lecture 10 **H** ETACL SCHOOLS đ F S bit.ly/atBIC

biologically-inspired computing

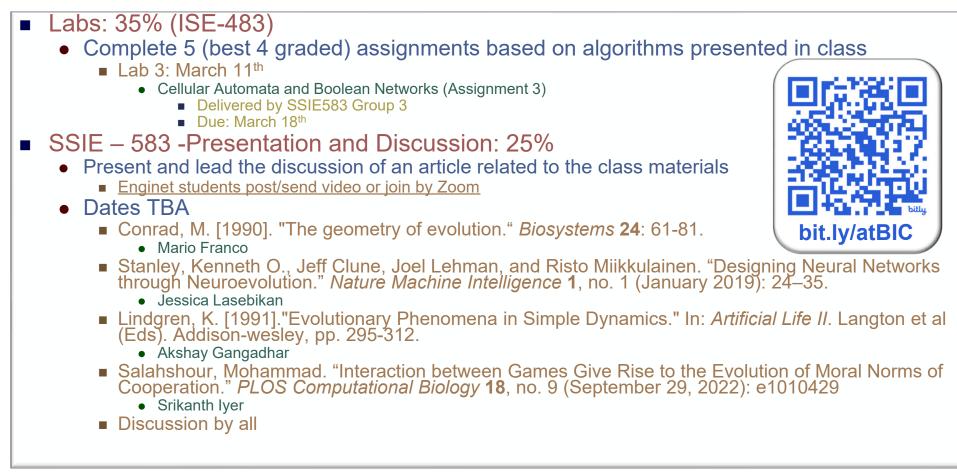
course outlook

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key events coming up



readings

until now **Class Book** Floreano, D. and C. Mattiussi [2008]. *Bio-Inspired Artificial Intelligence: Theories, Methods, and Technologies*. MIT Press. • Preface, Chapter 2. Nunes de Castro, Leandro [2006]. *Fundamentals of Natural Computing: Basic Concepts, Algorithms, and Applications*. Chapman & Hall. **Chapter 1**, pp. 1-23. Chapter 7, sections **7.1-7.4**, **Appendix B.3.1**, **Chapter 2**, Chapter 8, sections **8.1**, **8.2**, **8.3.10** Lecture notes Chapter 1: What is Life? Chapter 2: The logical Mechanisms of Life Chapter 3: Formalizing and Modeling the World Chapter 4: Self-Organization and Emergent Complex Behavior posted online @ http://informatics.indiana.edu/rocha/i-bic Papers and other materials Dynamical Systems Kauffman, S.A. [1969]. "Metabolic stability and epigenesis in randomly constructed genetic nets". Journal of Theoretical Biology 22(3):437-467. Optional Prusinkiewicz and Lindenmeyer [1996] The algorithmic beauty of plants. Chapter 1 Flake's [1998], The Computational Beauty of Life. MIT Press. Chapters 10, 11, 14 – Dynamics, Attractors and chaos BINGHAMTON

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final project schedule

Projects Due by May 6th in Brightspace, "Final Project Paper" assignment ALIFE 2023 Not to submit to actual conference due date (April 3rd, 2024) <u>https://2024.alife.org/</u> 8 pages, author guidelines: <u>https://2024.alife.org/call_paper.html</u> MS Word and Latex/Overleaf templates Preliminary ideas <u>by March 15</u> Submit to "Project Idea" assignment in Brightspace. Individual or group With very definite tasks assigned per member of group

ALIFE 2024

Tackle a real problem using bio-inspired algorithms, such as those used in the labs.



The 2024 Conference on Artificial Life

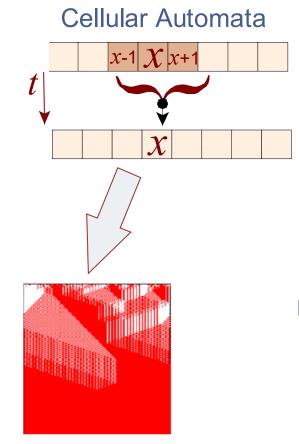
Copenhagen, Denmark | July 22-26, 2024

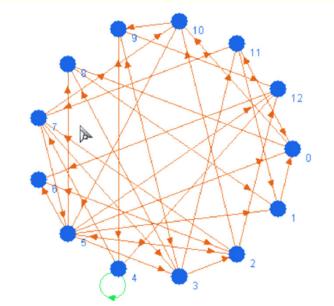


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discrete dynamical systems

examples





NK Boolean Network (N=13, K=3)

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dynamical models of regulation from qualitative data

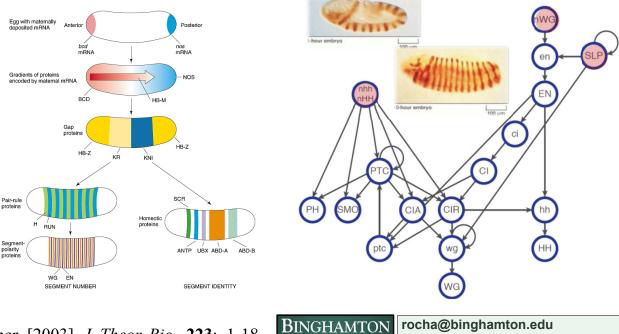
the drosophila segment polarity network



Based on the ODE model of von Dassow et al. (2000), consists of 4-cell parasegments, each cell with 15 interacting genes and proteins. 2⁶⁰ network configurations

