Exploring Disease Transmission On Networks with NetLogo

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December 12, 2014

Mathematical models of disease transmission

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.

At any given time each host is assumed to be in one of several states such as susceptible, infectious, or removed. The sets of hosts who are in these states are called the **S**-, **I**-, **R**-compartment, respectively.

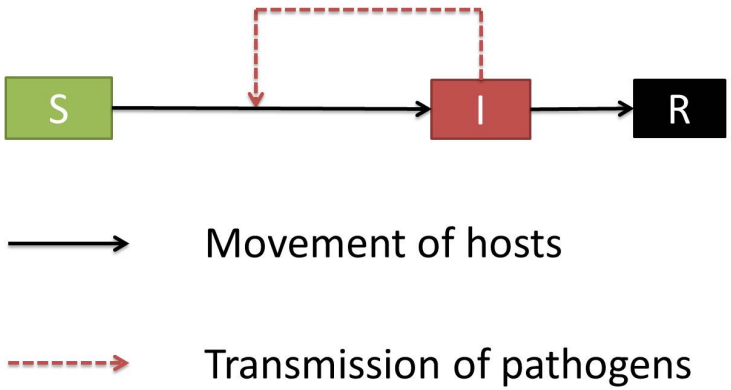


Figure: Schematic representation of the classical *SIR*-model.

Predictions of compartment-level *SIR*-models

In Compartment-level models the state of the population is represented by the numbers of hosts in each compartment. They are based on the assumptions of homogeneity of hosts and uniform mixing.

Of particular interest is the spread of the disease within a given initially entirely susceptible population during an outbreak that starts when a single infectious host (index case) gets introduced from outside of the population. The basic reproductive ratio R_0 is defined as the mean number of secondary infections caused by an average index case in a large population.

Compartment-level *SIR*-models predict that when $R_0 \leq 1$, all such outbreaks will be minor, that is, the fraction F of hosts who will experience infection will approach 0 as the population size $N \to \infty$. In contrast, when $R_0 > 1$, with positive probability the outbreak will be major and a fraction $F \approx F(R_0)$ of hosts will experience infection, where $0 < F(R_0) < 1$.

