

NETWORK MOTIFS

UNDERSTANDING BIOLOGY THROUGH MATHEMATICS

presented by Laura Martens & Arthur Heimbrecht

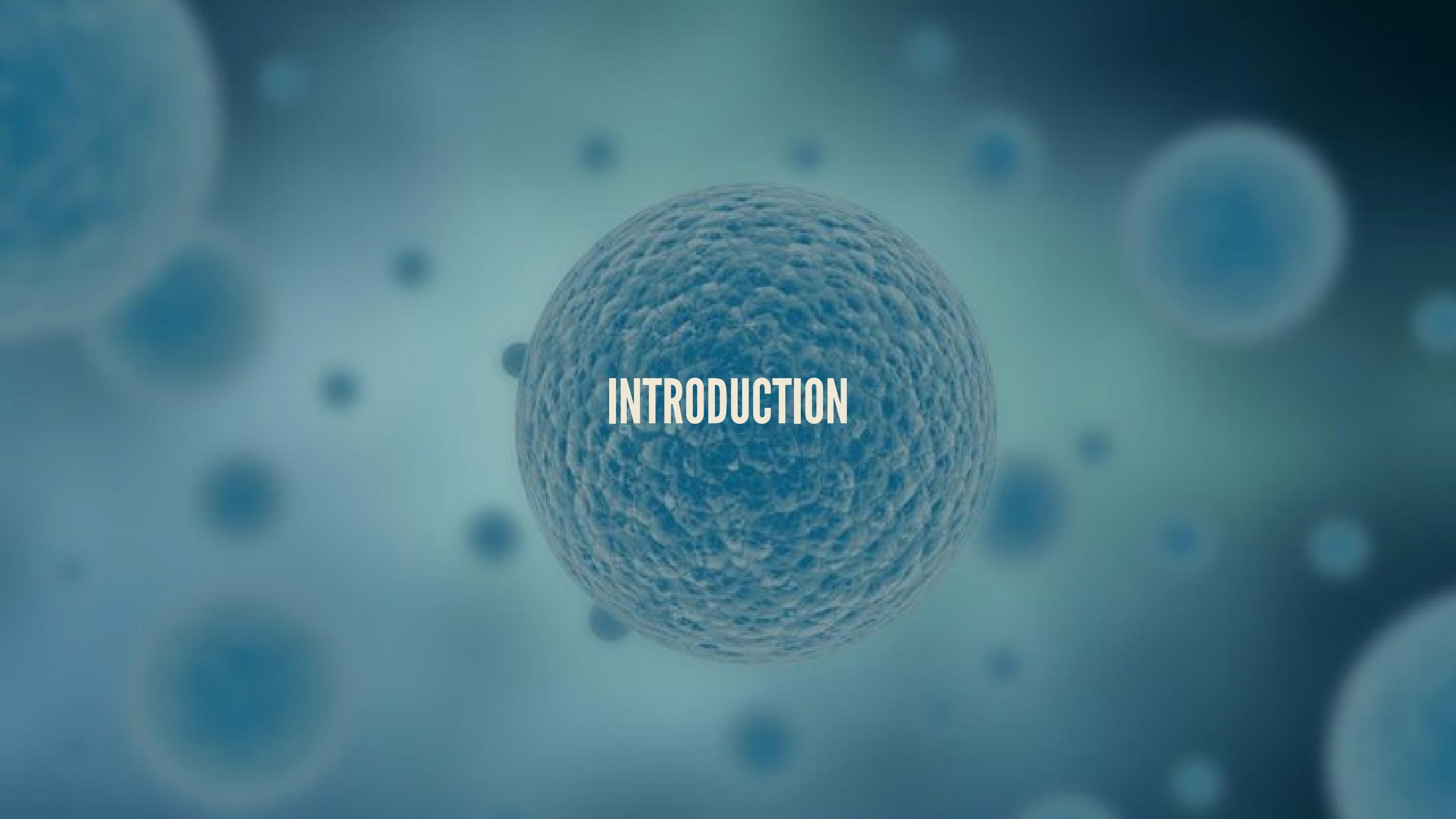
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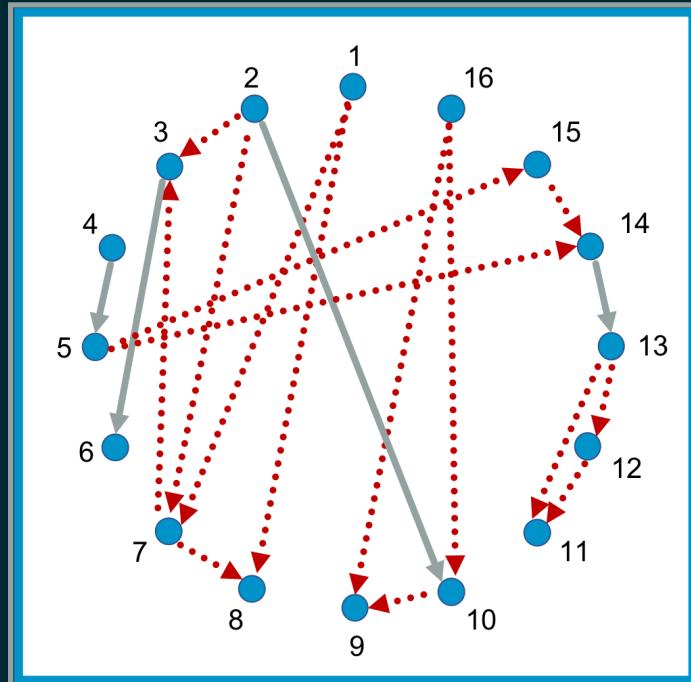


INTRODUCTION

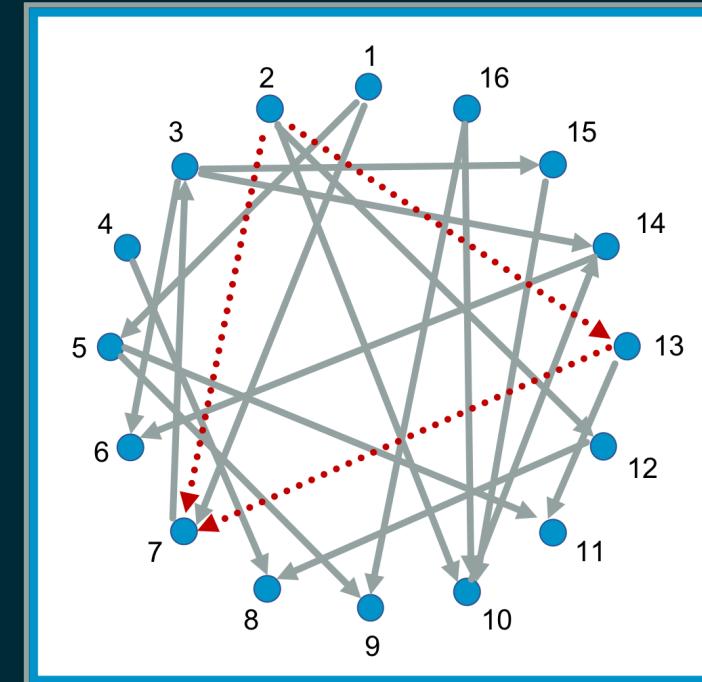
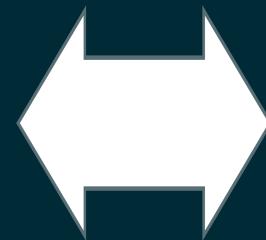
WHAT ARE NETWORK MOTIFS?

- Basic interaction patterns that recur throughout biological and non-biological networks much more often than in random networks
- Small set of network motifs serve as building blocks of large networks
- Each network has a defined function: e.g. filters, pulse generators

