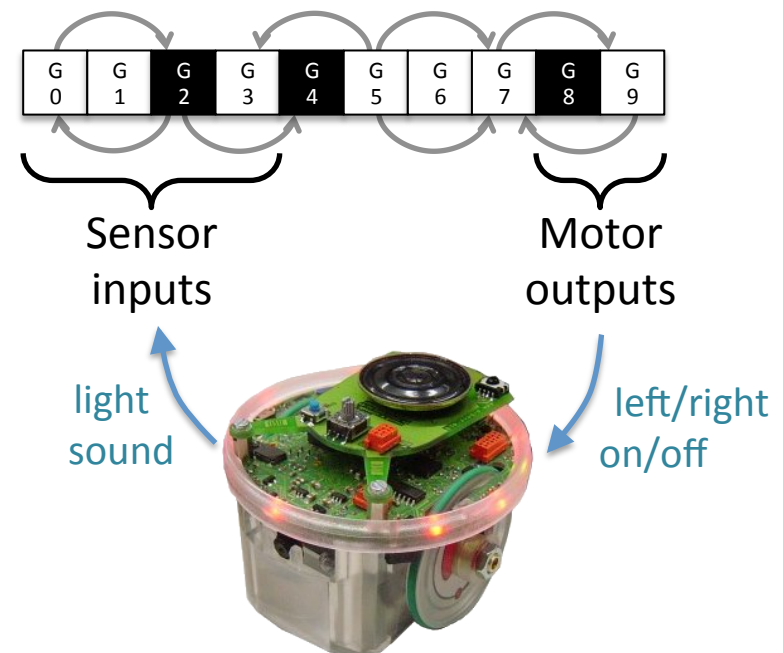


# Evolving Boolean Networks

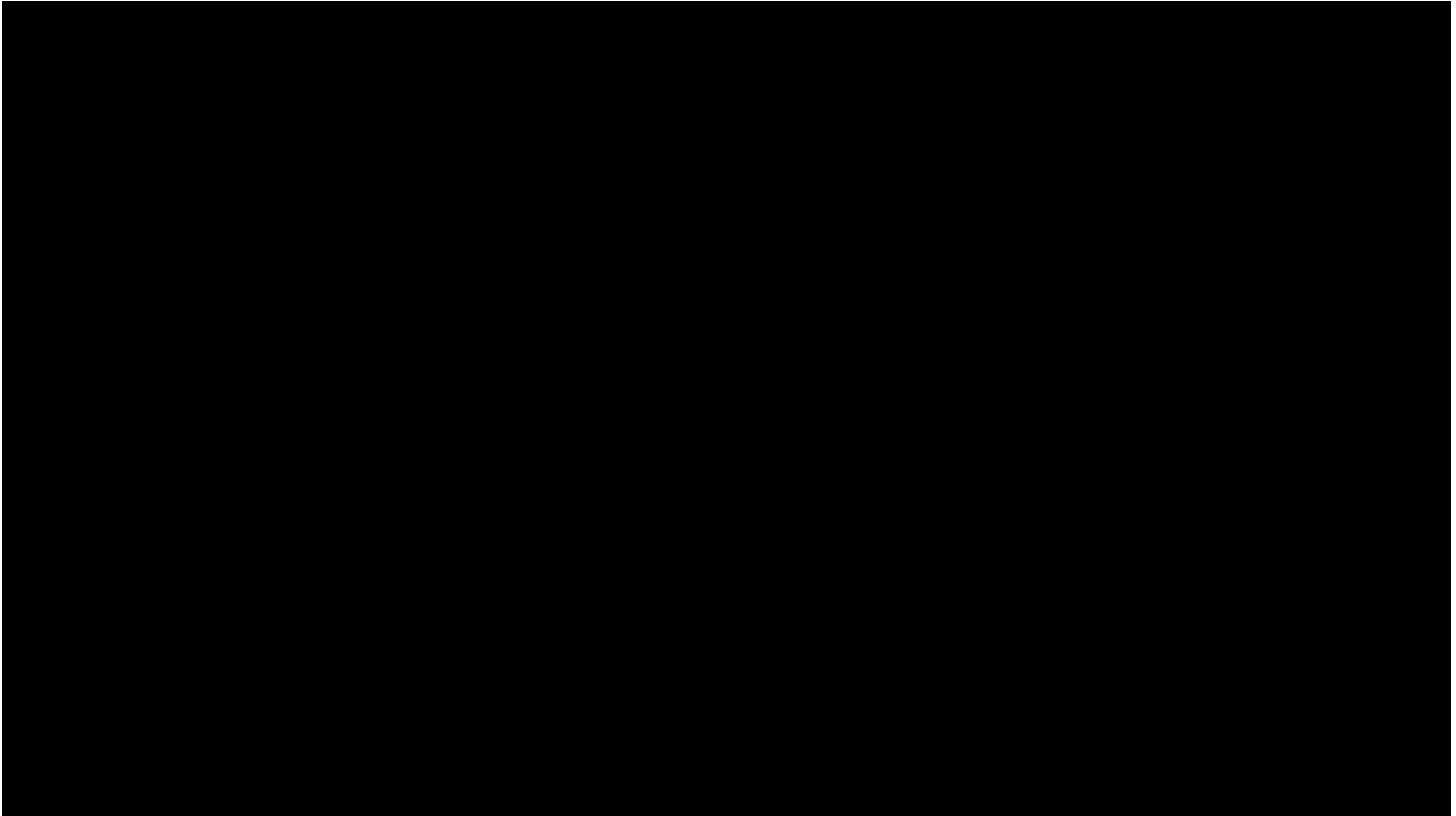
- ◆ Using EAs to find useful Boolean networks
  - ▷ Networks that solve a particular computational problem
  - ▷ Exhaustive search is not an option in this case
  - ▷ Another form of genetic programming