Reproduces wild-type and mutant gene expression patterns in development of fruit fly 2 intercellular inputs: **nhh** (*hedgehog*), **nWG** (*wingless*) 1 intracellular input: SLP (sloppy paired)

-		
	Node	State – TransitionFunction
	SLP_i^{t+1}	$\leftarrow 0 \text{ if } i=1 \lor i=2; 1 \text{ if } i=3 \lor i=4;$
	wg_i^{t+1}	$\leftarrow (\operatorname{CIA}_i^t \land \operatorname{SLP}_i^t \land \neg \operatorname{CIR}_i^t) \lor (wg_i^t \land (\operatorname{CIA}_i^t \lor \operatorname{SLP}_i^t) \land \neg \operatorname{CIR}_i^t)$
	WG_i^{t+1}	$\leftarrow wg_i^t$
	en_i^{t+1}	$\leftarrow (\mathbf{WG}_{i-1}' \lor \mathbf{WG}_{i+1}') \land \neg \mathbf{SLP}_i'$
	EN_i^{t+1}	$\leftarrow en_i^t$
	hh_i^{t+1}	$\leftarrow \mathbf{EN}_i^t \land \neg \mathbf{CIR}_i^t$
	HH_{i}^{t+1}	$\leftarrow hh_i^t$
	ptc_i^{t+1}	$\leftarrow \text{CIA}_i^t \land \neg \text{EN}_i^t \land \neg \text{CIR}_i^t$
	PTC_i^{t+1}	$\leftarrow ptc_i^t \lor (\operatorname{PTC}_i^t \land \neg \operatorname{HH}_{i-1}^t \land \neg \operatorname{HH}_{i-1}^t)$
	\mathbf{PH}_{i}^{t}	$\leftarrow \text{PTC}_i^t \land (\text{HH}_{i-1}^t \lor \text{HH}_{i+1}^t)$
	SMO_i^t	$\leftarrow \neg \text{PTC}_i^t \lor (\text{HH}_{i-1}^t \lor \text{HH}_{i+1}^t)$
	ci_i^{t+1}	$\leftarrow \neg \mathbf{EN}_i^t$
	$\operatorname{CI}_i^{t+1}$	$\leftarrow ci_i^t$
	CIA_i^{t+1}	$\leftarrow \mathbf{CI}_i^t \land (\neg \mathbf{PTC}_i^t \lor hh_{i-1}^t \lor hh_{i+1}^t \lor \mathbf{HH}_{i-1}^t \lor \mathbf{HH}_{i+1}^t)$
	$\operatorname{CIR}_{i}^{t+1}$	$\leftarrow \mathbf{CI}_{i}^{t} \land \mathbf{PTC}_{i}^{t} \land \neg hh_{i-1}^{t} \land \neg hh_{i+1}^{t} \land \neg \mathbf{HH}_{i-1}^{t} \land \neg \mathbf{HH}_{i+1}^{t}$



Albert & Othmer [2003]. J. Theor. Bio. 223: 1-18.

protein

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dynamical models of regulation from qualitative data

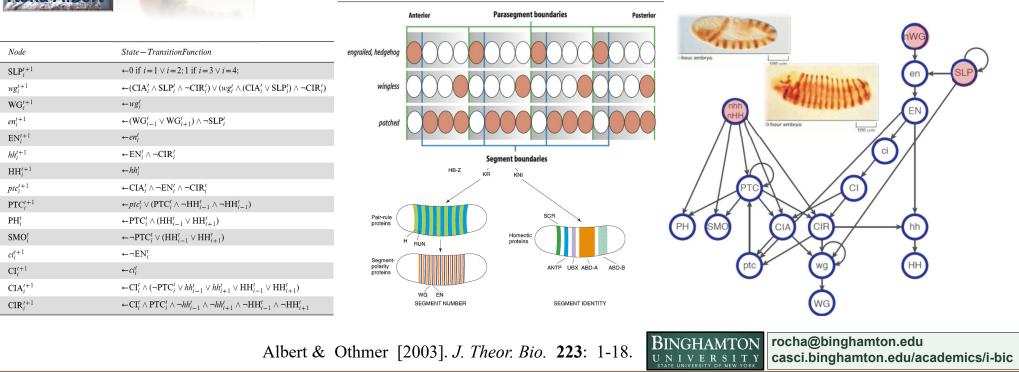
the drosophila segment polarity network



Based on the ODE model of von Dassow et al. (2000), consists of 4-cell parasegments, each cell with 15 interacting genes and proteins. **2**⁶⁰ **network configurations**