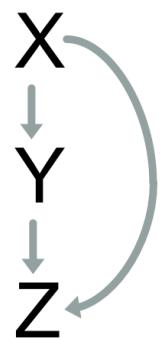
REAL NETWORK



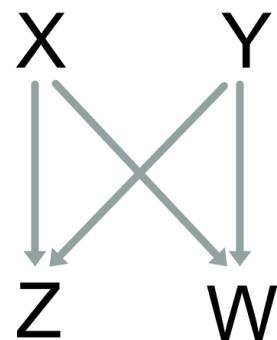
RANDOM NETWORK



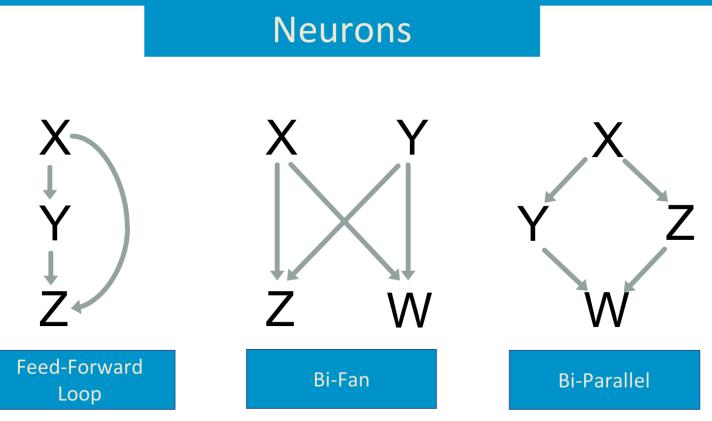
Transcription Network



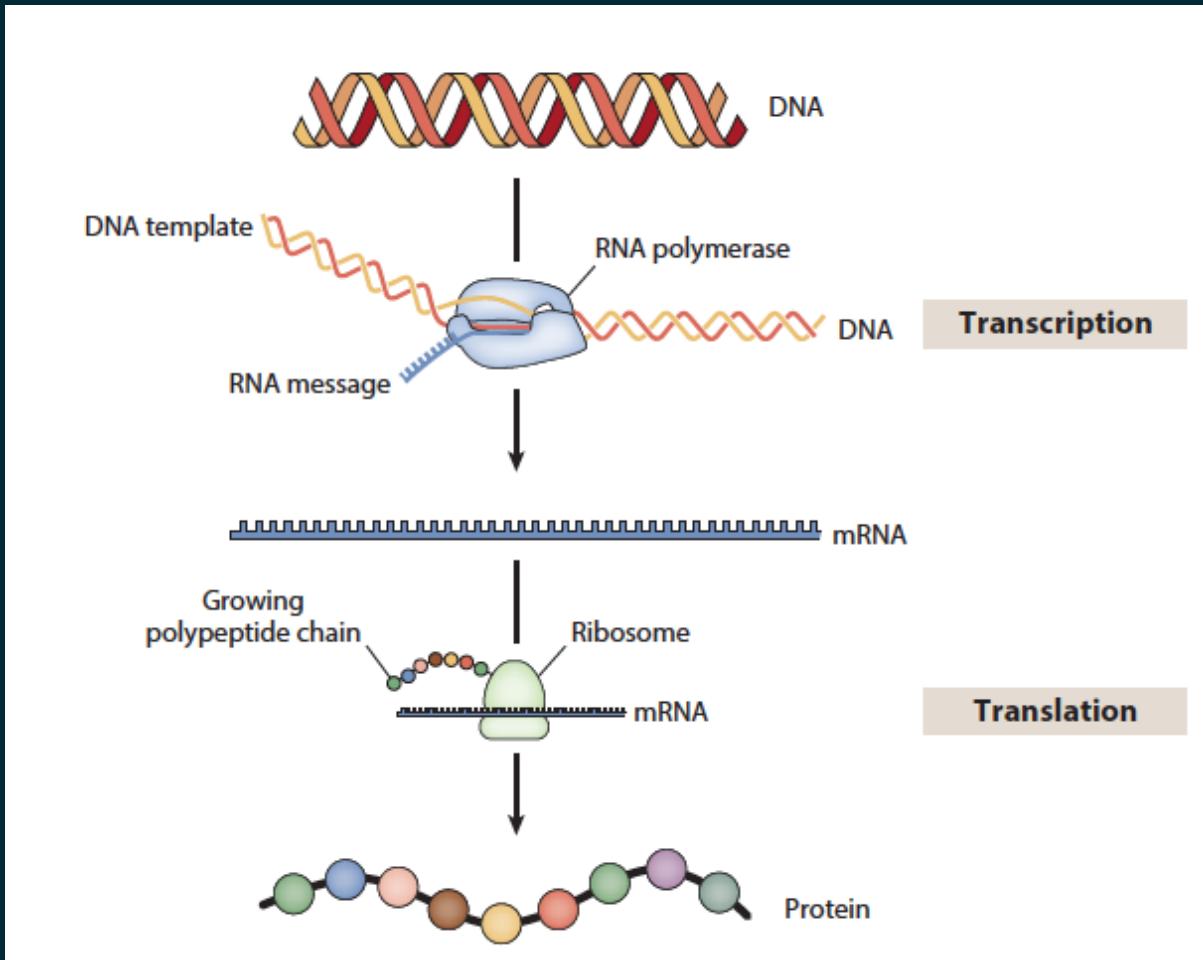
Feed-Forward
Loop



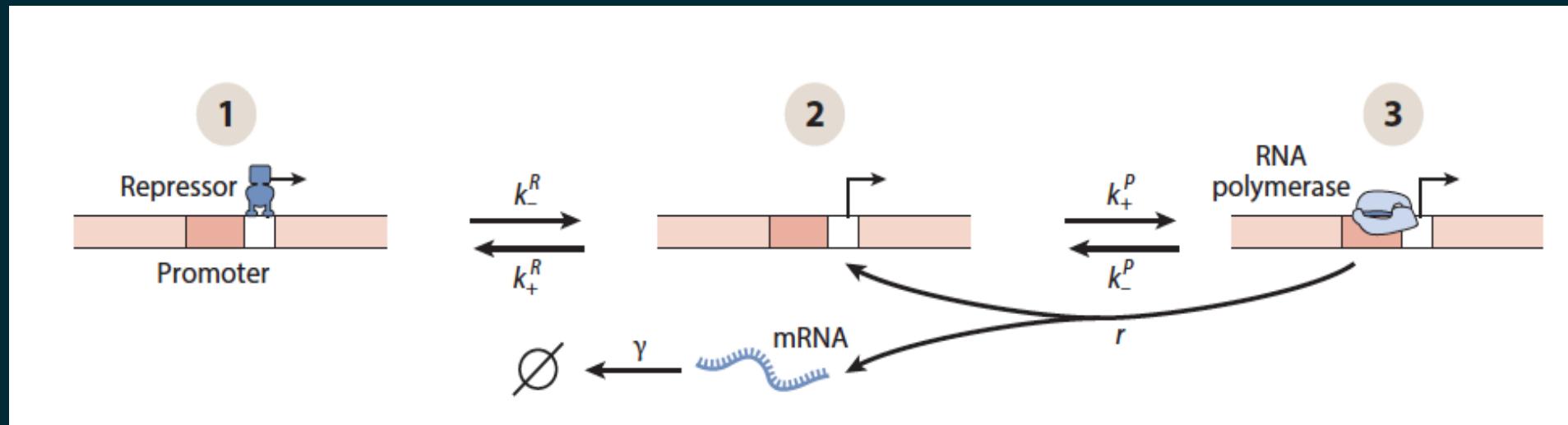
Bi-Fan



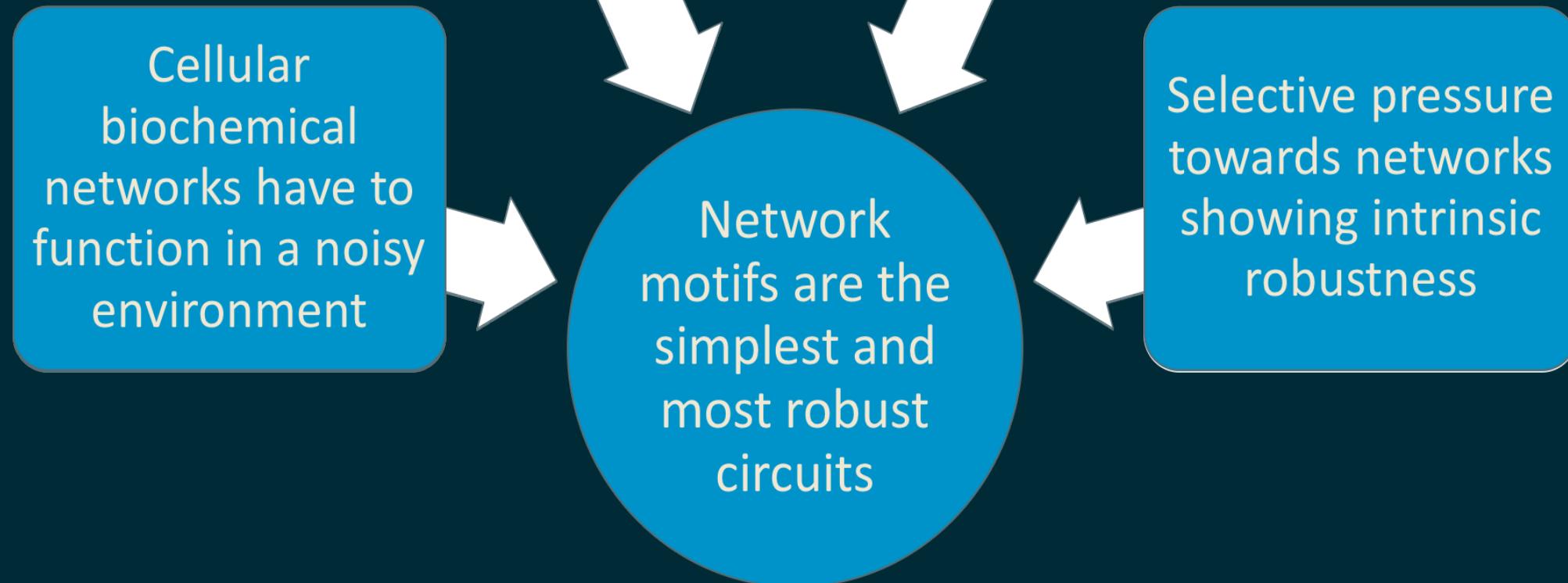
TRANSCRIPTION NETWORKS

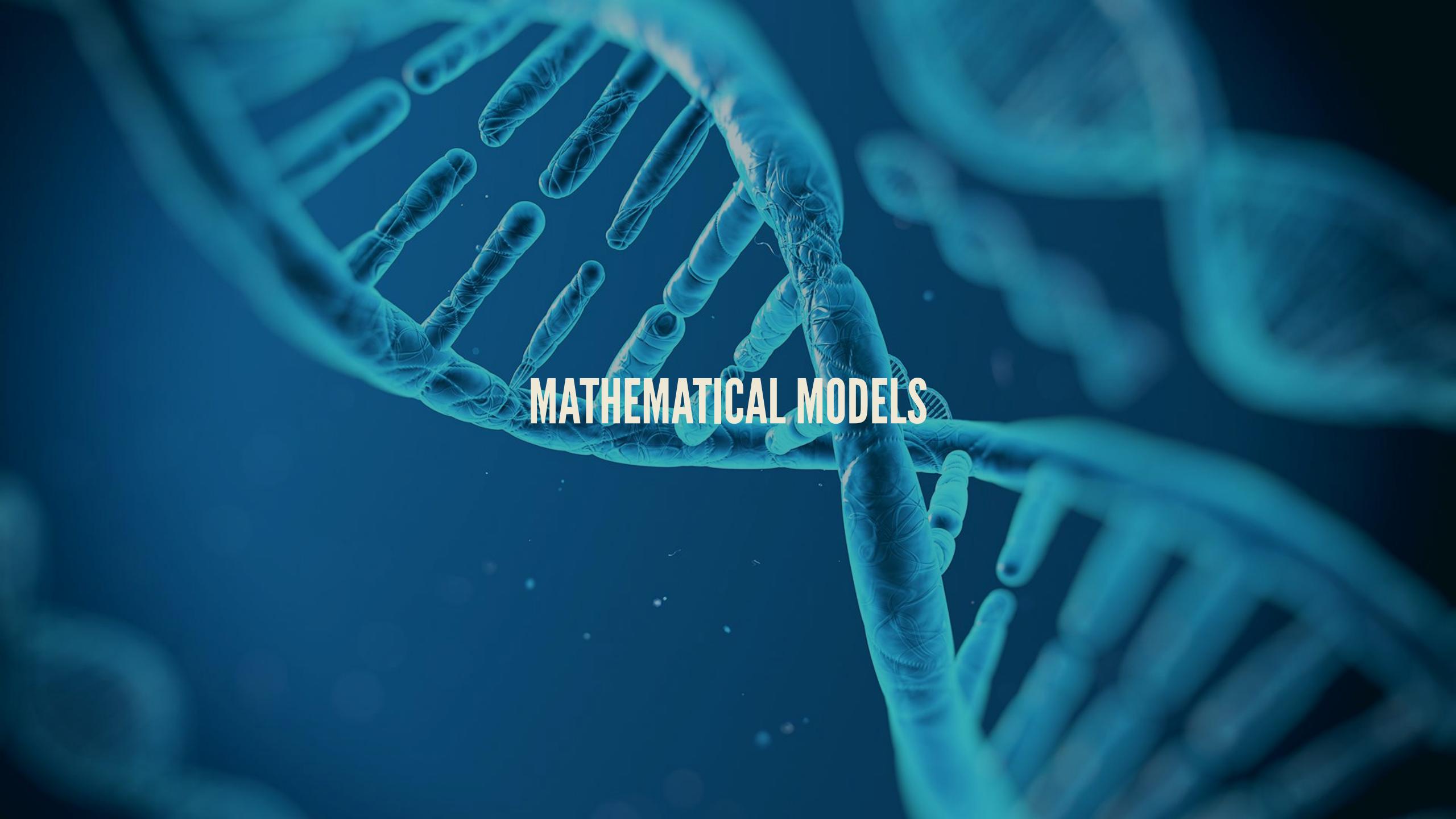


ACTIVATORS AND REPRESSORS



EVOLUTION OF NETWORK MOTIFS



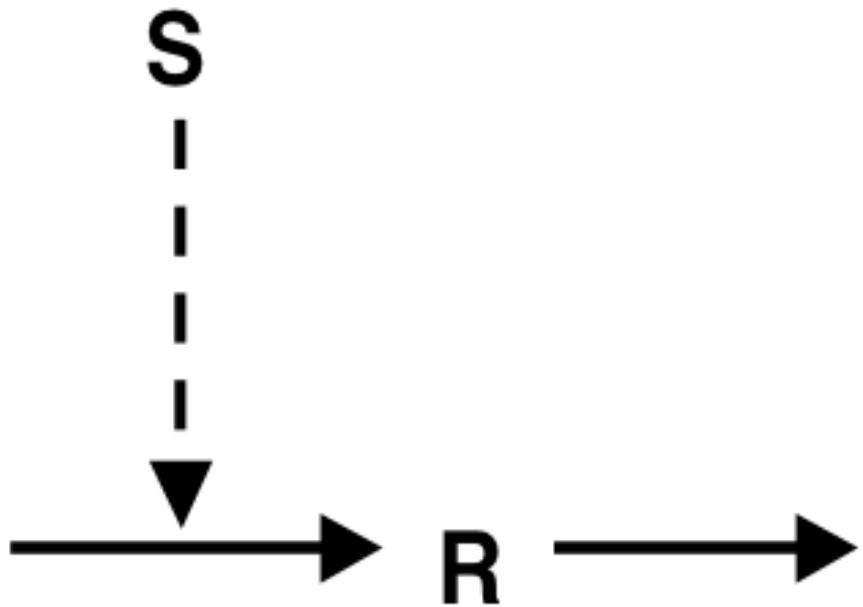


MATHEMATICAL MODELS

CLASSIFYING DEVELOPMENTAL AND SENSORY NETWORKS

- **Sensory networks**
 - Cell "senses" its surroundings/its own state
 - Response is a function of the signal
- **Developmental networks**
 - Response does not depend on the signal if threshold is reached
 - Cell fate decisions are final

