Complex Biological Systems: When are Simple Models Good Enough?

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Winfried Just at OU Simple Models of Complex Biological Systems

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Let's start from the beginning:

What are levels of biological organization? What is a complex (biological) system? What do we want to know about complex (biological) systems?

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Exhibit A: Cells





At the deepest level cells are giant networks of biochemical reactions. The products of these reactions somehow *self-organize* into organelles and whole cells that interact with other cells and the external environment.

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How does this happen? Why does this work?

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Exhibit B: Brains



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Human brains are composed of trillions of neurons that exhibit relatively simple firing patterns. Neurons are connected by dendrites and axons and communicate (receive and send signals) along these structures.



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How can the firing patterns of the neurons give rise to perceptions, feelings, thoughts, and actions?

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Exhibit C: Ant colonies



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fungi, which amounts to creating a habitat for another species?

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- Agents interact. The structure of these interactions is called the connectivity of the system.
- At the macroscopic level the system interacts with the environment **in complex ways**.
- The system may even shape its environment.

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When do interactions qualify as complex?

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Problem 1: Find the definition of "complexity" that works best for the context of your study.

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To get an idea what it takes to do systems biology, try to think simultaneously about trees and the forest. How does the (rather predictable) dynamics of forest growth *emerge* out of the growth of individual trees (that depends on many random events)?

How could we build mathematical models of forest growth? Obviously, if we were to assign variables to each individual tree, we would end up with too many variables to study the resulting models. We could try to work with variables that represent averages, but this may not work due to nonlinear interactions.

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Is (mathematical) systems biology even possible?

If mathematical models are to help us in studying problems as on the previous slide, they need to be simple enough to be **tractable** either mathematically or at least by computer simulations, and they need to incorporate enough details to make biologically realistic predictions or give us correct explanations of a phenomenon.

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Problem 2: Why does mathematical modeling in systems biology work as well as it does?

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- Study the time courses (trajectories) of the variables either by simulations or mathematical deductions (proofs).
- **Stochastic models** allow for some randomness in the trajectories, **deterministic models** assume that the current state uniquely determines the trajectory.
- **Continuous** (e.g. ODE, PDE) models assume that time can take any (nonnegative) real values; **discrete time** (e.g. difference equation, Boolean) models assume that time moves in discrete steps, that is, only takes integer values.

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For example, a model of a biochemical network as a stochastic process would keep track of actual numbers of molecules of each chemical species at a given time. A simpler ODE model would be based on concentrations instead of actual counts. A Boolean model would distinguish only between "high" and "low" concentrations. Usually, there are several different types of dynamical systems models that could be chosen for the same biological system.

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Problem 3: Under what conditions can we trust that the simpler models will make mathematically equivalent predictions to the more elaborate (and biologically more realistic) ones?

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An example: Dynamic clustering

In several neuronal networks, it has been observed that time appears to progress in distinct episodes in which some subpopulation of cells fire synchronously; however, membership within this subpopulation may change over time. That is, two neurons may fire together during one episode but not during a subsequent episode. This phenomenon is called **dynamic clustering.**



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Problem 4: Are there classes of DE models that exhibit dynamic clustering?

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A theorem

Terman D, Ahn S, Wang X, Just W, Physica D, 2008

Theorem

There exist a broad class of ODE models M for neuronal networks such that every model in this class exhibits dynamic clustering. Moreover, for every such M there exists a discrete model N with a finite state space that accurately predicts which neurons will fire in any given episode.

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Simultaneously, the theorem assures us that the ODE models in this class can be **simplified** to the corresponding discrete models.

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- Neurons fire or are at rest.
- After a neuron has fired, it has to go through a certain **refractory period** when it cannot fire.
- A neuron will fire when it has reached the end of its refractory period and when it receives firing input from at least as many other neurons as are required by its **firing threshold**.

Ahn S, Smith BH, Borisyuk A, Terman D, Physica D, 2010

A directed graph $D = [V_D, A_D]$ and integers *n* (size of the network), p_i (refractory period), th_i (firing threshold).

A state $\vec{s}(t)$ at the discrete time t is a vector: $\vec{s}(t) = [s_1(t), \dots, s_n(t)]$ where $s_i(t) \in \{0, 1, \dots, p_i\}$ for each i. The state $s_i(t) = 0$ means neuron i fires at time t.

Dynamics on the discrete network $N = \langle D, \vec{p}, t\vec{h} \rangle$:

- If $s_i(t) < p_i$, then $s_i(t+1) = s_i(t) + 1$.
- If $s_i(t) = p_i$, and there exists at least th_i neurons j with $s_j(k) = 0$ and $\langle j, i \rangle \in A_D$, then $s_i(t+1) = 0$.
- If $s_i(t) = p_i$ and there do not exist th_i neurons j with $s_j(t) = 0$ and $\langle j, i \rangle \in A_D$, then $s_i(t+1) = p_i$.

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How do these features of the network dynamics depend on the network connectivity and the firing thresholds and refractory periods of individual neurons? We can study these questions for special connectivities:

- Directed cycle graphs.
- Strongly connected digraphs: There is a directed path from every node to every other node.
- Complete digraphs.
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Alternatively, we can study expected properties of the dynamics if the connectivity is a **random digraph**. There are several models for generating random digraphs, the most important ones being the **Erdős-Rényi model** and the **preferential attachment model**.

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Many results on how the connectivity of the discrete model influences its dynamics under suitable assumptions on the refractory periods and firing thresholds are reviewed in the chapter

Neuronal Networks: A Discrete Model, Just W, Ahn S, Terman D of the forthcoming volume

Mathematical Concepts and Methods in Modern Biology, Robeva R and Hodge T eds., Elsevier 2013. Many results on how the connectivity of the discrete model influences its dynamics under suitable assumptions on the refractory periods and firing thresholds are reviewed in the chapter

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The chapter also includes eight research projects that gradually lead students from relatively easy exercises to unsolved open problems. Most of these are at a level that is accessible to undergraduates.