- ◆ Robot controllers [Roli, 2011]

- ▷ Used inputs and outputs →
- ▷ Searched for networks with light following behaviour
- ▷ Controlled a real ePuck
- ▷ Networks were robust to sensor noise



# Roli et al.



<https://www.youtube.com/watch?v=6ZF9Ijpwk8>

# Inputs and Outputs

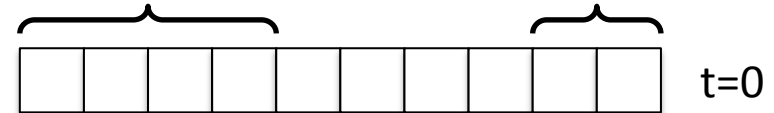
## Initial State

No sensor signals  
Not moving



Sensor inputs

Left/right motors



Note: This is a simplified example. See paper for full details of how this works.



# Inputs and Outputs

## Initial State

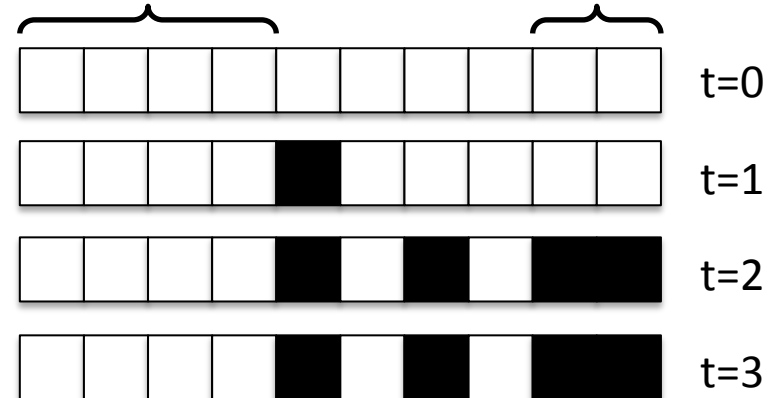
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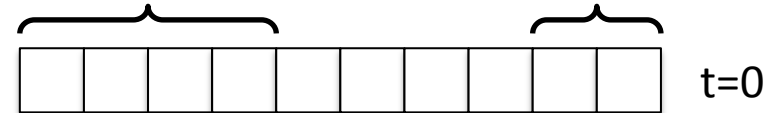
## Initial State

No sensor signals  
Not moving



Sensor inputs

Left/right motors



## First Update

No sensor signals  
Moving forward



Note: This is a simplified example. See paper for full details of how this works.