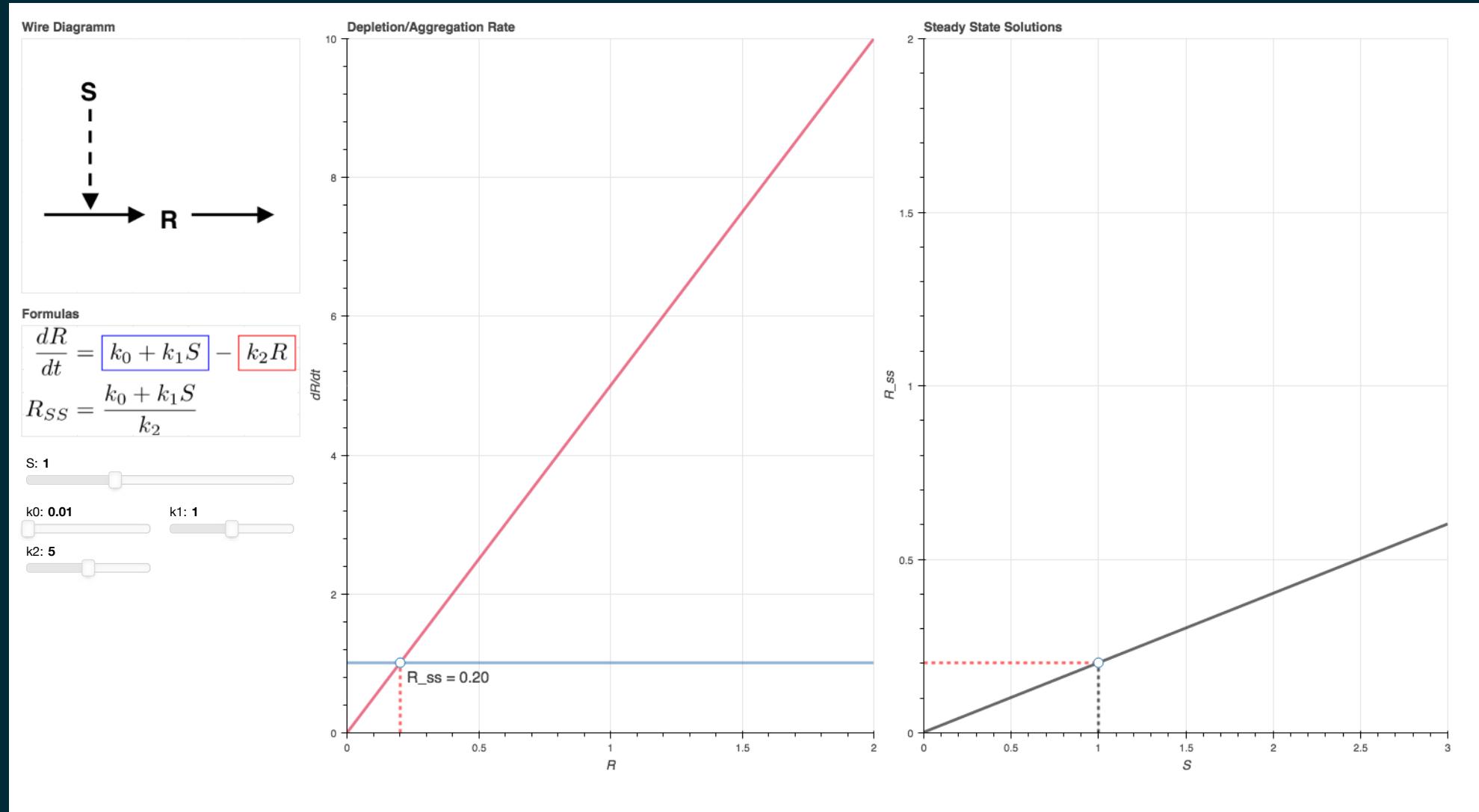
PRELIMINARY EXAMPLE



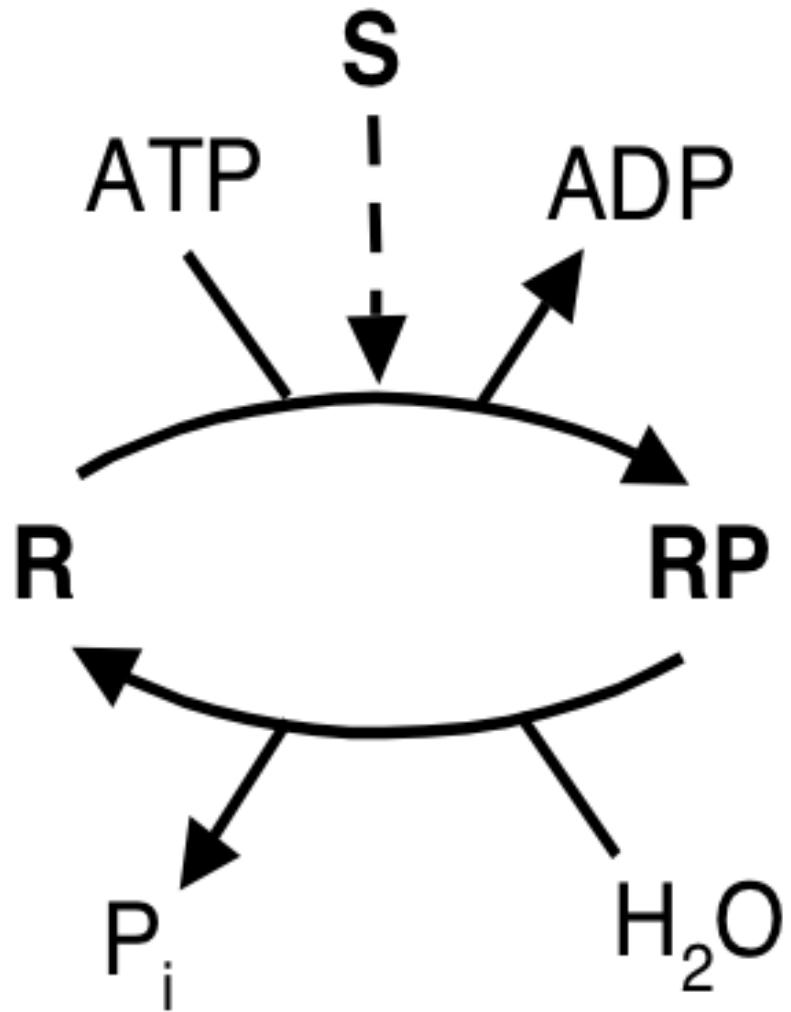
$$\frac{dR}{dt} = \boxed{k_0 + k_1 S} - \boxed{k_2 R}$$

$$R_{SS} = \frac{k_0 + k_1 S}{k_2}$$

PRELIMINARY EXAMPLE



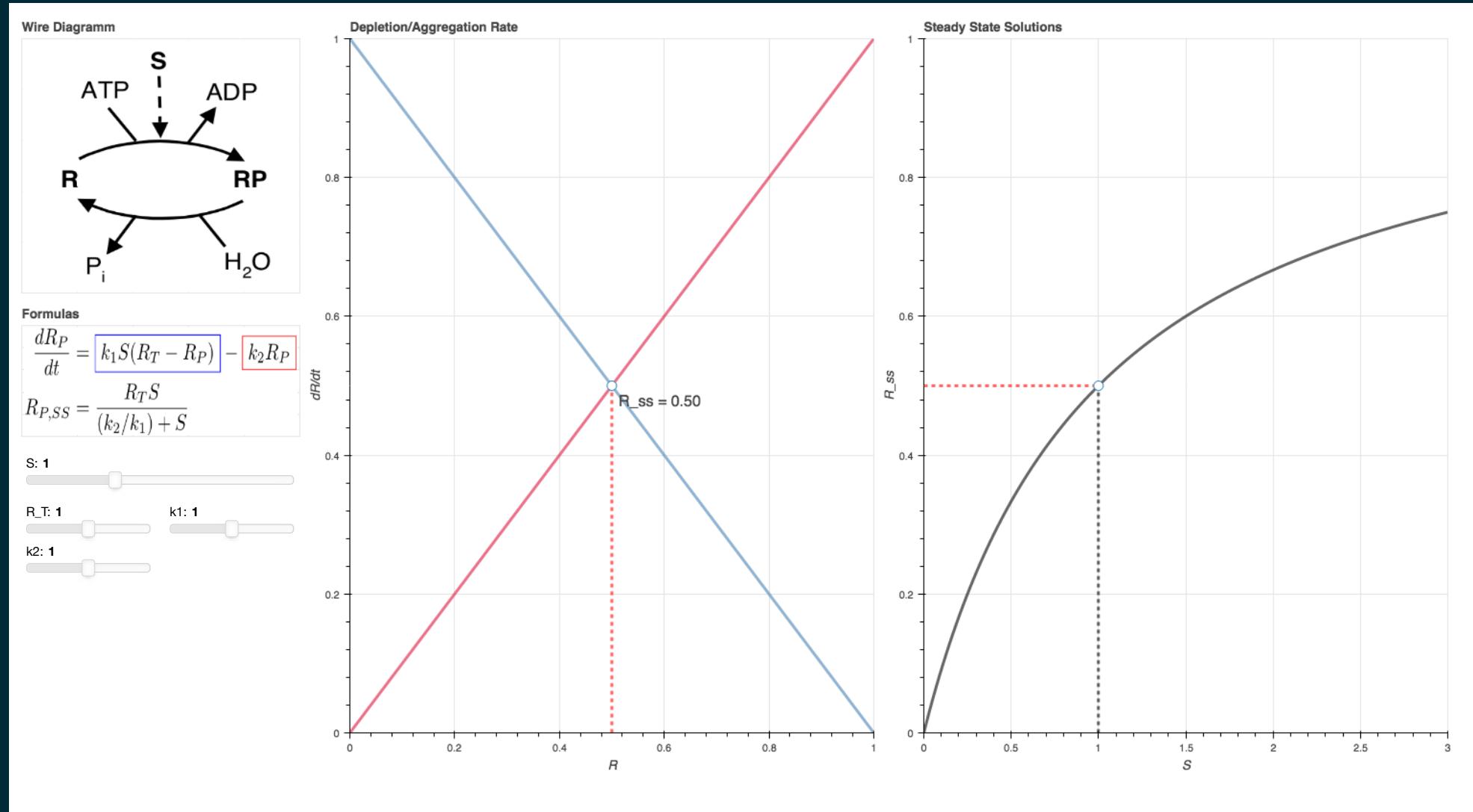
BIOLOGICAL EXAMPLE



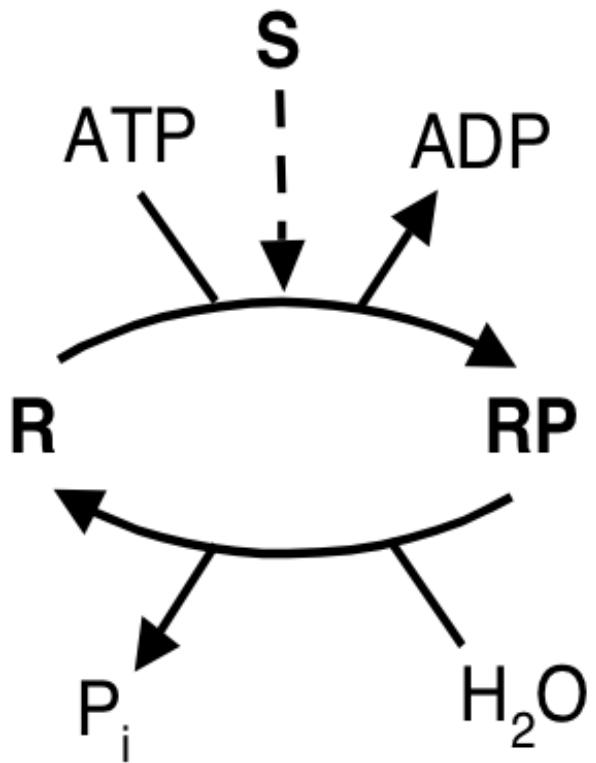
$$\frac{dR_P}{dt} = \boxed{k_1 S (R_T - R_P)} - \boxed{k_2 R_P}$$

$$R_{P,SS} = \frac{R_T S}{(k_2/k_1) + S}$$

BIOLOGICAL EXAMPLE



BUZZER

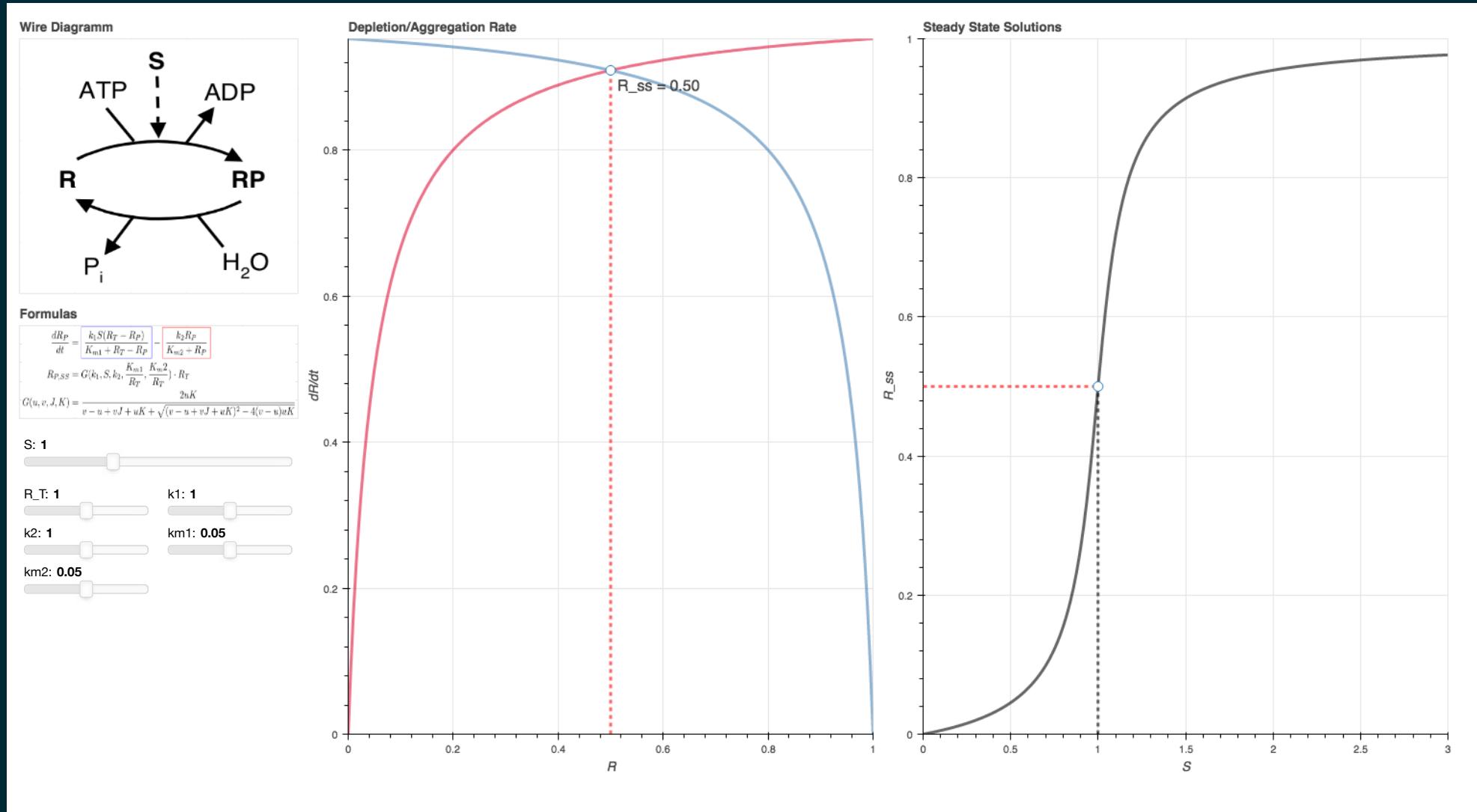


$$\frac{dR_P}{dt} = \frac{k_1 S (R_T - R_P)}{K_{m1} + R_T - R_P} - \frac{k_2 R_P}{K_{m2} + R_P}$$

