biologically-inspired computing

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lecture 7

course outlook



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final project schedule

Projects

bit.lv/atBIC

Due by May 7th in Brightspace, "Final Project 483/583" assignment

ALIFE 2025

- Not necessarily to submit to actual conference due date
 - May 4 full paper, July 4, abstract
- https://2025.alife.org/
- Max 8 pages, author guidelines:
- https://2025.alife.org/calls#paper-call
- MS Word and Latex/Overleaf templates
- Preliminary ideas by March 7
 - Submit to "Project Idea" assignment in Brightspace.
- Individual or group
 - With very definite tasks assigned per member of group

ALIFE 2025

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



Reusing and expanding labs is highly encouraged.

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readings for this class

Additional information

- Floreano, D. and C. Mattiussi [2008]. *Bio-Inspired Artificial Intelligence: Theories, Methods, and Technologies*. MIT Press. Preface, Sections 4.1, 4.2. **Chapter 2.**
 - Nunes de Castro, Leandro [2006]. Fundamentals of Natural Computing: Basic Concepts, Algorithms, and Applications. Chapman & Hall. Chapter 1, pp. 1-23. Sections 7.1 to 7.4, Appendix B.3.1. Chapter 2, 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 @ casci.binghamton.edu/academics/i-bic
- Papers and other materials
 - Optional
 - Prusinkiewicz and Lindenmeyer [1996] The algorithmic beauty of plants.
 - Chapter 1
 - Flake's [1998], *The Computational Beauty of Life*. MIT Press.
 - Chapters 1, 5, 6 (7-9).
 - Chapters 10, 11, 14



natural design principles

modeling similarities across nature

- self-similar structures
 - Trees, plants, clouds, mountains
 - morphogenesis
 - Mechanism
 - Iteration, recursion, feedback
- dynamical systems and unpredictability
 - From limited knowledge or inherent in nature?
 - Mechanism
 - Chaos, measurement
- self-organization, collective behavior, emergence
 - Complex behavior from collectives of many simple units or agents
 - cellular automata, dynamical networks, morphogenesis, swarms, brains, social systems
 - Mechanism
 - Parallelism, multiplicity, multi-solutions, redundancy
- evolution
 - Adaptation, learning, social evolution
 - Mechanism
 - Reproduction, transmission, variation, selection, Turing's tape
- Network causality (heterogenous complexity)
 - Behavior derived from many inseparable sources
 - Immune system, anticipatory systems, brain-body-environment-culture, embodiment, epigenetics, culture
 - Mechanism
 - Modularity, control, hierarchy, connectivity, stigmergy, redundancy





discrete dynamical systems or automata networks



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

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examples



networks with (automata) dynamics

canonical complex systems

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





different Boolean networks for same structure (256¹³)

Multivariate Dynamical Systems: *Structure*: Variable interactions, associations, influence *Dynamics*: variable *states* (micro) network *configurations* (macro)

> Minimal networks with both structure and dynamics. Interactions and variables with binary states. Huge statespaces and **ensembles** for same structure. Full range of **attractor behavior**

 $2^N \rightarrow$ Network configurations (state-space) $2^{2^K} \rightarrow$ possible Boolean functions of k inputs (k=3 \rightarrow 256)

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

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NK-networks

Stuart Kauffman's version



simple Boolean network

small example NK-network of 3 variables



or

or

р	q	p ∨ q
0	0	0
0	1	1
1	0	1
1	1	1



State	space

t		t+1					
	n ₁	n ₂	n ₃	n ₁	n ₂	n ₃	
0	0	0	0	0	0	0	0
1	0	0	1	0	1	0	2
2	0	1	0	0	0	1	1
3	0	1	1	1	1	1	7
4	1	0	0	0	1	1	3
5	1	0	1	0	1	1	3
6	1	1	0	0	1	1	3
7	1	1	1	1	1	1	7

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simple Boolean network

attractors and state-space



Boolean network dynamics

ensemble dynamics for same structure



Small Boolean network

SimpleNet



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dynamical landscape of SimpleNet

State-transition graph (basins of attraction)



Basin	Size	Attractor	Attractor Period
8	22	1,0,1,1,0,1,1,0 1,0,1,0,1,1,1,0 1,0,1,1,1,0,1,0	3
9	2	1,0,1,1,1,1,1,0	1
10	2	1,0,1,1,1,1,1,0	1
11	12	1,1,1,1,1,1,0,1	1
12	12	1,1,1,1,1,1,0,1	1
13	12	0,1,1,1,1,1,1,0	1
14	12	0,1,1,1,1,1,1,1	1

