Exploring Transmission of Infectious Diseases on Networks with NETLOGO

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The purpose of this talk

- **Quoting the abstract:** In this talk we will present a set of teaching materials for introducing network-based models of disease transmission.

- **In plain English:** The presenter is going to give a sales talk, shamelessly bragging about his materials, and will tell us to adopt them.

- **Putting it more diplomatically:** I will tell you what makes these materials different from other sources and what teaching objectives the authors had in mind when designing them.

The materials: Book chapters

We have two book chapters in

Raina Robeva (ed.), *Algebraic and Discrete Mathematical Methods for Modern Biology,* Academic Press, 2015:

[1] Winfried Just, Hannah Callender, M. Drew LaMar, and Natalia Toporikova; *Transmission of infectious diseases: Data, models, and simulations.* 193-215.

[2] Winfried Just, Hannah Callender, and M. Drew LaMar; *Disease transmission dynamics on networks: Network structure vs. disease dynamics.* 217-235.

Both chapters come with extensive online supplements.

M. Drew LaMar, in consultation with the other authors, developed a customized simulation tool called **IONTW**, which stands for **I**nfections **O**n **N**e**TW**orks.

It is written in the NETLOGO programming language.

IONTW can be downloaded for free and used to some extent independently of the book chapters.

The materials: Modules published on the web

A number of modules for more in-depth student explorations are published at

http://www.ohio.edu/people/just/IONTW/

https://qubeshub.org/iontw

They form a natural continuation of the book chapters, but can also be used independently, based on the condensed introduction to network-based models of disease transmission posted at these websites.

We encourage submission of additional web-based modules by our colleagues and students. So far, three of them have been co-authored by my Ph.D. student Ying Xin.

For whom did we write?

- Our first book chapter is intended for undergraduate students of the life sciences and mathematics .

- The second book chapter targets advanced undergraduate and beginning graduate students of mathematics or with a strong mathematical background.

- The modules on the web vary in level from elementary to topics leading into open research problems.

What makes us different from the competition?

Several existing books have chapters devoted network-based models of disease transmission, and there exists one book-length treatment at a high level of mathematical abstraction.

All of these sources are pretty much "read-only."

In contrast, our treatment of the material is discovery-based, with numerous student exercises of varying levels of difficulty forming an integral part of the text, accompanied by "modules" and "projects" for further exploration.

A typical exercise uses the **IONTW** simulation tool and guides students towards discovering a particular mathematical insight.

We believe that this format makes our materials suitable as a basis for REU projects, whose intended outcome may well be design of an additional module to be posted at our websites, or expansion of an existing one.

[1] Winfried Just, Hannah Callender, M. Drew LaMar, and Natalia Toporikova (2015); *Transmission of infectious diseases: Data, models, and simulations.*

This one has a dual purpose:

1. Introduce models of transmission of infectious diseases (obviously).

2. Introduce students to the process of mathematical modeling itself, starting from the kind of data we can collect and the questions we want to answer with the help of the model, through establishing terminology and spelling out the simplifying assumptions, specifying the model itself, to exploring its predictions and deriving conclusions in terms of the goals of our modeling.

Infectious diseases are caused by pathogens (such as viruses, bacteria, fungi, or protozoans) that spread in populations of hosts (humans, animals, or plants). We focus on pathogens that are transmitted during direct contacts between hosts.

We may want to predict the final size of an outbreak.

The final size is the fraction F of hosts who experience infection during the outbreak.

How does the expected value of F behave if we increase population size N?

If $\lim_{N \to \infty} F = 0$, we predict only minor outbreaks, when $\lim_{N \to \infty} F > 0$, there is a risk of major outbreaks.

A (the?) goal of epidemiological modeling

The ultimate goal of modeling the spread of infectious diseases is to design effective control measures, such as vaccination, quarantine, culling (for animal and plant diseases), behavior modification (for human diseases).

Models allow us to compare the predicted effectiveness of several feasible control measures.

Effectiveness may often be measured in terms of expected reduction of the final size of outbreaks.

Our models: Conceptual framework

Technically, we build individual-based stochastic dynamical systems models.

In both book chapters we present them as embodied in computer code aka agent-based models rather than formal mathematical constructs.

Our first chapter has two sections that explain in some detail what is going on behind the screen when a simulation runs on a computer.