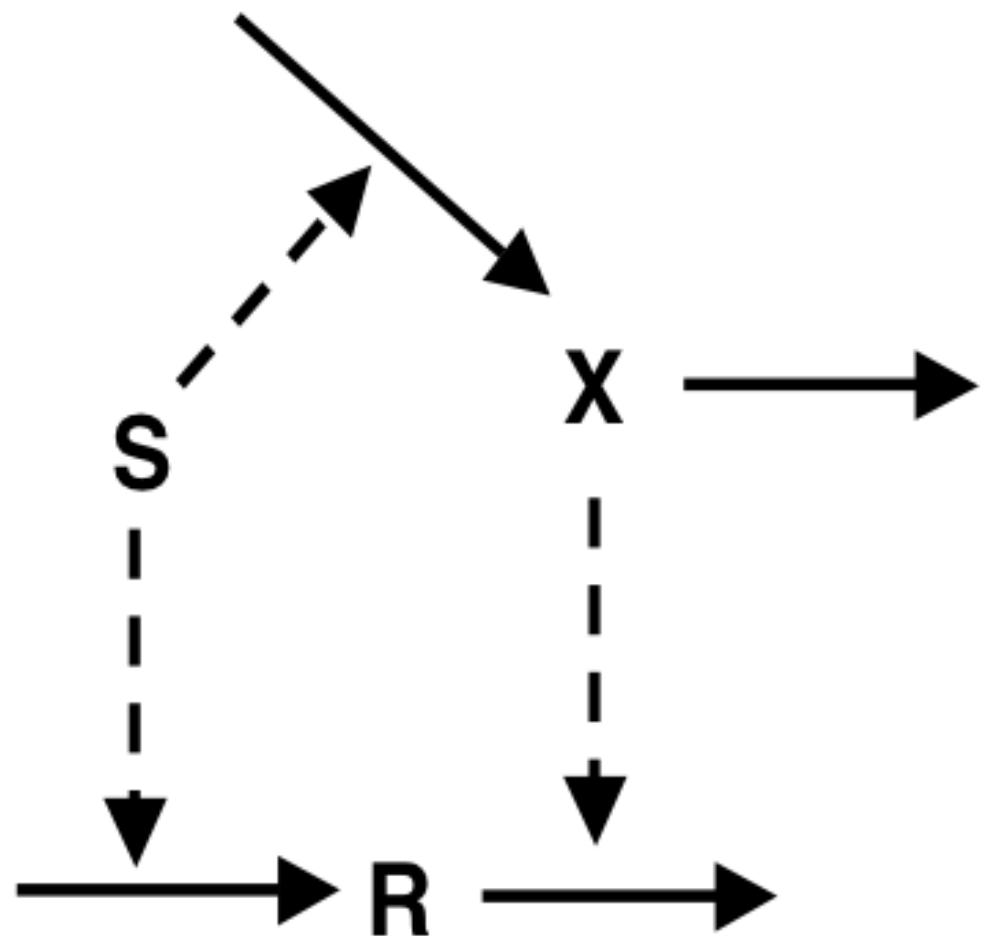
$$R_{P,SS} = G(k_1, S, k_2, \frac{K_{m1}}{R_T}, \frac{K_{m2}}{R_T}) \cdot R_T$$

$$G(u, v, J, K) = \frac{2uK}{v - u + vJ + uK + \sqrt{(v - u + vJ + uK)^2 - 4(v - u)uK}}$$

BUZZER



SNIFFER



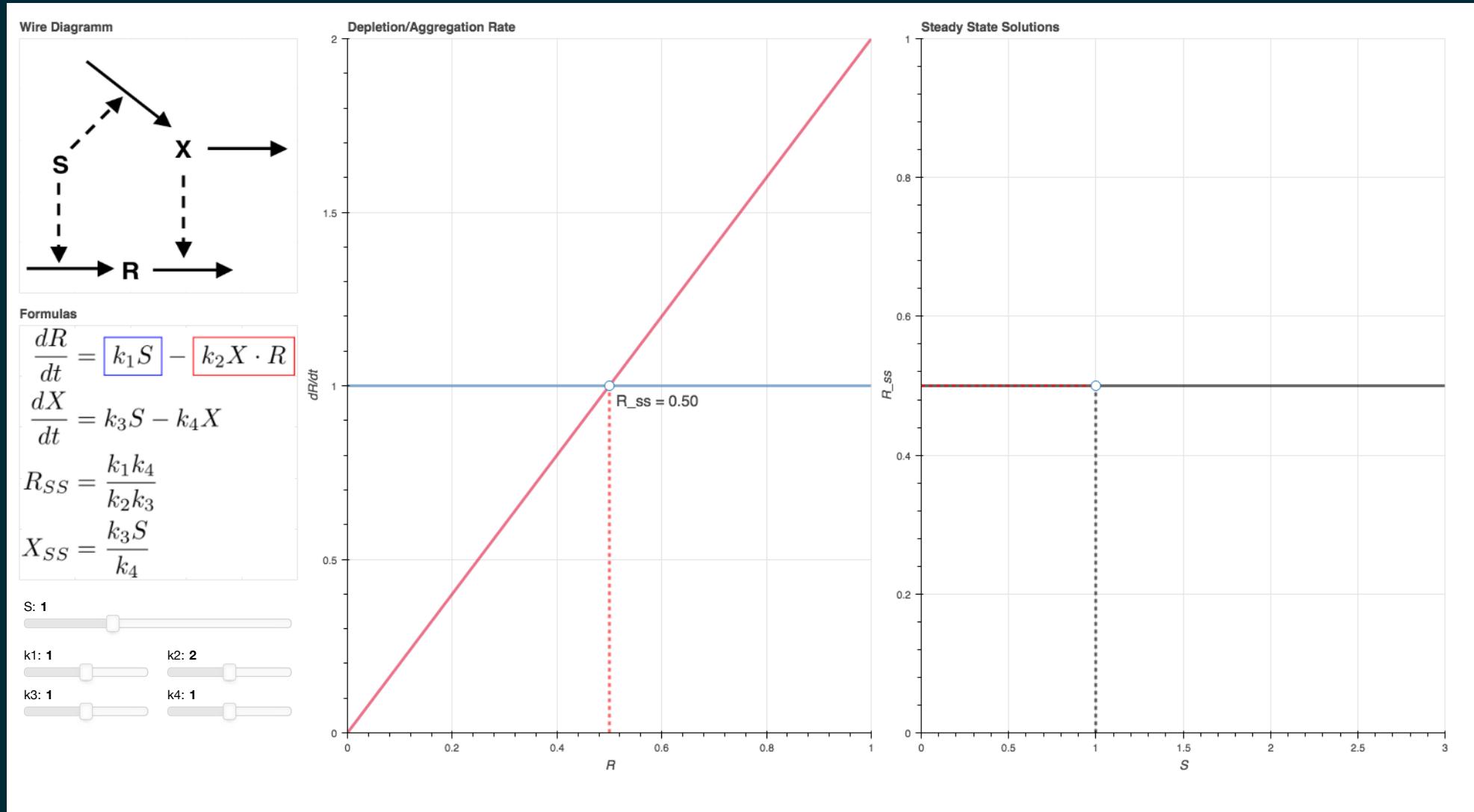
$$\frac{dR}{dt} = k_1 S - k_2 X \cdot R$$

$$\frac{dX}{dt} = k_3 S - k_4 X$$

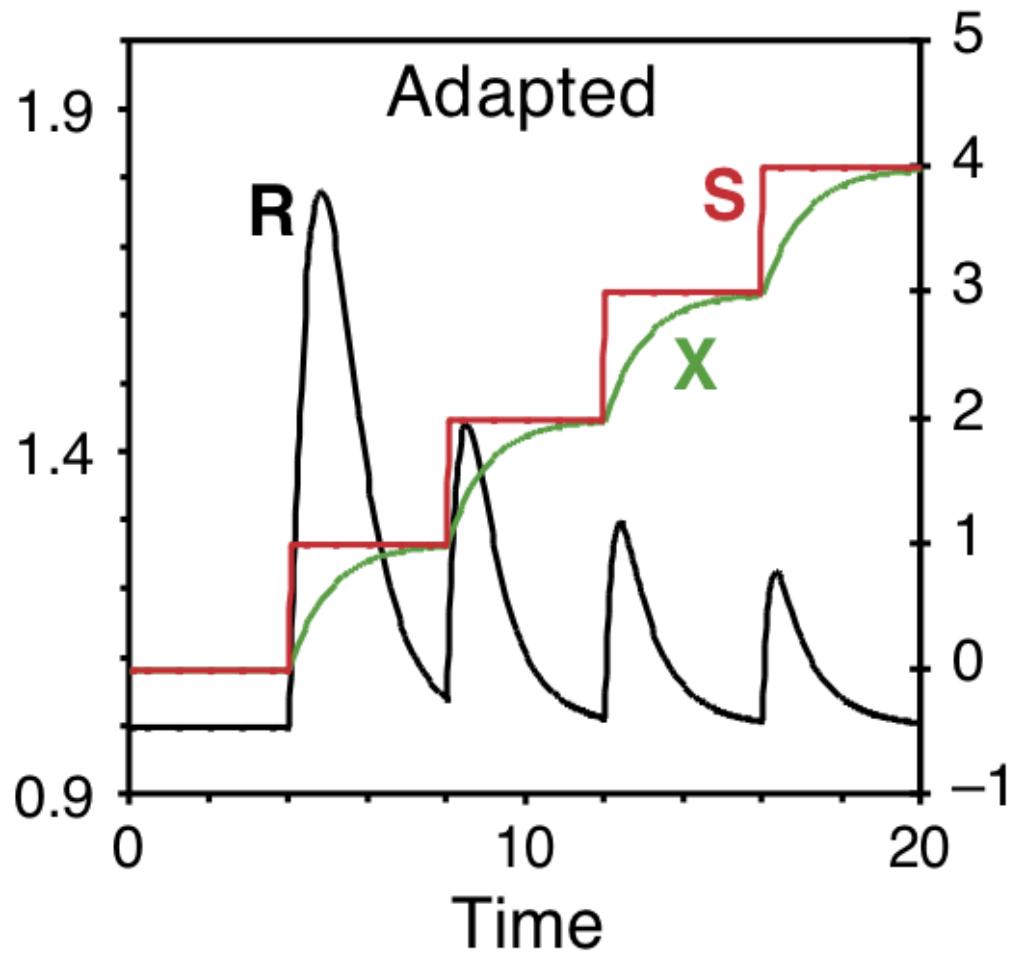
$$R_{SS} = \frac{k_1 k_4}{k_2 k_3}$$

$$X_{SS} = \frac{k_3 S}{k_4}$$

SNIFFER



SNIFFER



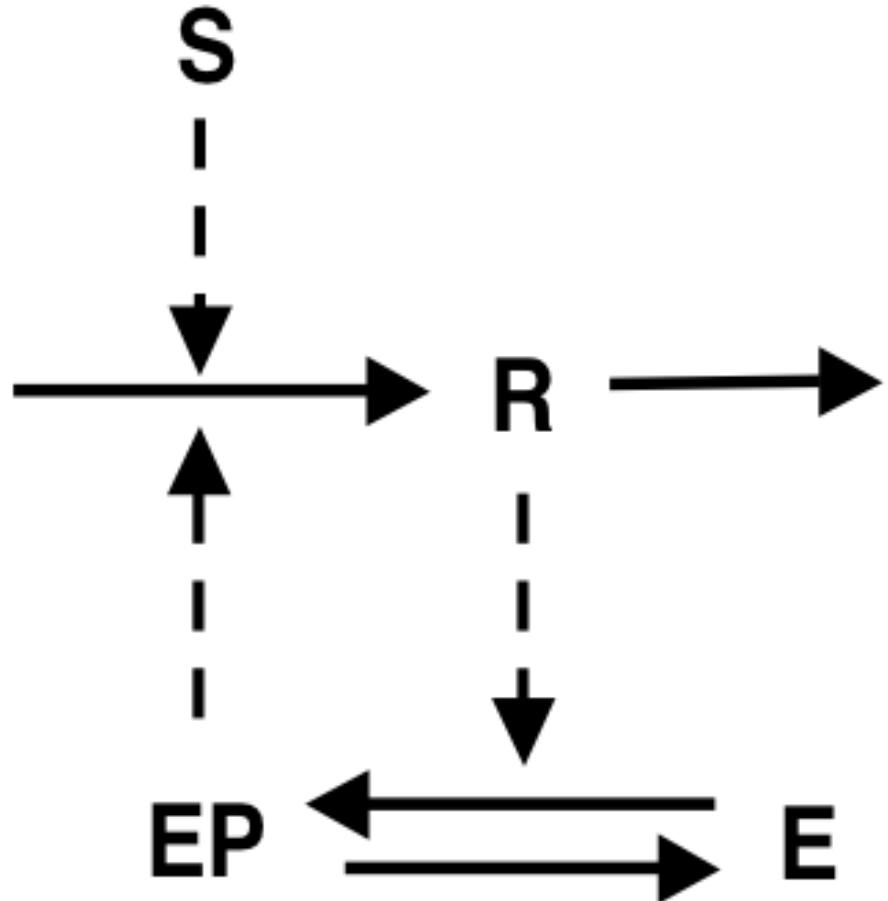
$$\frac{dR}{dt} = k_1 S - k_2 X \cdot R$$