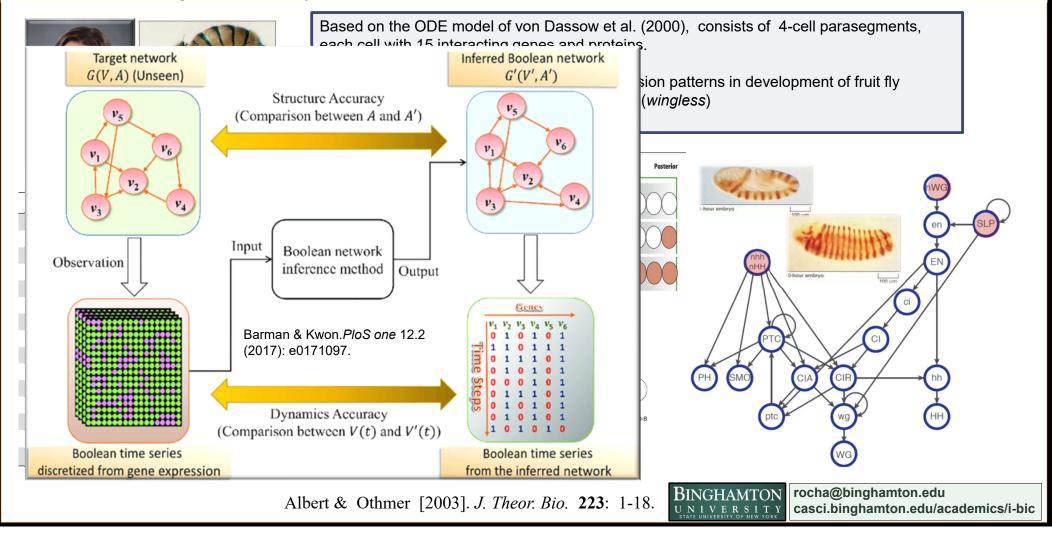
Reproduces wild-type and mutant gene expression patterns in development of fruit fly 2 intercellular inputs: **nhh** (*hedgehog*), **nWG** (*wingless*)

1 intracellular input: **SLP** (*sloppy paired*)



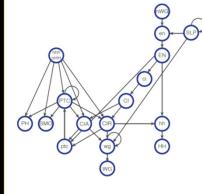
dynamical models of regulation from qualitative data

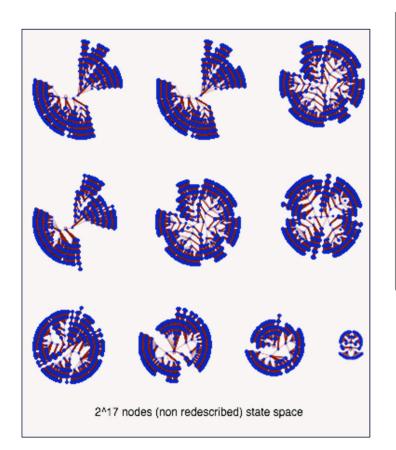
the drosophila segment polarity network



dynamical behavior

cell-types in a spatial arrangement





- Observing the state-transition graph
 converges to one of 10 possible stable configurations

 Steady-state attractors

 observed experimentally
 - wildtype
 - plus 3 variants
 - broad stripe
 - no-segmentation
 - Ectopic

B

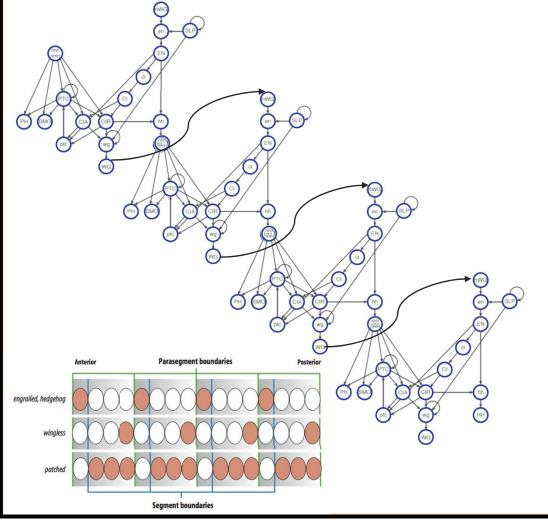
plus 3 variants

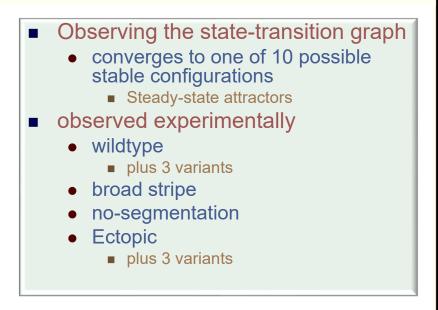
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dynamical behavior