Network models of disease transmission

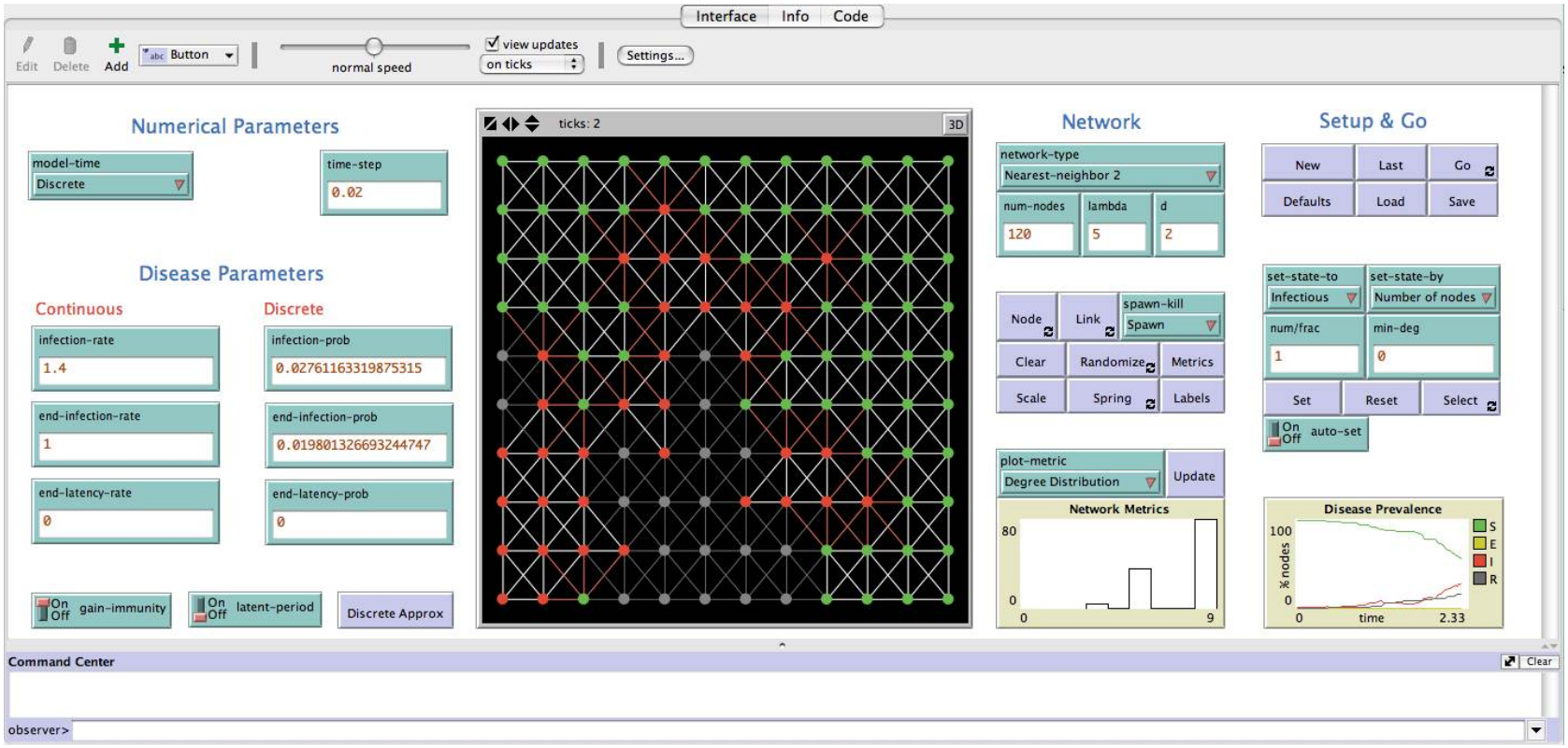
For populations with a well-defined social or territorial structure, the uniform mixing assumption is unrealistic. Some pairs of individuals will have contact relatively frequently (think of co-workers or neighbors in human populations), while other pairs of individuals will almost certainly never encounter each other.

For more realistic modeling one can assume the existence of a contact network that determines whether it is even possible for the pathogens to be transmitted between two given hosts. The nature of the required contact, and thus the relevant contact network, depends on the particular disease. Think of the flu *vs.* a computer virus *vs.* a sexually transmitted infection.

In network models of disease transmission the contact network is represented by a graph. The assumption of homogeneity of hosts is retained, and transmission rates or probabilities between any pair of hosts that are connected by an edge of the contact network are assumed identical. Such models can be embodied in computer code as agent-based models.

The IONTW software

IONTW, which stands for **I**nfections **O**n **N**e**TW**orks is a NetLogo-based tool for teaching network models of disease transmission. It was developed by M. Drew LaMar (College of William and Mary) in consultation with Winfried Just, Hannah Callender (University of Portland), and Natalia Toporikova (Washington and Lee University).



Exploring networks with IONTW

Currently IONTW supports the following network types: complete graphs, empty graphs, Erdős-Rényi , 1- and 2-dimensional nearest-neighbor and small-world networks, the preferential attachment model, generic scale-free, spatially clustered, and random regular graphs, regular trees, as well as custom networks or generic networks with specified degree sequences or degree distributions.

Apart from visualization, the software allows for exploration of certain structural properties of a given network. Histograms of degree distributions, node clustering coefficients and distributions of distances can be displayed to the screen. The mean degree, edge density, network clustering coefficients, number of connected components, relative size, diameter, and mean distance between nodes of the largest component can be looked up by the user.

Defining models of disease transmission in IONTW

IONTW can simulate disease outbreaks both in continuous-time and discrete-time models. The user chooses the rates or probabilities of movement of hosts between the compartments.

Currently IONTW supports the following model types: *SI*, *SEI*, *SIR*, *SEIR*, *SIS*, *SEIS*.

SI- or *SEI*-models can be enforced by setting the rate or probability of leaving the **I**-compartment to 0.

Toggle switches control whether the disease is assumed immunizing (of type *SIR* or *SEIR*) or of type *SIS* or *SEIS* and whether an **E**-compartment is included in the model.