$$\frac{dX}{dt} = k_3 S - k_4 X$$

$$R_{SS} = \frac{k_1 k_4}{k_2 k_3}$$

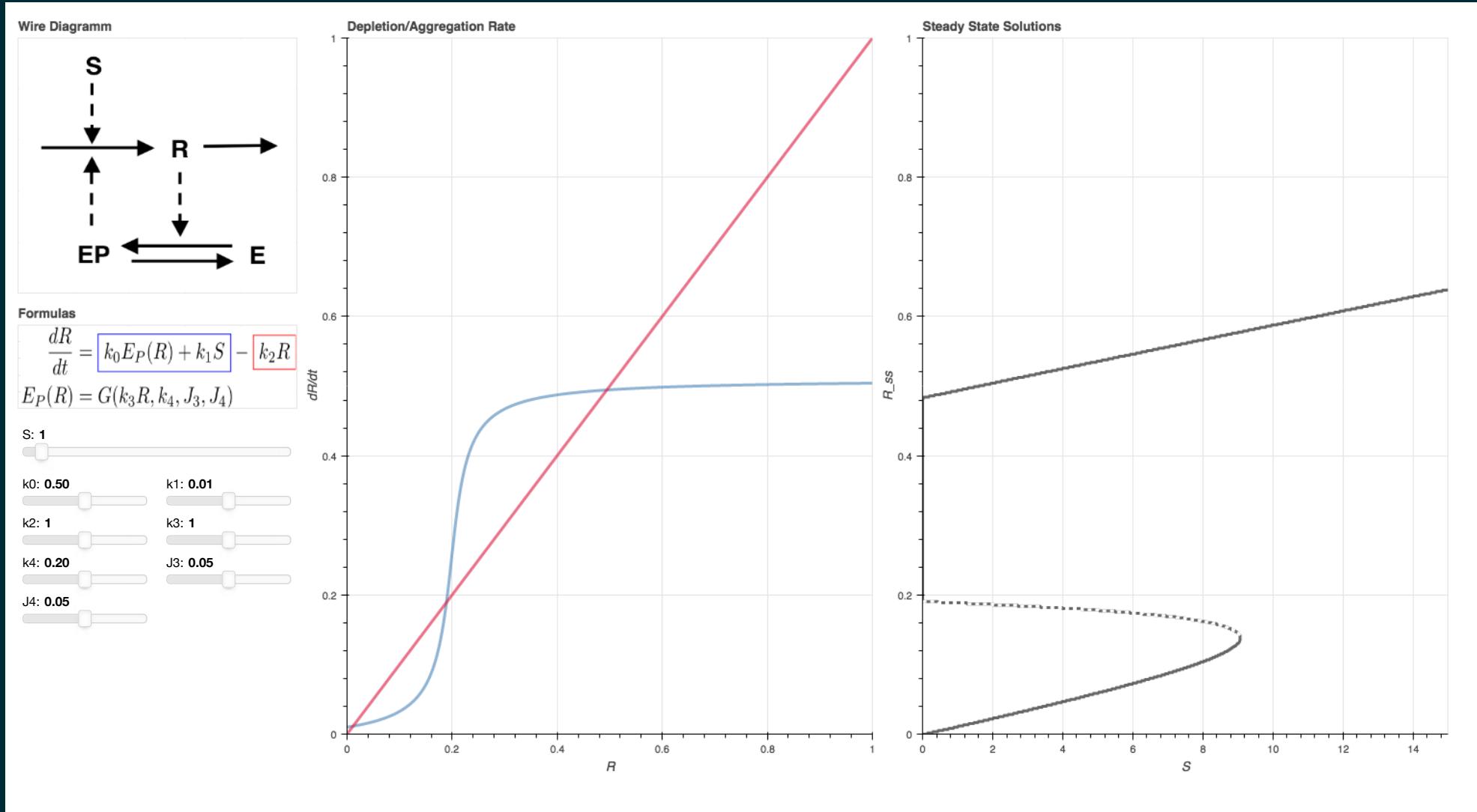
$$X_{SS} = \frac{k_3 S}{k_4}$$

IRREVERSIBLE SWITCH



$$\frac{dR}{dt} = [k_0 E_P(R) + k_1 S] - [k_2 R]$$
$$E_P(R) = G(k_3 R, k_4, J_3, J_4)$$