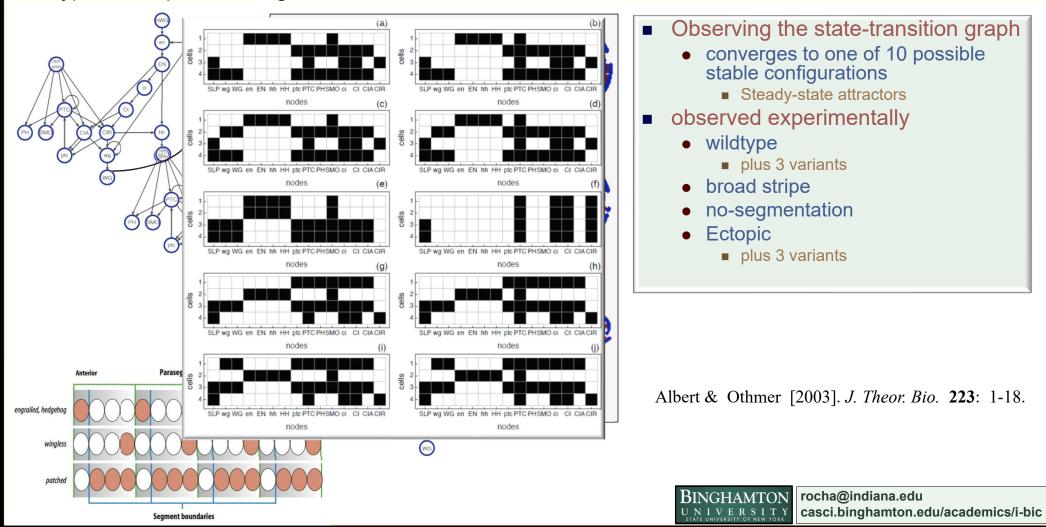




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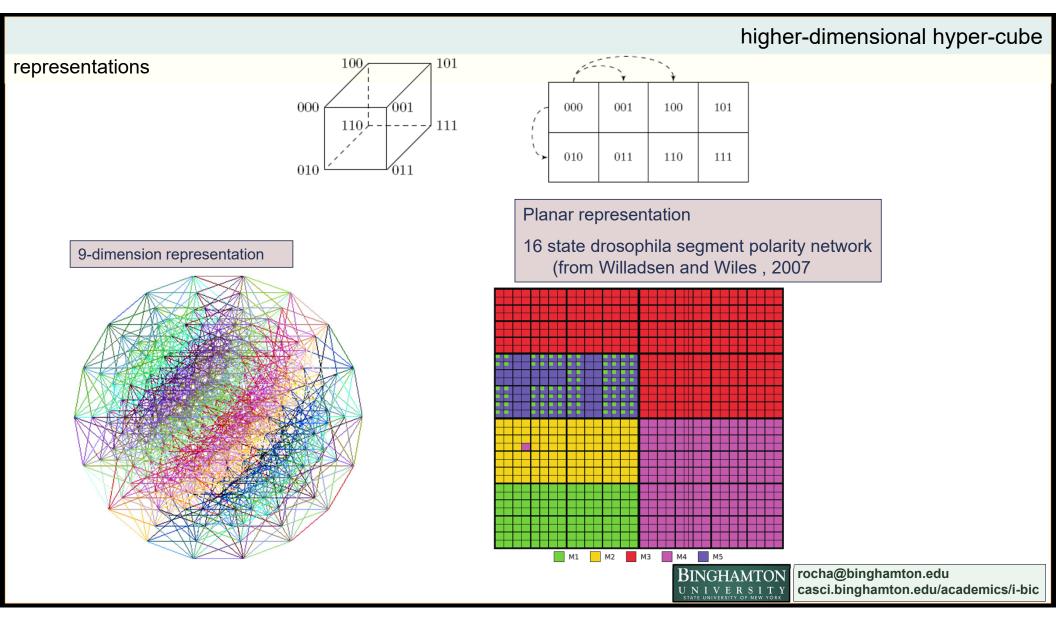
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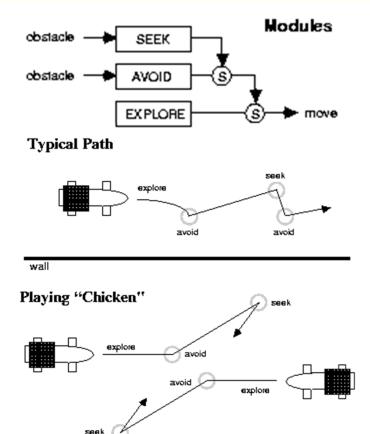
cell-types in a spatial arrangement

dynamical behavior



Self-organization

Robot example





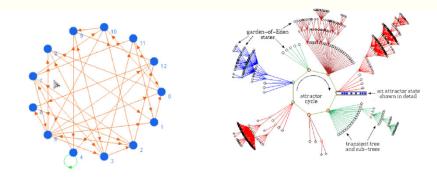
Jonathan Connell 's Muramator

- Emergent Behavior from system/environment coupling
 - Classifies Walls and Other Robots
 - Self-organization
 - Embodied cognition



random Boolean networks

self-organization



Discrete dynamical systems

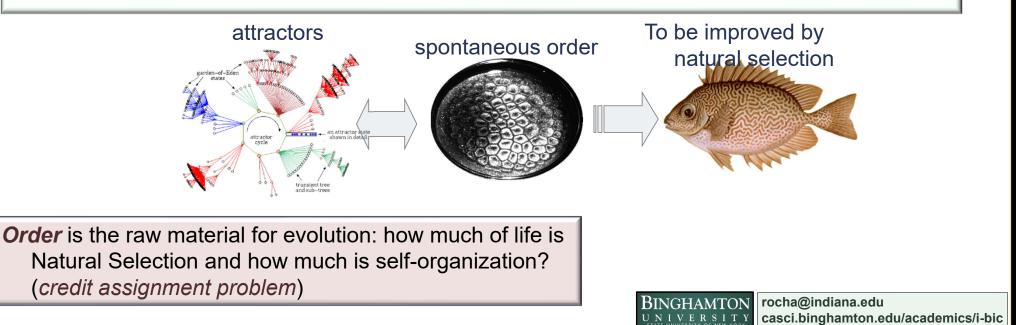
- Extremely large number o coupled elements
- Systems of binary variables (0,1), coupled to one another in a network
 The activity of each element depends on previous state of other elements
- Simplifies continuous systems while maintaining essential behavior
- Statistical properties of sets of networks
 - Understanding of macroscopic, emergent properties
 - Similar to temperature
- Typically irreversible