These are primarily aimed at undergraduate life sciences majors with no computer science background.

Some of our web modules study models analytically as mathematical objects.

Observed outcomes will greatly vary from simulation run to simulation run.

In our exercises, we teach students some rudiments of statistical inference, in particular, on how to choose appropriate batch sizes.

For the first few simulation exercises, very detailed guidance to data analysis is given.

We put great emphasis on clearly spelling out the simplifying assumptions that lead to a given model and discussing how they might distort the predictions.

Our particular focus is on the related, but different assumptions of homogeneity of hosts and the uniform mixing assumption that underly all compartment-level models.

In a sense, the entire second chapter explores how the uniform mixing assumption might distort predictions if the disease is in fact only transmitted along the edges of a contact network.

Homogeneity of hosts via cartoon characters

Each host is treated as a mathematical version of "Joe Average."

Objection: You should have written "Joe or Jane Average."

You are correct: We call our hosts Joene Average.

But you are wrong: Don't think of Joene as "Joe or Jane." S&he is actually Joe and Jane.

Joene will sometimes recover quickly from a bout of the flu and sometimes slowly, will sometimes be warm and fuzzy and sometimes be emotionally withdrawn, will sometimes act in a stereotypically male and sometimes in a stereotypically female way.

Joene is all of us.

Uniform mixing via cartoon characters

What would it be like to be married to Joene?

Joene Choosy is Average only in the sense of homogeneity of hosts and may still be quite selective about with whom and how frequently s&he makes contact.

In particular, s&he may be good spouse material.

Joene Butterfly embodies the uniform mixing assumption. At all times s&he will be equally likely to make contact with every other host of the population.

Forget about getting a commitment from Joene.

You can have some exciting moments with Joene, but you shouldn't even invite him&er to dinner.

Joene just will not sit in one place for two hours.

Network-based models of disease transmission

The host population consists of copies of Joene Choosy.

Thus the assumption of homogeneity of hosts is retained.

However, instead of uniform mixing, we assume that two hosts can make contact only if they are connected by an edge of a given graph G that represents the contact network.

The uniform mixing assumption becomes the special case when G is the complete graph.

Our second book chapter

[2] Winfried Just, Hannah Callender, and M. Drew LaMar (2015); Disease transmission dynamics on networks: Network structure vs. disease dynamics.

- Contains some theoretical results on the role of R_0 under uniform mixing.
- Introduces notions from graph theory in context.
- Explores the relation between the structure of the underlying contact network and the predicted dynamics.

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But how do we know the contact network?

For any real population of realistic size we simply don't.

But we can estimate some structural parameters, like the mean degree of the nodes, based on statistical sampling, and treat the contact network as a random graph that shares these empirically verified properties with high probability.

Quite a few types of random graphs are implemented in **IONTW** and introduced in our second chapter or our web modules.

They include Erdős-Rényi, small world (1 and 2 dimensions), preferential attachment, generic scale-free, spatially clustered, random regular graphs, as well as random graphs with a user-specified degree distribution.

Sorry, no. Out of time.

Get **IONTW** and play yourself!

The software can be accessed at:

http://www.ohio.edu/people/just/IONTW/

(For download, together with viewing our web modules.)

http://booksite.elsevier.com/9780128012130/chapters.php

(For download, together with online parts of our book chapters.)

https://qubeshub.org/iontw

(A version that runs on a web server; also modules for download.)

Or best: Go to Hannah Callender's presentation at noon to see a detailed description of **IONTW**.

Chapters on network-based models of disease transmission are contained in several books, such as:

[1] MJ Keeling and P Rohani; *Modeling infectious diseases in humans and animals.*Princeton U Press, 2008.

[2] MEJ Newman; *Networks: an introduction.* Oxford U Press 2010.

[3] E Vynnycky and R White; *An introduction to infectious disease modelling.* Oxford U Press 2010.

[4] O Diekmann, H Heesterbeek, and T Britton *Mathematical tools for understanding infectious disease dynamics.* Princeton U Press, 2012.

[5] A-L Barabási *Network Science.* (2015)
http://barabasi.com/networksciencebook/

There is also a book-length mathematical treatment:

[6] M. Draief and L. Massoulié *Epidemics and Rumors in Complex Networks.* Cambridge U Press 2010.