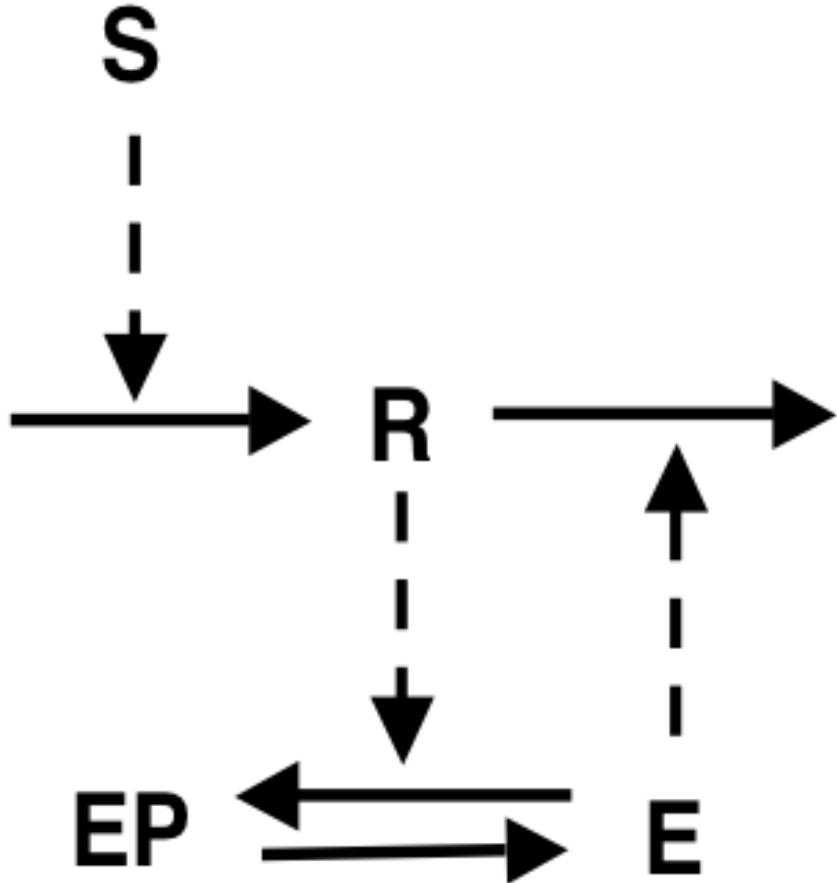
IRREVERSIBLE SWITCH



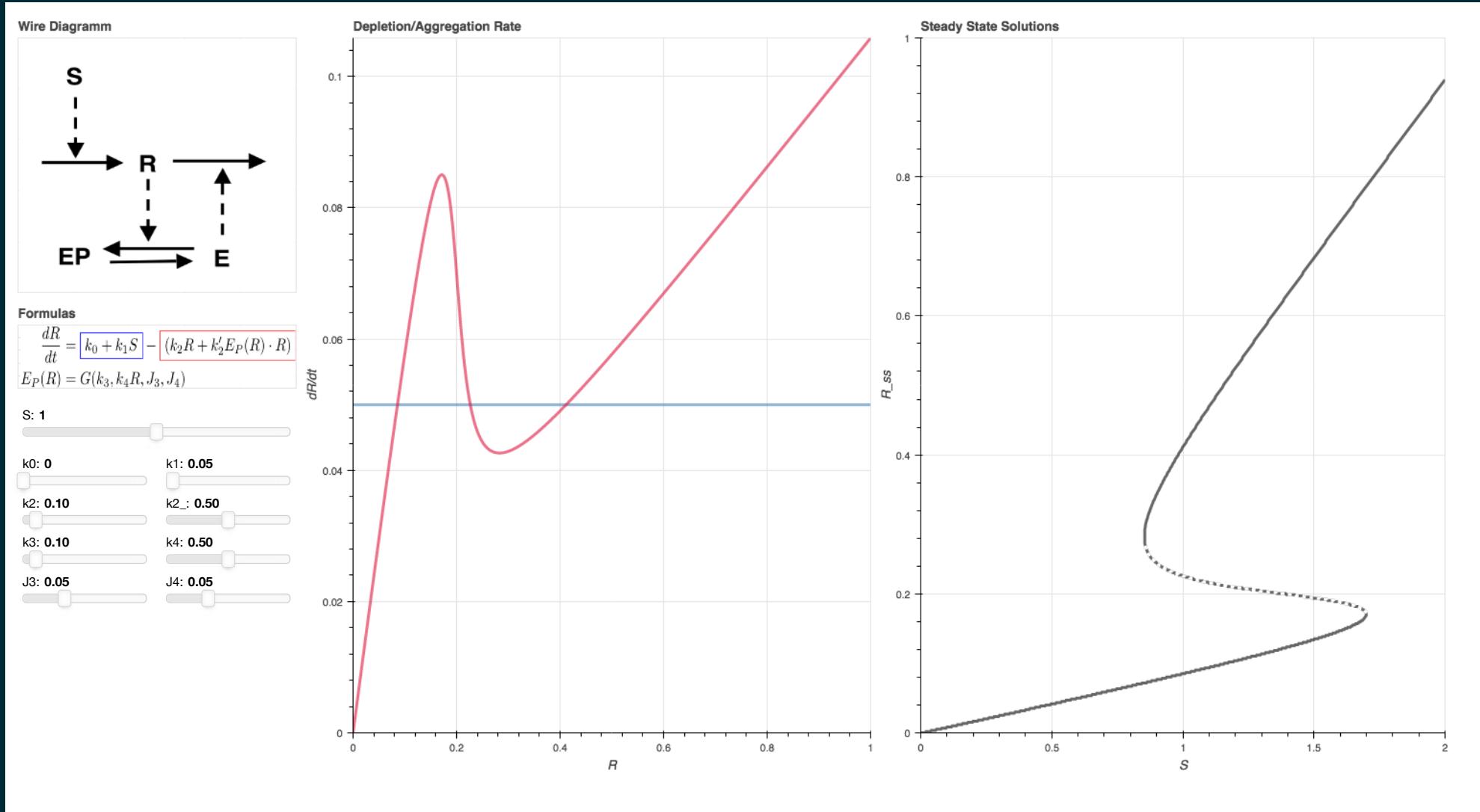
REVERSIBLE SWITCH

$$\frac{dR}{dt} = [k_0 + k_1 S] - [(k_2 R + k'_2 E_P(R) \cdot R)]$$

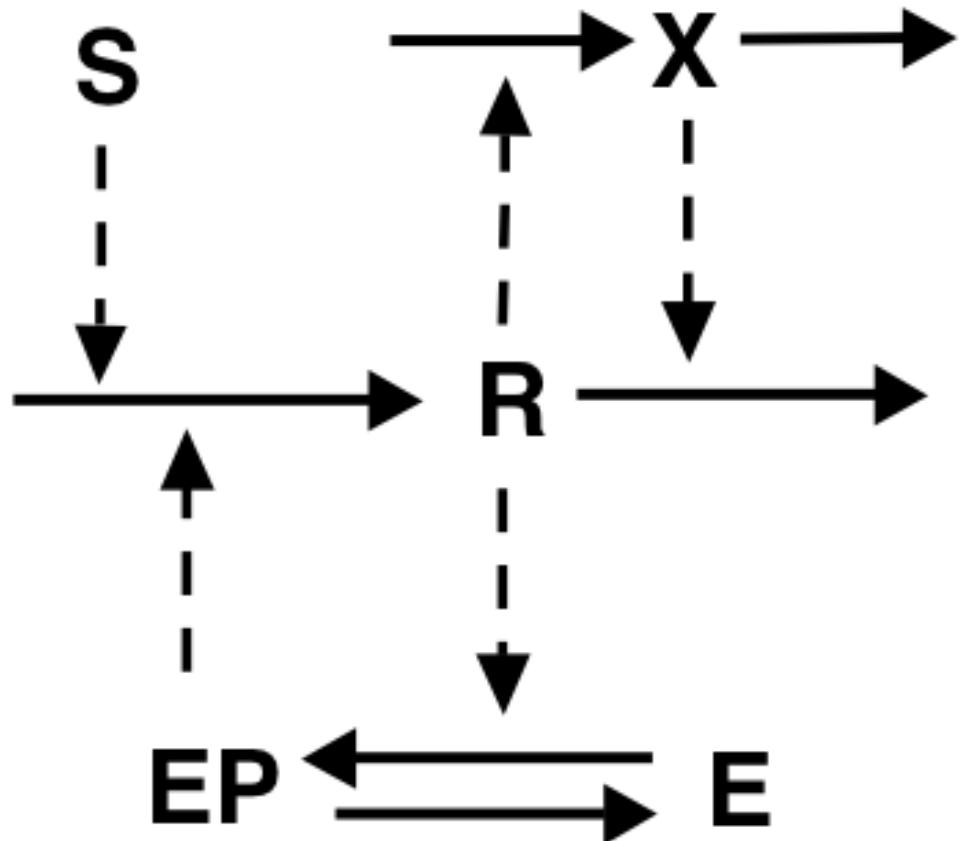
$$E_P(R) = G(k_3, k_4 R, J_3, J_4)$$



REVERSIBLE SWITCH



POSITIVE FEEDBACK OSCILLATOR

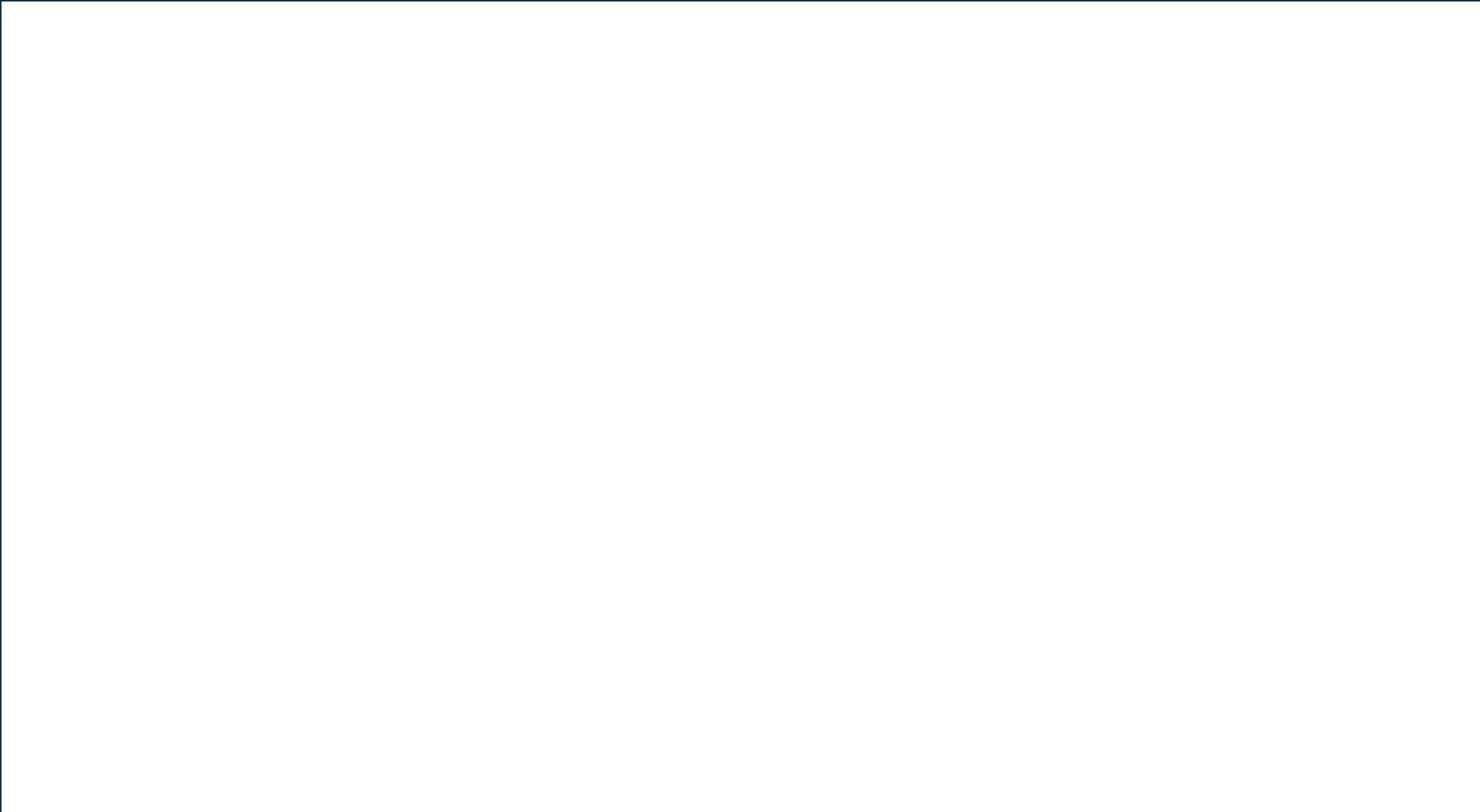


$$\frac{dR}{dt} = k_0 E_P(R) + k_1 S - k_2 R - k'_2 X \cdot R$$

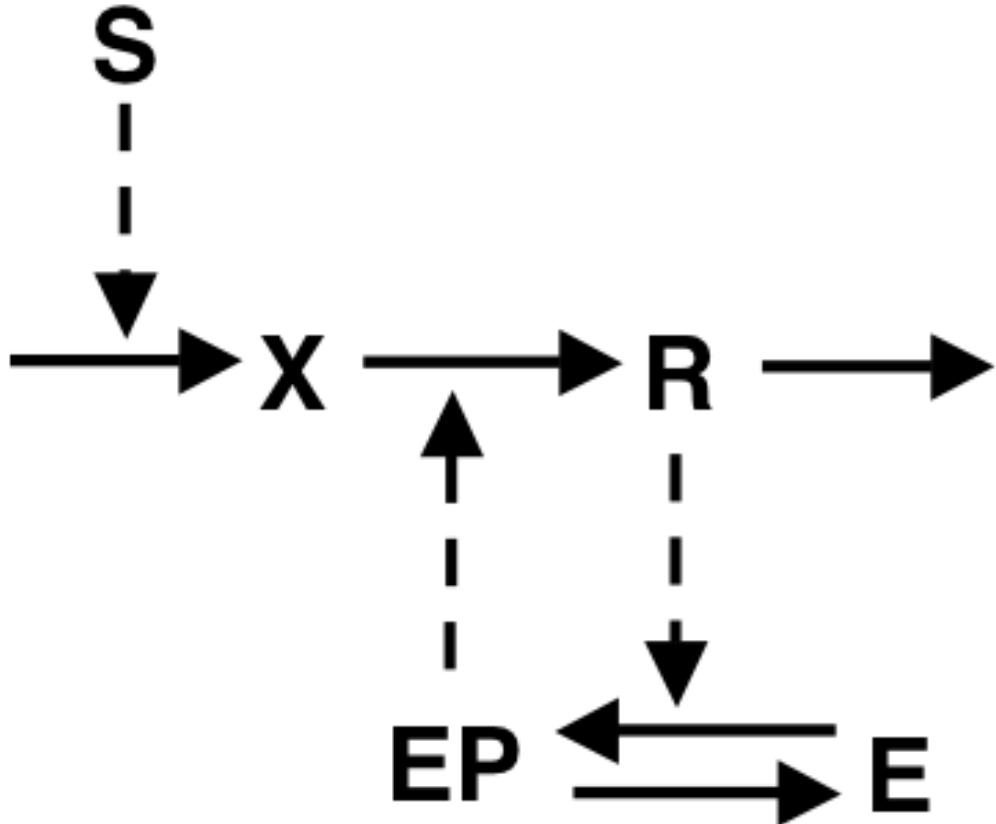
$$\frac{dX}{dt} = k_5 R - k_6 X$$

$$E_P(R) = G(k_3 R, k_4, J_3, J_4)$$

POSITIVE FEEDBACK OSCILLATOR



NEGATIVE FEEDBACK OSCILLATOR



$$\frac{dR}{dt} = [k'_0 + k_0 E_P(R)] \cdot X - k_2 R$$

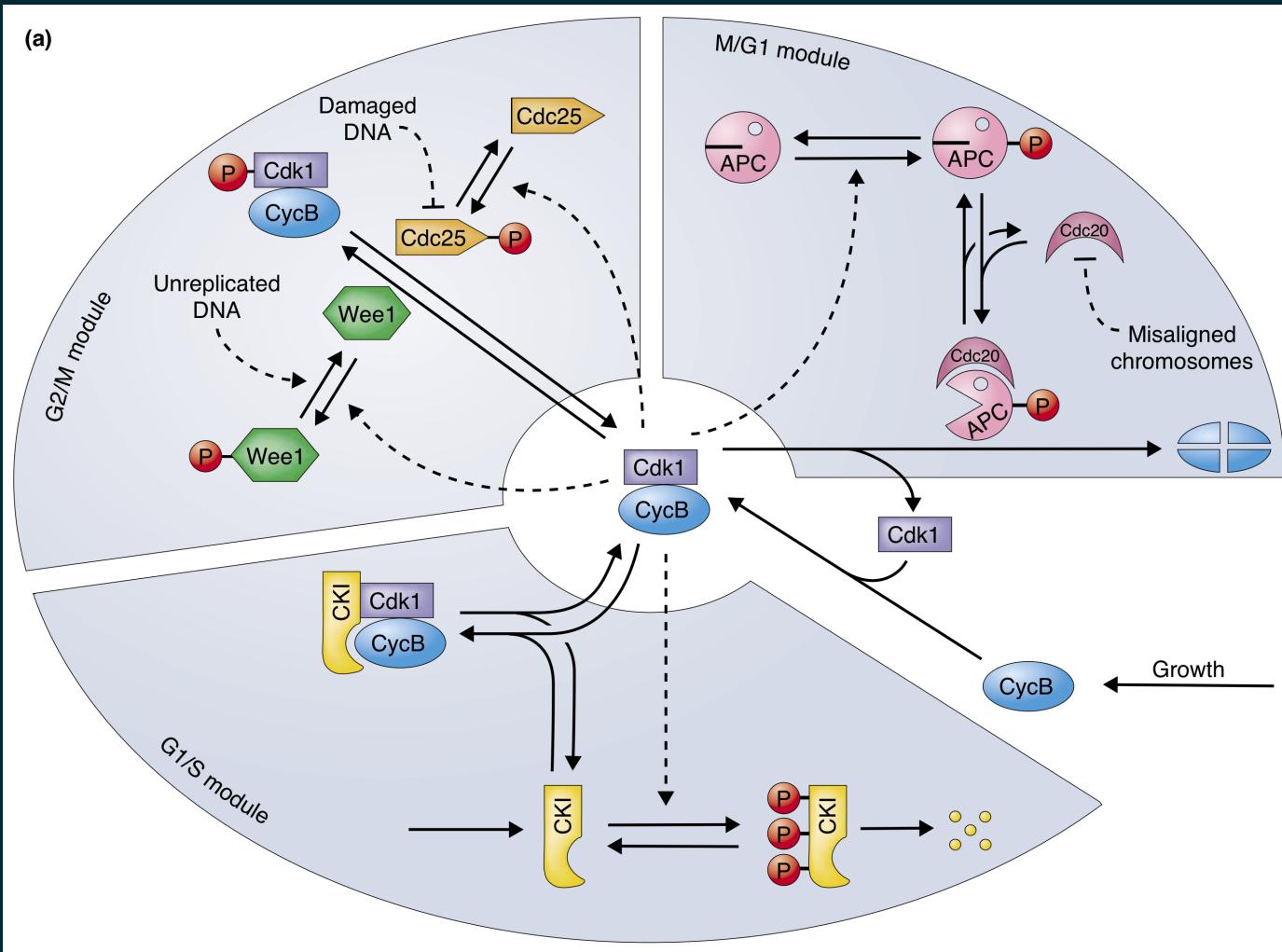
$$\frac{dX}{dt} = k_1 S - [k'_0 + k_0 E_P(R)] \cdot X$$