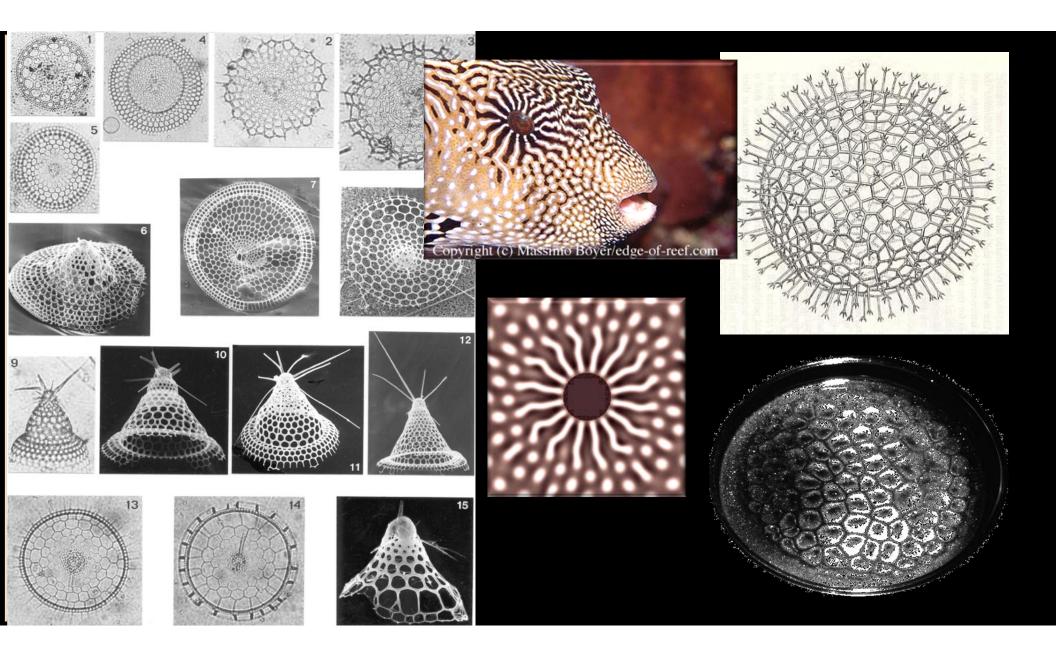


biological interpretations of attractor behavior

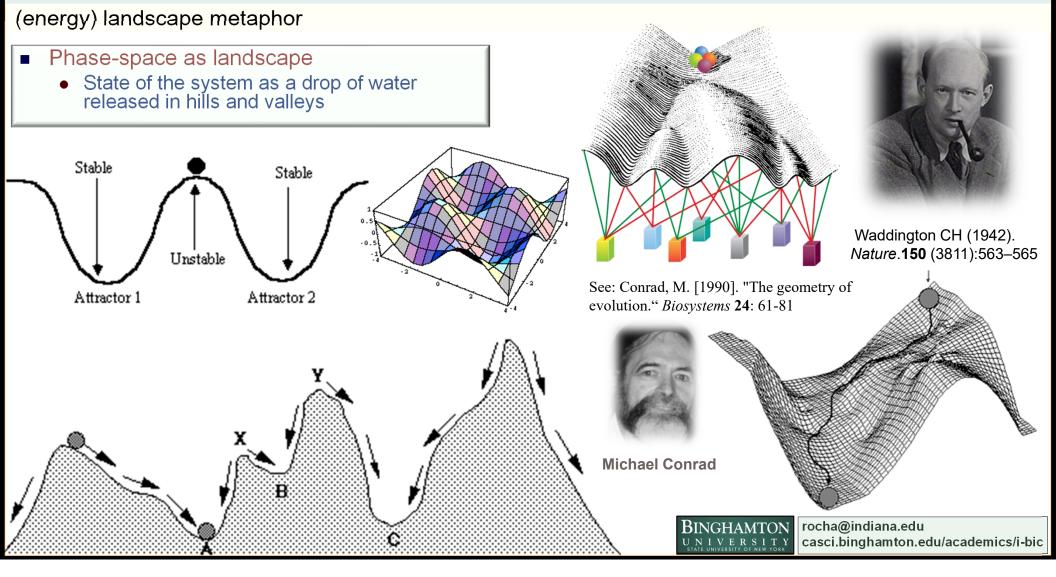
self-organization

- Genetic regulatory networks
 - Genes are on or off
 - Development, morphogenesis
 - Attractors interpreted as different cell types
- Classification in Immune networks
- Representation in artificial neural networks
- Stable patterns of species abundances in ecosystems



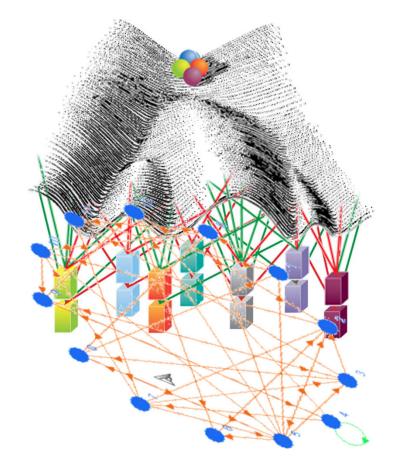


attractors



self-organization as a key mechanism for order and robustness

evolution does not need to encode all details and is constrained







Kauffman, S. A. (1984). *Phys. D Nonlinear Phen*.**10**,145–156.

Waddington CH (1942). *Nature*.**150** (3811):563–565

robustness of phenotypes is the result of a *buffering* of the developmental process.