# Inputs and Outputs

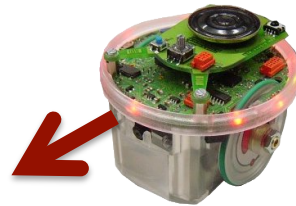
## Initial State

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Not moving



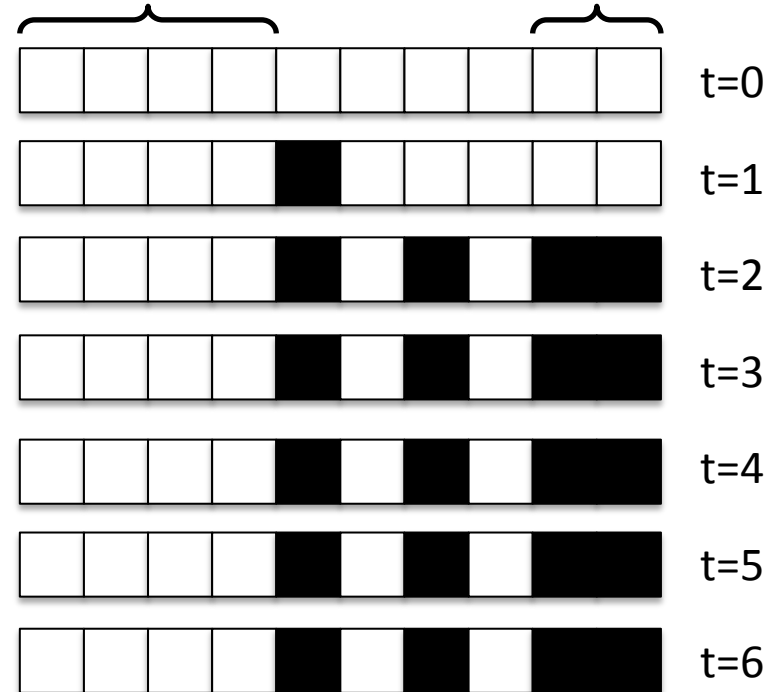
## First Update

No sensor signals  
Moving forward



Sensor inputs

Left/right motors



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# Inputs and Outputs

## Initial State

No sensor signals  
Not moving



Sensor inputs

Left/right motors



t=0



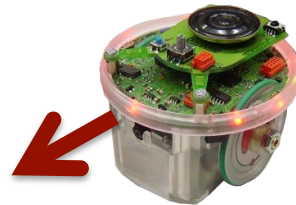
t=1



t=2

## First Update

No sensor signals  
Moving forward



t=3



t=4



t=5

## Second Update

Light on left  
Moving forward



t=6

Note: This is a simplified example. See paper for full details of how this works.

# Inputs and Outputs

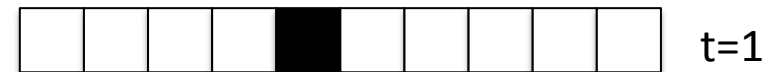
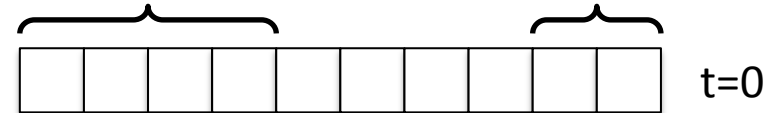
## Initial State

No sensor signals  
Not moving



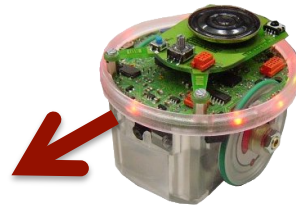
Sensor inputs

Left/right motors



## First Update

No sensor signals  
Moving forward



## Second Update

Light on left  
Moving forward



Note: This is a simplified example. See paper for full details of how this works.

# Inputs and Outputs

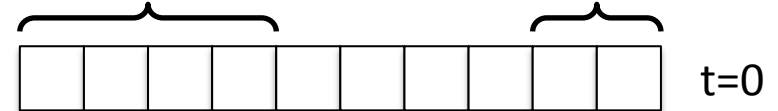
## Initial State

No sensor signals  
Not moving



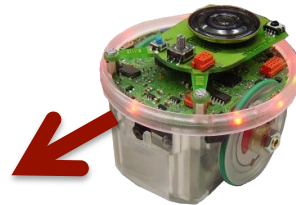
Sensor inputs

Left/right motors



## First Update

No sensor signals  
Moving forward



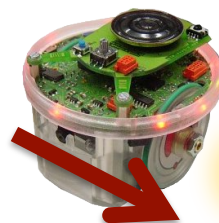
## Second Update

Light on left  
Moving forward



## Third Update

Light on left  
Turning left



Note: This is a simplified example. See paper for full details of how this works.



# Limitations of Boolean Networks

## ◇ From a practical perspective

- ▷ Inputs and outputs must be binary encoded
- ▷ Difficult to handle large/continuous/many values
- ▷ E.g. Pi in binary: 0100000001001001000011111111001

## ◇ From a biological perspective

- ▷ Gene expression levels are not discrete
- ▷ Regulatory functions are not always Boolean functions
- ▷ *However, Boolean networks are computationally efficient and can be implemented directly in hardware*

# To be continued...

- ◇ GRN models that look more biological
- ◇ Using GRN models for development
- ◇ Interesting applications

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