$$E_P(R) = G(k_3 R, k_4, J_3, J_4)$$

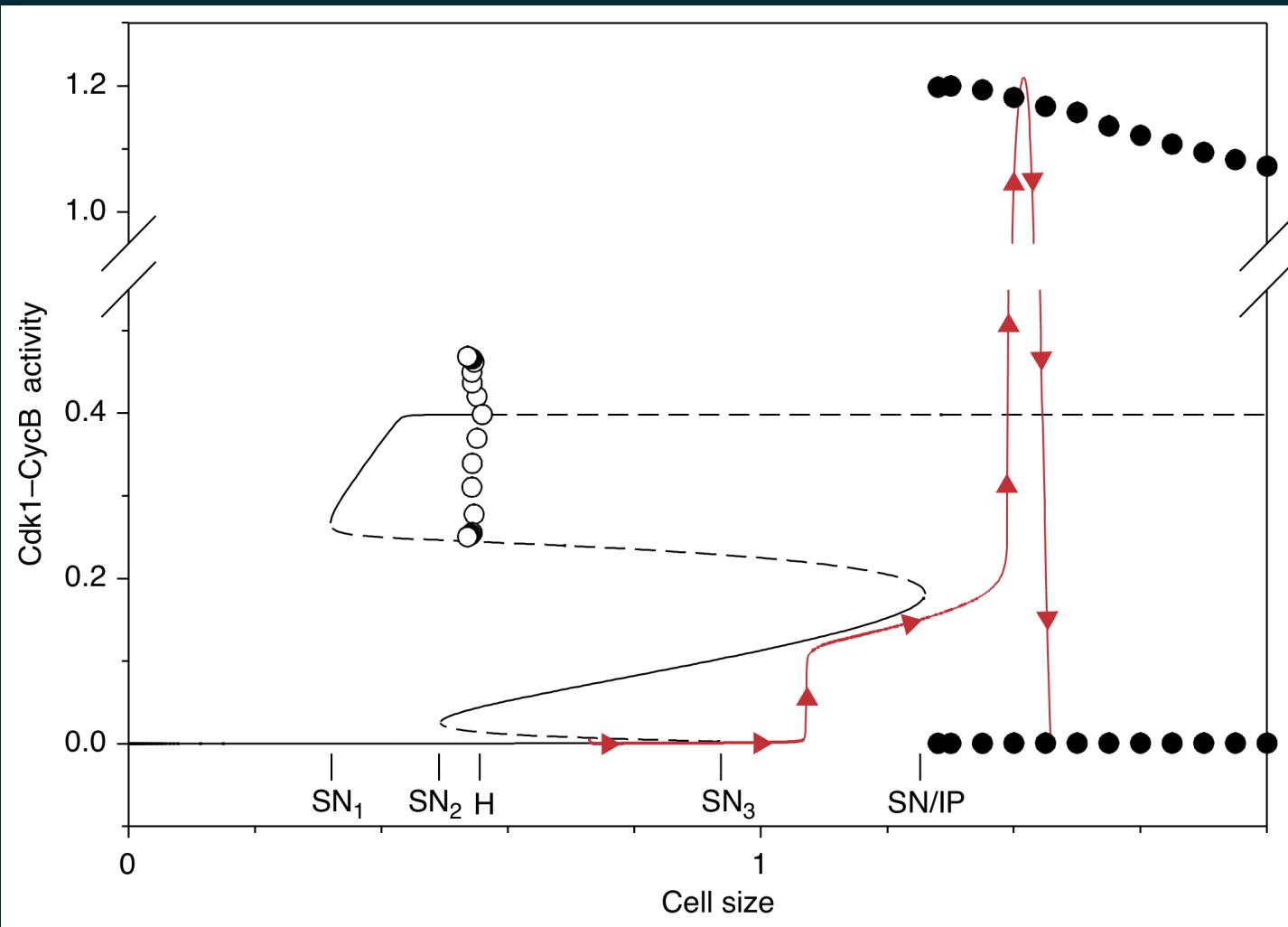
NEGATIVE FEEDBACK OSCILLATOR

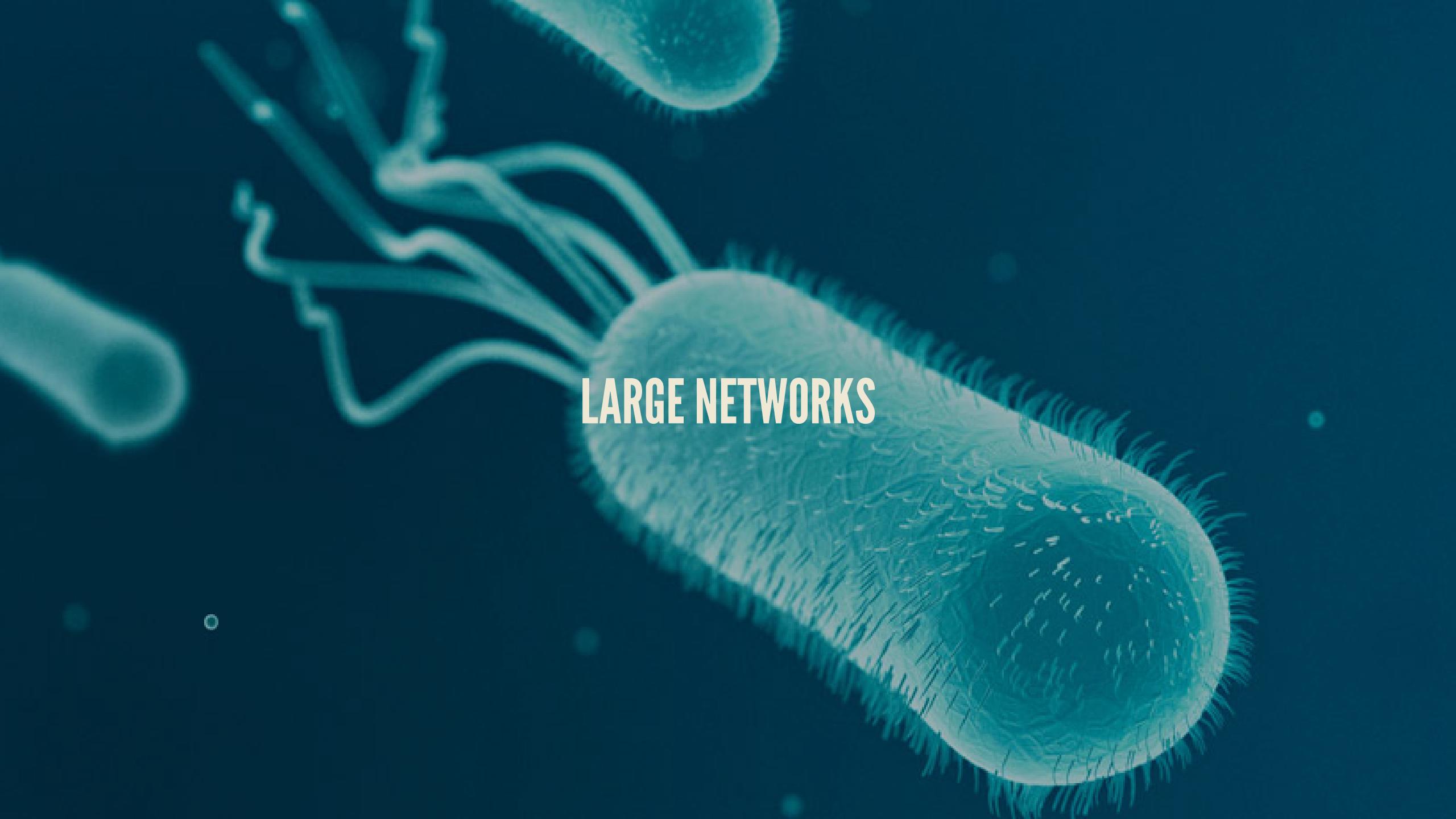


LARGE NETWORK EXAMPLE



LARGE NETWORK EXAMPLE

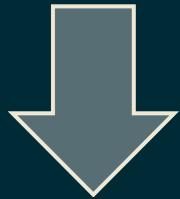




LARGE NETWORKS

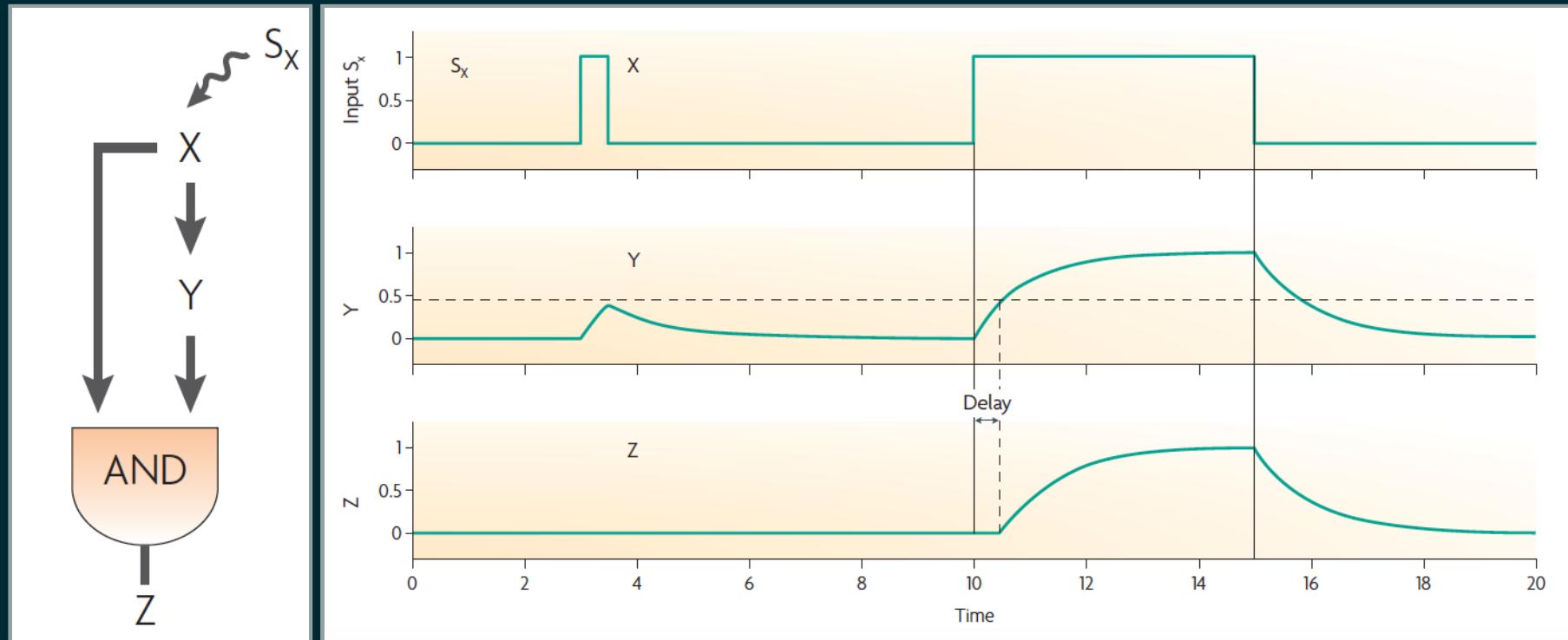
LOGIC OPERATORS

There are different ways how X and Y can be integrated to regulate the Z promoter

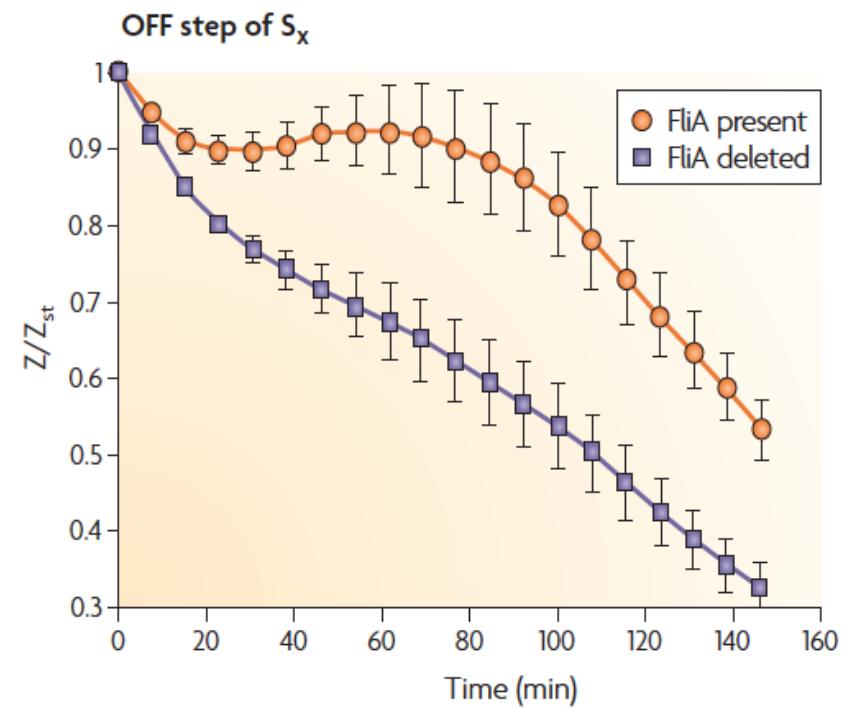
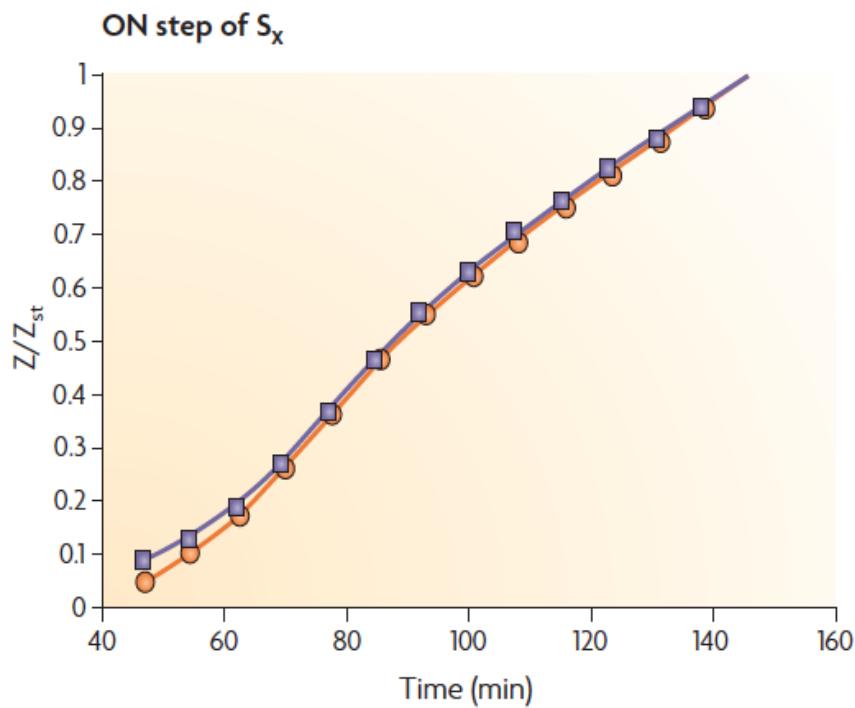
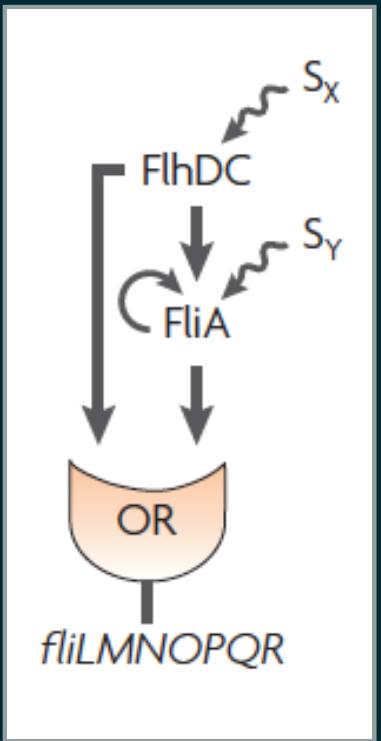


Two common input functions are the **AND** gate and **OR** gate.