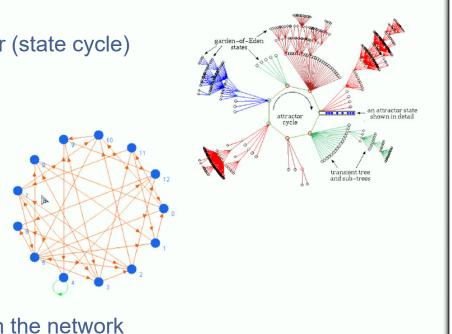
dynamics of gene networks provides buffering (*self-organization*).

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Boolean networks

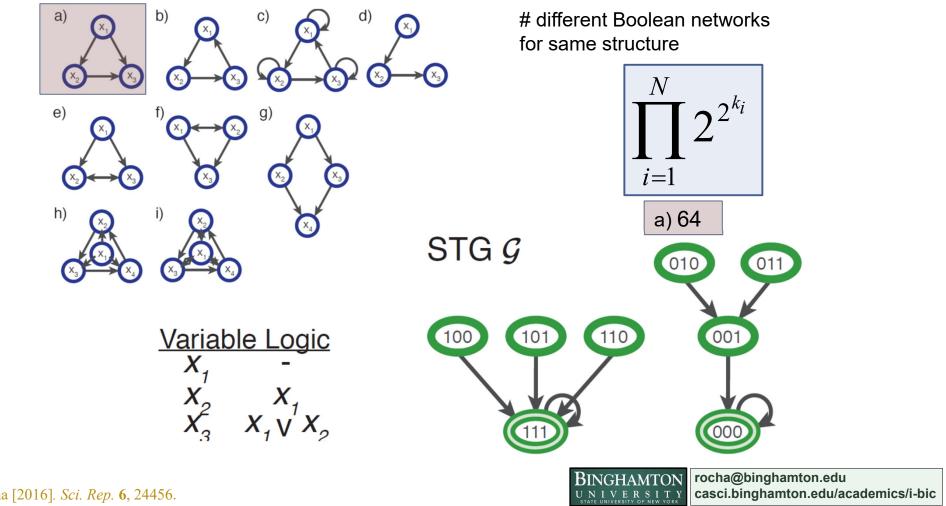
definitions

- basin of attraction
 - All states in trajectories leading to an attractor (state cycle)
- length of cycle
 - Number of states in cycle
 - 1 to 2^N
- perturbation (minimal)
 - Flipping of one node to the opposite state
- Damage
 - Change in behavior from a perturbation
- Structural perturbation
 - Permanent in connections or Boolean rules in the network



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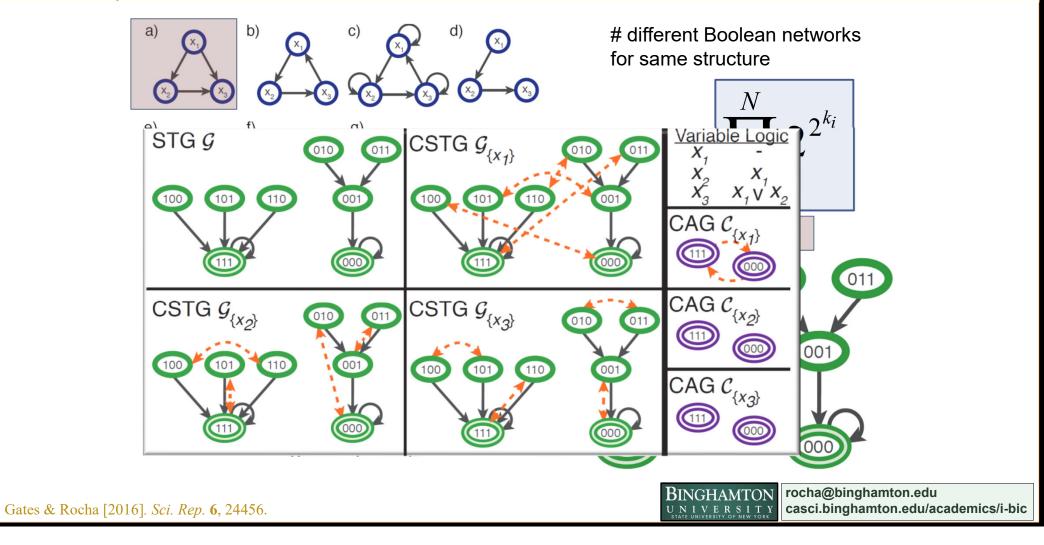
ensemble dynamics for same structure



Gates & Rocha [2016]. Sci. Rep. 6, 24456.

