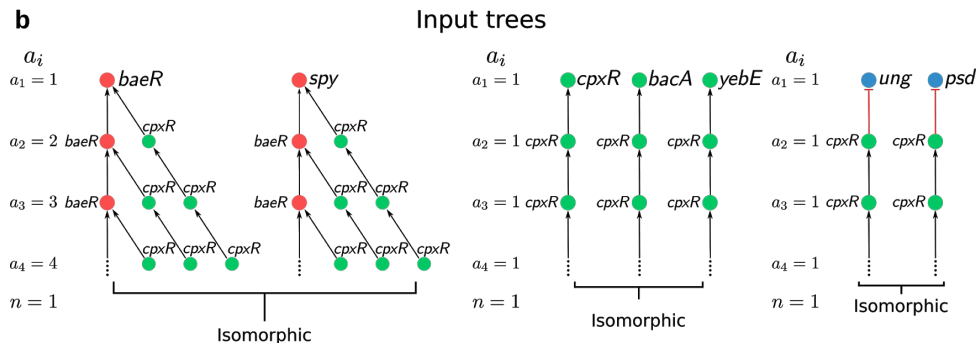
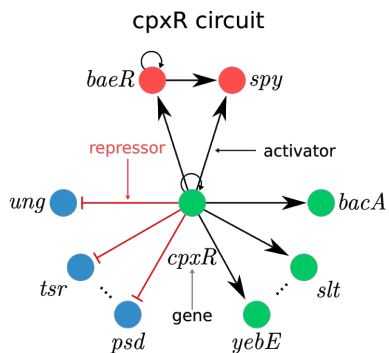

Fibration symmetries uncover the building blocks of biological networks

— Ian Leifer, Flaviano Morone, —
Hernan Makse

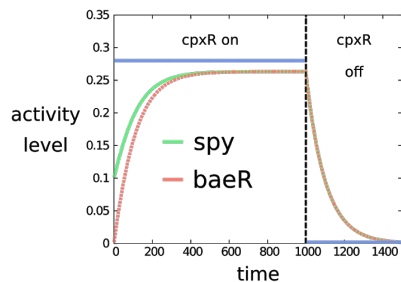
Introduction

- Decomposing systems into building blocks provides a great way to study them
- Symmetry considerations provide a way to find building blocks in real large-scale networks
- The way building blocks function and interact can shed some light on how the complex behavior in networks emerges
- Here we talk about applications to transcriptional regulatory networks and use examples from bacteria, but this can be applied to any directed network

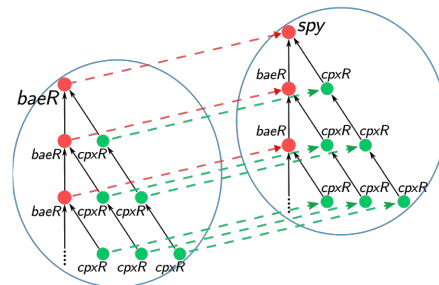
Methods. Input-trees, fibers, branching ratios, synchronization



Synchronization



Isomorphism

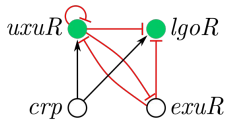
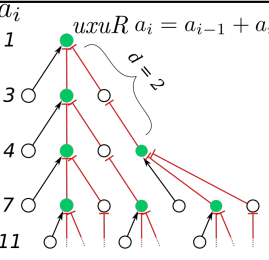
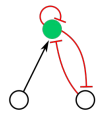
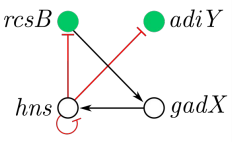
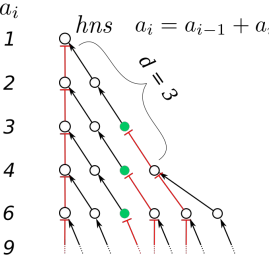
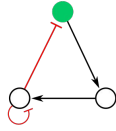