Basin	Size	Attractor	Attractor Period
1	6	1,0,1,0,0,0,0,0	1
2	52	1,0,1,1,1,1,0,1	1
3	6	1,0,1,0,0,0,1,0	1
4	52	1,0,1,1,1,1,1,1	1
5	22	1,0,1,0,0,1,0,0 1,0,1,0,1,0,0,0 1,0,1,1,0,0,0	3
6	22	1,0,1,0,0,1,1,0 1,0,1,0,1,0,1,0 1,0,1,1,0,0,1,0	3
7	22	1,0,1,1,0,1,0,0 1,0,1,0,1,1,0,0 1,0,1,1,1,0,0	3

There are 2⁸=256 possible states but only a small set (14) of attractors

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attractor behavior

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how to control?



dynamical (qualitative) models of regulation from experimental 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)

Egg with maternally deposited mPNA Anterior		
	State – TransitionFunction	Node
bcd mRt	$\leftarrow 0 \text{ if } i=1 \lor i=2; 1 \text{ if } i=3 \lor i=4;$	SLP_i^{t+1}
Gradients of proteins	$\leftarrow (\mathbf{CIA}_i^t \land \mathbf{SLP}_i^t \land \neg \mathbf{CIR}_i^t) \lor (wg_i^t \land (\mathbf{CIA}_i^t \lor \mathbf{SLP}_i^t) \land \neg \mathbf{CIR}_i^t)$	wg_i^{t+1}
encoded by maternal mRNA	$\leftarrow wg_i^t$	WG_i^{t+1}
BĆE	$\leftarrow (\mathrm{WG}'_{l-1} \lor \mathrm{WG}'_{l+1}) \land \neg \mathrm{SLP}'_l$	en_i^{t+1}
Gap	$\leftarrow en'_i$	EN_i^{t+1}
proteins	$\leftarrow \mathbf{EN}_i^t \land \neg \mathbf{CIR}_i^t$	hh_i^{t+1}
HB-	$\leftarrow hh'_i$	$\mathbf{H}\mathbf{H}_{i}^{t+1}$
	$\leftarrow \mathbf{CIA}_i^t \land \neg \mathbf{EN}_i^t \land \neg \mathbf{CIR}_i^t$	$ptc_i^{\prime+1}$
	$\leftarrow ptc_i^t \lor (PTC_i^t \land \neg HH_{i-1}^t \land \neg HH_{i-1}^t)$	PTC_i^{t+1}
Pair-rule proteins	$\leftarrow \mathbf{PTC}_i^t \land (\mathbf{HH}_{i-1}^t \lor \mathbf{HH}_{i+1}^t)$	\mathbf{PH}_{i}^{t}
H RUN	$\leftarrow \neg PTC_i' \lor (HH_{i-1}' \lor HH_{i+1}')$	\mathbf{SMO}_i^t
Segment-	$\leftarrow \neg \mathbf{EN}_{i}^{t}$	ci_i^{t+1}
polarity proteins	$\leftarrow ci_i^t$	$\operatorname{CI}_{i}^{t+1}$
WGEN	$\leftarrow \mathbf{CI}_i^t \wedge (\neg \mathbf{PTC}_i^t \vee hh_{i-1}^t \vee hh_{i+1}^t \vee \mathbf{HH}_{i-1}^i \vee \mathbf{HH}_{i+1}^t)$	CIA_i^{t+1}
SEGMENT NUMB	$\leftarrow \mathbf{CI}_{i}^{t} \land \mathbf{PTC}_{i}^{t} \land \neg hh_{i-1}^{t} \land \neg hh_{i+1}^{t} \land \neg \mathbf{HH}_{i-1}^{t} \land \neg \mathbf{HH}_{i+1}^{t}$	CIR_i^{t+1}



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

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dynamical (qualitative) models of regulation from experimental data

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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 (qualitative) models of regulation from experimental data

the drosophila segment polarity network



dynamical behavior

rocha@indiana.edu

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cell-types in a spatial arrangement

dynamical behavior

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cell-types in a spatial arrangement

dynamical behavior

self-organization

robot example with Brooks' subsumption architecture

wall

Jonathan Connell 's Muramator

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

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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

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

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

BINGHAMTON UNIVERSITY casci.binghamton.edu/academics/i-bic self-organization as a key mechanism for order and robustness

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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

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

Boolean network dynamics, perturbations, and control

ensemble dynamics for same structure

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

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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?

homogenous lattice of state-determined systems

Parallel updating Artificial physics Local interactions only No actions at a distance • Homogeneous Unpredictable global behavior • Emergence 2-levels: rules (micro-level) and attractor behavior (macro-level) Irreversible Self-organization Example rules • Rug (diffusion) 256 states Average of 8 neighbors in 2-d grid, if state is 255 -> 0. Vote/majority binary

rocha@indiana.edu casci.binghamton.edu/academics/i-bic

elementary CA rules

http://mathworld.wolfram.com/CellularAutomaton.html

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Living patterns easily replicated in CA

Next lectures

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