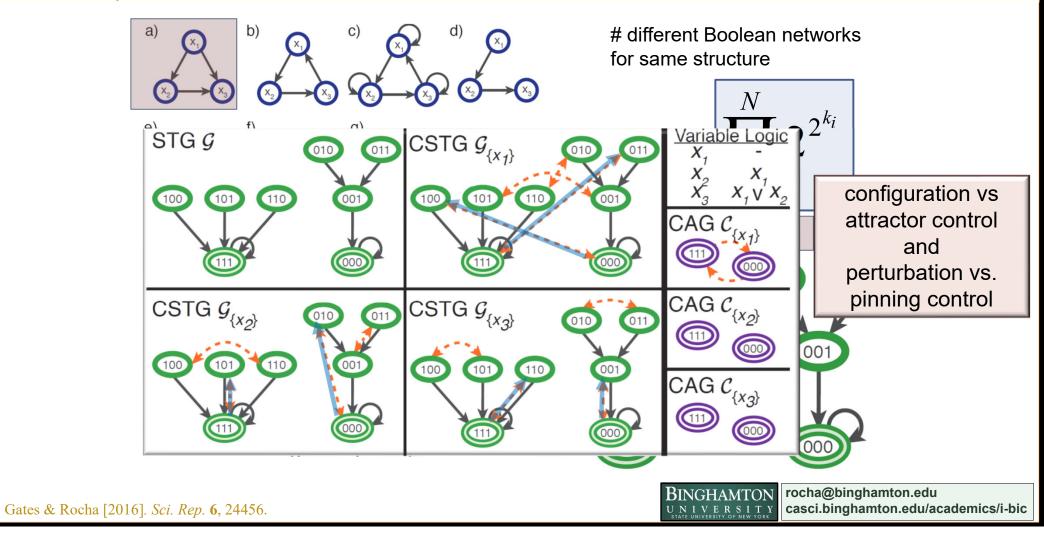
Boolean network dynamics, perturbations, and control

ensemble dynamics for same structure



Boolean network dynamics, perturbations, and control

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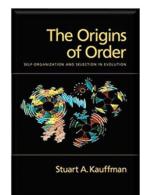


Kauffman's statistical analysis

Of NK-Boolean Networks

- Random networks
 - Started with random initial conditions
 - Self-organization is not a result of special initial conditions
- Statistical analysis
 - $K \le 2$
 - Steady state, ordered, crystallization
 - (5 \leq K to) K=N
 - Disordered, chaotic
 - Mean length of cycles: 0.5 x 2^{N/2}
 - Mean number of cycles: N/e
 - High reachability, sensitive to perturbation
 - Number of other state cycles system can reach after perturbation
 - K=2
 - Mean length: n^{1/2}
 - Mean number of cycles: n^{1/2}
 - Low reachability
 - Percolation of frozen clusters (isolated subsets)
 - Not very sensitive to perturbation

Kauffman, S. A. (1984). *Phys. D Nonlinear Phen*.**10**,145–156.



Kauffman, SA. J. theoretical biology 22.3 (1969): 437-467.

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edge of chaos on Boolean Networks

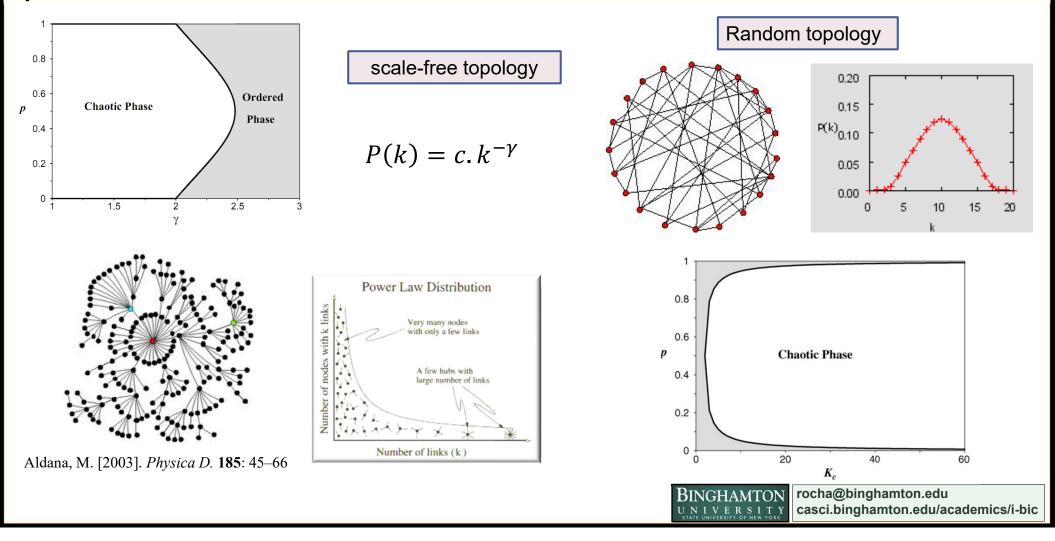
criticality

• $2 \le K \le 5$

- Good for evolvability?
- Some changes with large repercussions
- Best capability to perform information exchange
 - Information can be propagated more easily
- Problems with analysis
 - Network topology is random
 - Not scale-free, as later explored by Aldana
 - Real genetic networks tend to have lower values of K (in ordered regime)
 - Genes as simply Boolean may be oversimplification
 - Though a few states can approximate very well continuous data