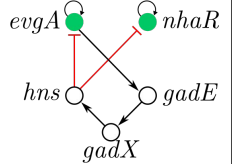
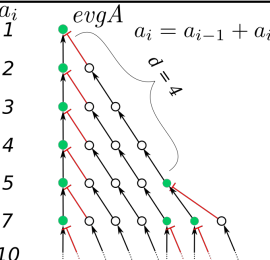
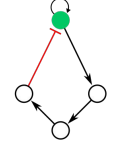
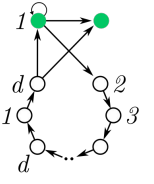
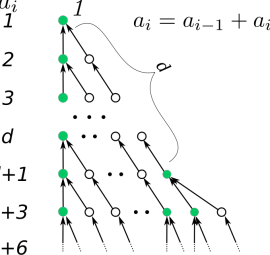
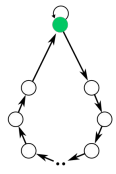
Building blocks. Integer branching ratios

| $ n, \ell\rangle$ | Genetic circuit | Input tree | Base |
|-------------------|-----------------|-------------------------------------|------|
| $ 0, 1\rangle$ | | a_i 1 $a_{1,2} = 1$ | |
| $ 0, 2\rangle$ | | a_i 1 $a_1 = 1$ $a_2 = 2$ | |
| $ 0, 3\rangle$ | | a_i 1 $a_1 = 1$ $a_2 = 3$ | |

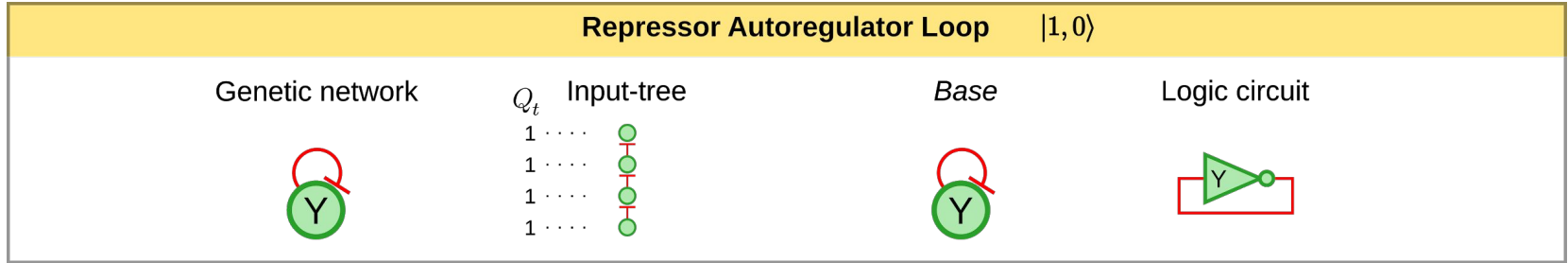
| $ n, \ell\rangle$ | Genetic circuit | Input tree | Base |
|--------------------------|-----------------|---|------|
| $ 2, 1\rangle$ | | a_i 1 $a_1 = 1$ $a_{i>2} = 3 * 2^{i-1}$ | |
| $ n \geq 3, \ell\rangle$ | | $a_1 = 1$ $a_{i>2} = (n + l) * n^{i-1}$ | |

Building blocks. Fibonacci branching ratios

| $ \varphi_d, \ell\rangle$ | Genetic circuit | Input tree | Base |
|---------------------------|---|---|---|
| $ 1.6180\dots, 2\rangle$ |  <p>2-Fibonacci Fiber (2-FF)</p> |  <p>a_i 1 3 4 7 11</p> <p>$urxR$ $a_i = a_{i-1} + a_{i-2}$ $d=2$</p> |  |
| $ 1.4655\dots, 1\rangle$ |  <p>3-Fibonacci Fiber (3-FF)</p> |  <p>a_i 1 2 3 4 6 9</p> <p>hns $a_i = a_{i-1} + a_{i-3}$ $d=3$</p> |  |