The user can choose the numbers of infectious, removed, and susceptible hosts in the initial state, can specify which particular set of nodes in a given network is infectious or removed in the initial state, or that initially removed hosts will be randomly chosen among all nodes with a specified minimum degree.

Simulating outbreaks with IONTW

Users can adjust execution speed in real time using NetLogo's built-in speed control slider. In slow motion the graphic display in the **World** window shows how the states of hosts change over time.

States of hosts are color-coded, little green discs represent susceptible hosts, yellow ones exposed, red ones infectious, and grey discs removed hosts.

Edges of the contact network will also change color during a simulation, with red edges indicating that an effective contact along this edge at the given time will lead to successful transmission of the pathogen from the infectious to the susceptible endpoint of the edge.

The IONTW interface has a **Disease Prevalence** plot that is continuously updated during a given simulation. Its color-coded curves show how the percentages of nodes in the relevant compartments change over time.

Analyzing predictions of models with IONTW

Suppose we have set up a network model of type *SIR* and want to compare its predictions with the corresponding model for the same population size N and basic reproductive ratio R_0 that assumes uniform mixing.

Will the structure of the contact network make major outbreaks more or less likely? On average, will a larger or a smaller proportion of hosts experience infection?

Due to the stochastic nature of disease transmission, we will need to collect and analyze statistics on a large batch of simulated outbreaks. NetLogo's batch processing mode allows us to do this. The user defines an experiment with a specified number of repetitions and instructs the software to save the output statistics of interest to a spreadsheet that permits subsequent data analysis.

IONTW completes such experiments with 100 repetitions within minutes for densely connected networks with several hundred nodes and sparsely connected networks with several thousand nodes.

Exploring control measures with IONTW

Ultimately, mathematical epidemiology aims at predicting the effectiveness of control measures for preventing or reducing the spread of an infection in a given population. Conceivable control measures include vaccination, quarantine, culling (for animal or plant diseases), and behavior modifications (for human diseases).

Vaccination can be modeled by moving some hosts to the **R**-compartment prior to the start of an outbreak. The uniform mixing assumption predicts that a proportion of at least $HIT = 1 - \frac{1}{R_0}$ of the population needs to be vaccinated to prevent major outbreaks. HIT is called the herd immunity threshold.

IONTW allows explorations of various vaccination strategies by modifying the initial state. Depending on the network type, randomly vaccinating hosts with probability HIT may no longer be (most) effective. For some network types, targeting vaccination at highly connected nodes works best; for other network types the best strategy boils down to creating barriers in specific places.

Teaching mathematical epidemiology with IONTW

[1] Winfried Just, Hannah Callender, M. Drew LaMar, and Natalia Toporikova; *Transmission of infectious diseases: Data, models, and simulations.*
[2] Winfried Just, Hannah Callender, and M. Drew LaMar; *Disease transmission dynamics on networks: Network structure vs. disease dynamics.*
In: Raina Robeva (ed.), *Algebraic and Discrete Mathematical Methods for Modern Biology,* Academic Press, March 1, 2015.

The first chapter discusses in detail the process of mathematical modeling in epidemiology, including data collection, development of models, and deriving and interpreting predictions of models, while the second largely focuses on network-based models.
The models of each chapter are explored with IONTW in numerous exercises and projects, using discovery-based learning.
Suitable for use as modules in a course on mathematical modeling in biology or as reading for an individual study or REU offering.
Level: advanced undergraduate majors of biology or mathematics.

Advanced teaching materials that use IONTW

The book chapter [2] gives a more detailed exposition of network models of disease transmission than existing introductory texts, but still has limited scope. Its authors see a need for materials on more in-depth explorations and aim at filling this gap in the literature with a sequence of modules at

http://www.ohio.edu/people/just/IONTW/
(also to be posted at https://www.qubeshub.org/IONTW)

Existing modules cover topics such as assortativity and the differences between disease transmission on Erdős-Rényi and random regular networks. Modules on friendship paradox, clustering coefficients, the small-world property, and scale-free networks are in preparation and will be posted soon.

Current authors of modules are Just, Callender, LaMar, and Xin. The web site welcomes submission of similar modules that are authored by other colleagues and students.