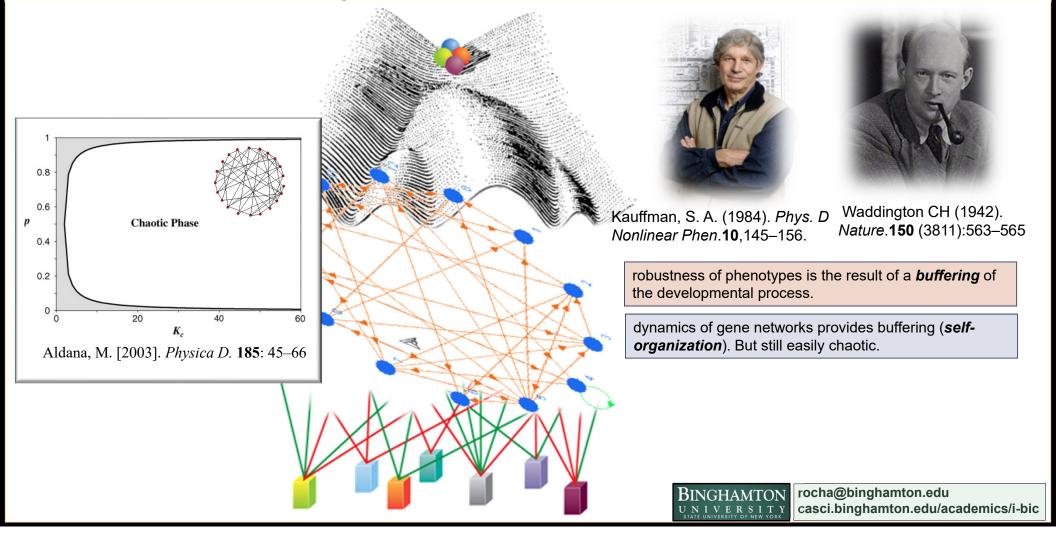
criticality in Boolean networks

dynamical behavior of ensembles of networks



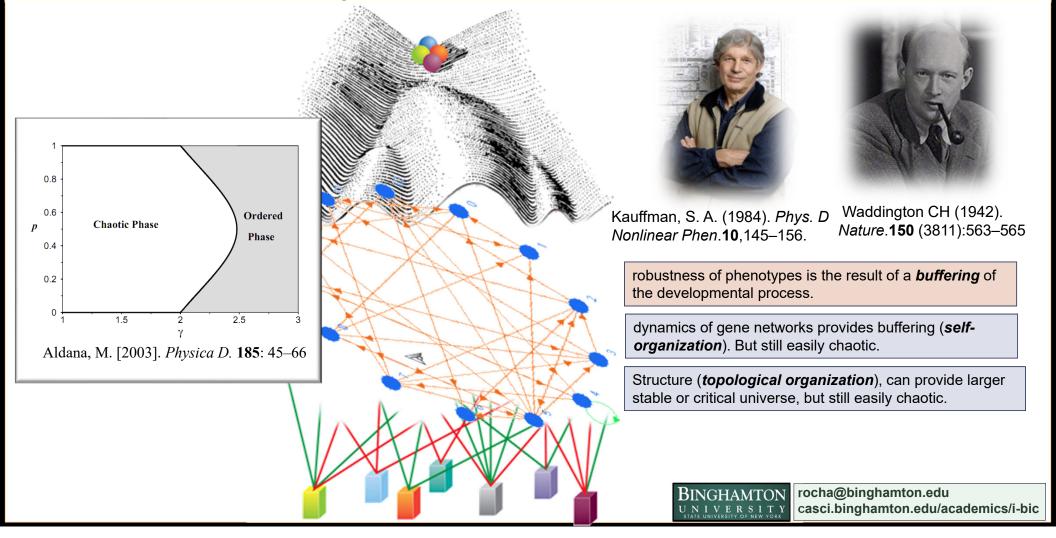
self-organization easily chaotic

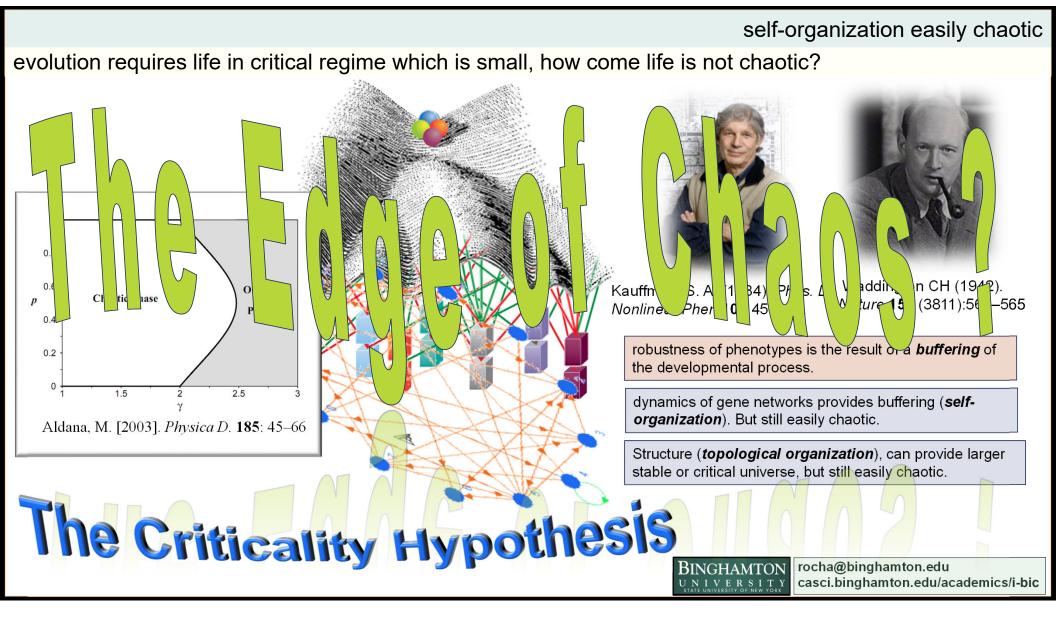
evolution requires life in critical regime which is small, how come life is not chaotic?



self-organization easily chaotic

evolution requires life in critical regime which is small, how come life is not chaotic?





Next lectures

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