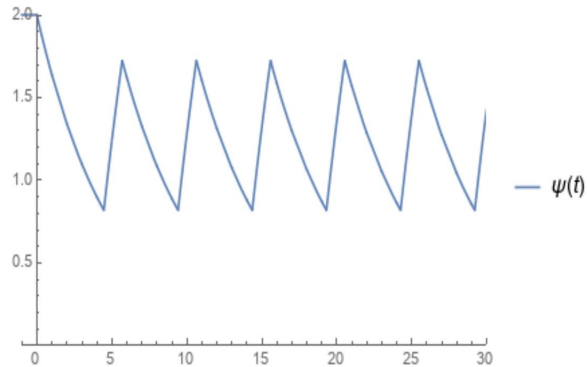
| $ \varphi_d, \ell\rangle$ | Genetic circuit | Input tree | Base |
|---------------------------|---|--|---|
| $ 1.3802\dots, 1\rangle$ |  <p>4-Fibonacci Fiber (4-FF)</p> |  <p>a_i 1 2 3 4 5 7 10</p> <p>$evgA$ $a_i = a_{i-1} + a_{i-4}$ $d=4$</p> |  |
| $ \varphi_d, \ell\rangle$ |  <p>d-Fibonacci Fiber (d-FF)</p> |  <p>a_i 1 2 3 \dots d $d+1$ $d+3$ $d+6$</p> <p>1 $a_i = a_{i-1} + a_{i-d}$ d</p> |  |

Analogy to electronic circuits (clock)



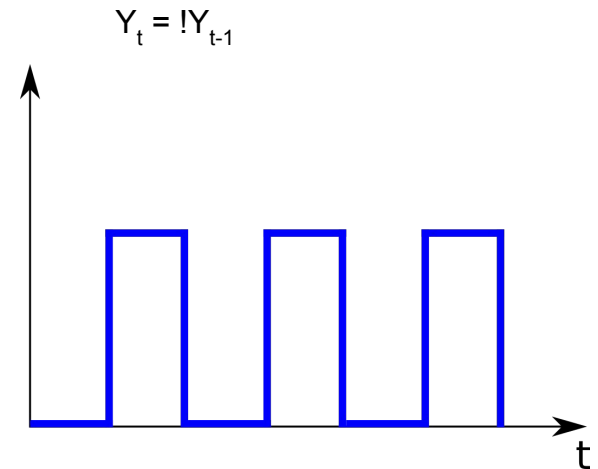
Continuous model

$$\dot{\psi} = -\alpha\psi(t) + \delta \theta(1 - \psi(t - \tau))$$

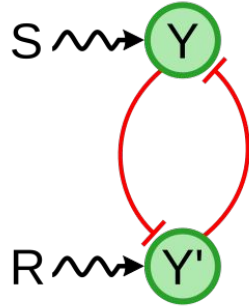


Boolean model

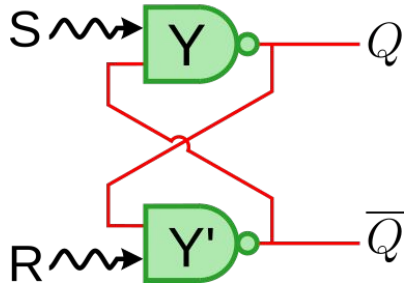
| t | Y_t |
|---|-------|
| 0 | 1 |
| 1 | 0 |
| 2 | 1 |
| 3 | 0 |
| 4 | 1 |



Analogy to electronic circuits (memory)



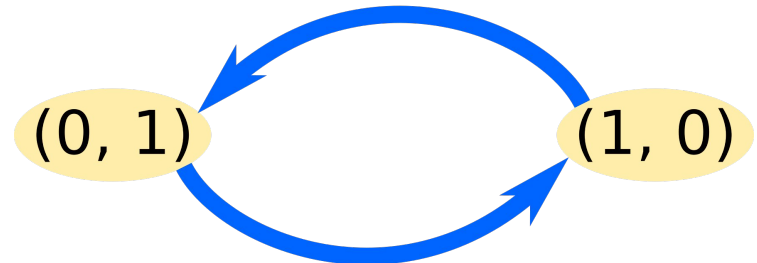
SR flip-flop



State map



$S = 1, R = 0$



$S = 0, R = 1$



Conclusions

- Fibration symmetry is a type of symmetry that can provide the way to analyze biological (or any other directed) network
- Symmetries of the network help uncover new functional building blocks related to synchronization
- This provides a theoretically principled and algorithmically supported strategy to search for computational building blocks in biological networks

Further reading:
Morone, Leifer, Makse, PNAS (2020)
Leifer, et al. Plos. Comp. bio (2020)

Algorithm availability:
<https://github.com/ianleifer/fibrationSymmetries>
<https://github.com/makselab>