AND GATE



OR GATE



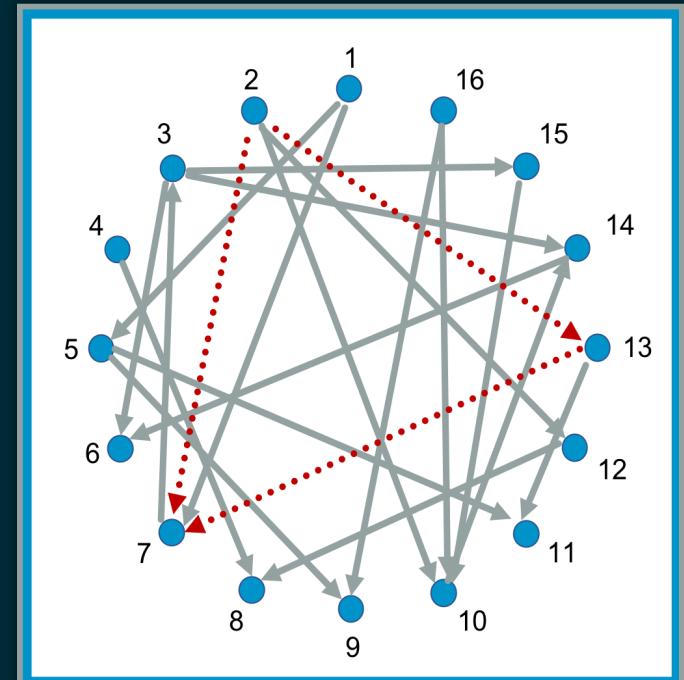
DETECTION OF NETWORK MOTIFS

Theoretically and Experimentally

FINDING NETWORK MOTIFS THEORETICALLY

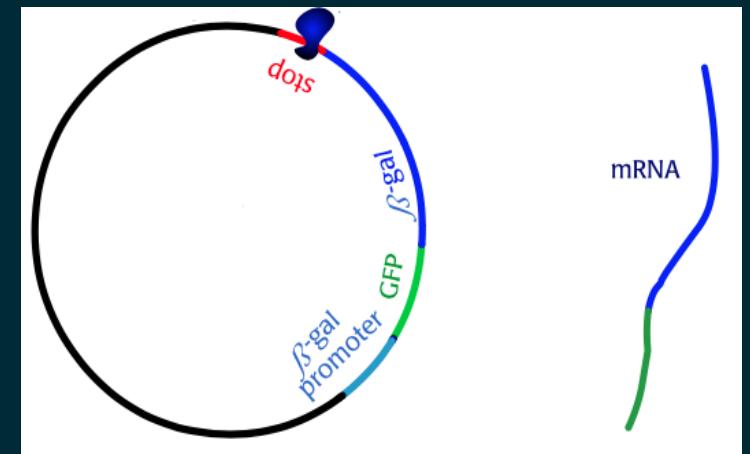
Algorithm to detect network motifs:

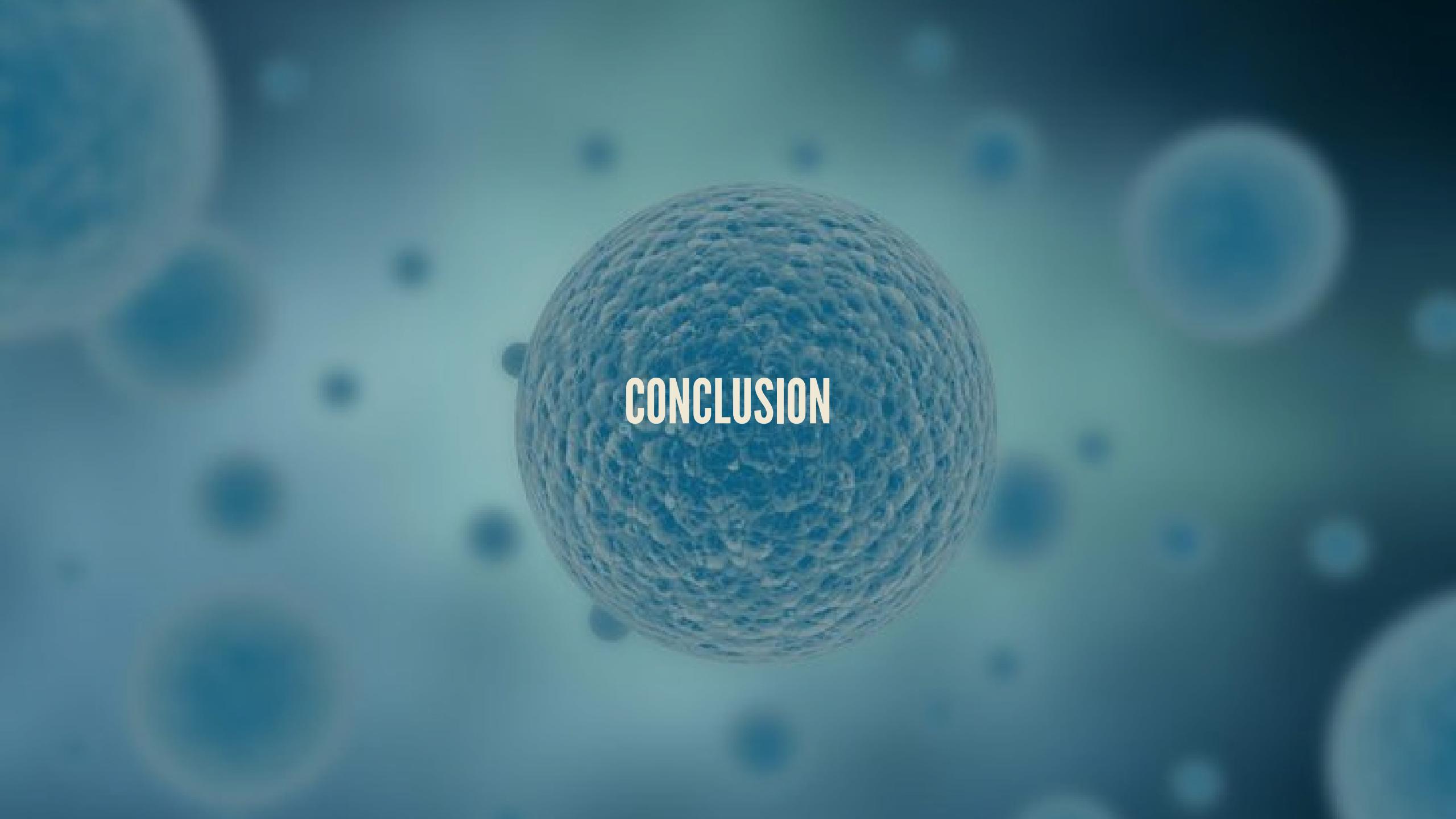
- Create a network with same number of nodes as the real network
- Assign the same number of incoming and outgoing edges to each node as has the corresponding node in the real network
- Scan network for all possible n-node subgraphs and record the number of occurrences of each subgraph
- Compare probabilities → cut-off probability



STUDY NETWORK MOTIFS EXPERIMENTALLY

- Measure the transcriptional activity of promoters by means of reporter genes
- Widely used: Green Fluorescent Protein (GFP)
- Promoter activation is detected by increased fluorescent signal
- Fast-folding GFP variants become fluorescent within minutes after transcription initiation





CONCLUSION

CONCLUSION

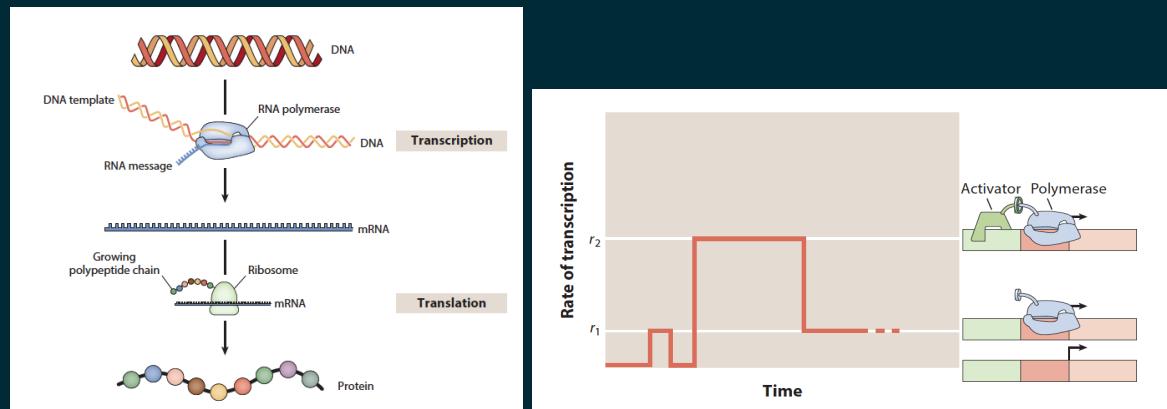
- Complex biological networks contain a limited set of network motifs
- Networks can be broken down into smaller understandable motifs
- Certain network motifs have been selected again and again in evolution
- Mathematical modeling has helped to define functions of network motifs
- How do network motifs work in large networks?
- Further research on other networks

THANK YOU FOR LISTENING!

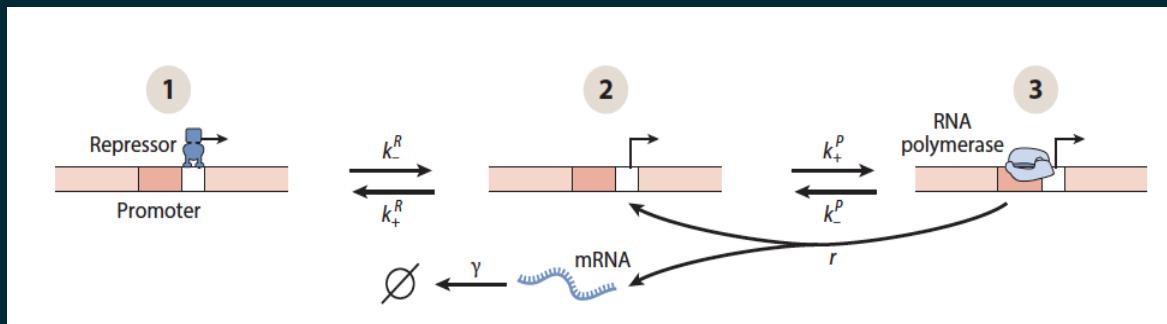
LITERATURE

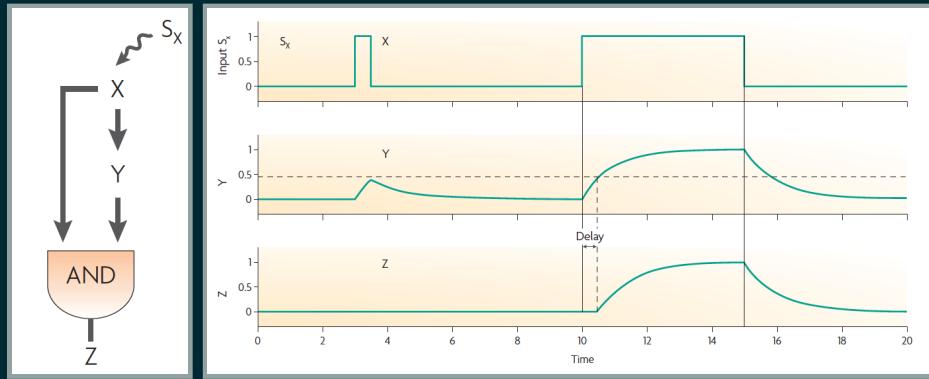
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PICTURES

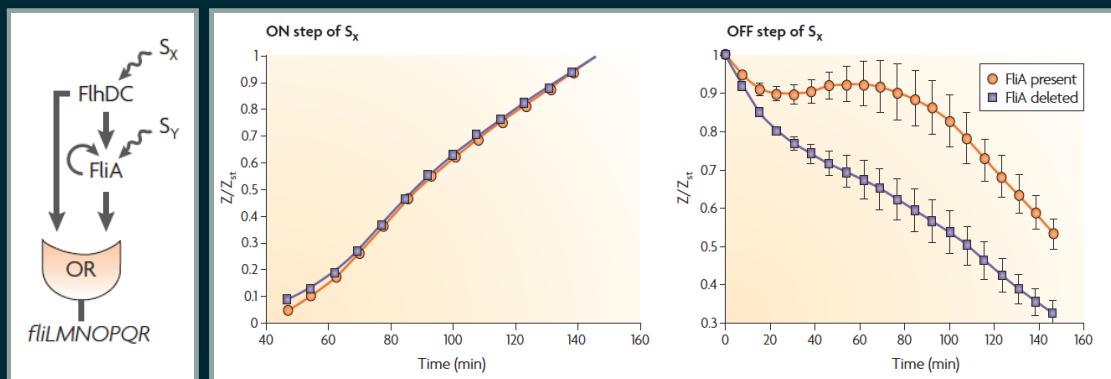


Phillips, Rob. "Napoleon is in equilibrium." *Annu. Rev. Condens. Matter Phys.* 6.1 (2015): 85-111.





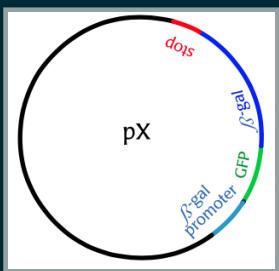
Alon, Uri. "Network motifs: theory and experimental approaches." *Nature Reviews Genetics* 8.6 (2007): 450



- [https://www.gettyimages.de/-video/green-jellyfish?
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popular&offlinecontent=include&phrase=green-%20jellyfish



- <http://www.dnabtb.org/34/problem.html>



- <http://tracks.arte.tv/fr/surveillance-deni-de-facies>



- <https://www.utahpeoples-post.com/2016/10/human-cell-atlas/>



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