Visualization and modelling of the spread and treatment of an infectious disease in non-homogenous populations using a simple random walk approach.

Motive of this model

The motive of this model is to simulate the spread of an infectious disease in a non-homogenous population. The model also heals the infected nodes using three stages of available antibiotics with increasingly better chances of curing the infection.

In a simulation based on this model, users will have an idea of how a random population reacts to the administration of antibiotics and how likely it is that an antibiotic-resistant strain will develop.

The population

The model assumes that the population is randomly composed of three kinds of interconnected participants: Adults, Children and Old persons. Each of these participants have varying levels of susceptibility to an infection, they also have different probability of success of a full recovery with antibiotic administration.

Eg, children and old persons are more susceptible to an infection. They also may respond differently to the administration of an antibiotic. ***The model also assumes that the relationships between nodes remain static, no new nodes are added and no nodes are removed.***

The antibiotics

The model is composed of 3 stages of antibiotics with which infected nodes are treated. The stage 1 antibiotic being the first line of defense while stage 3 antibiotic being the last line of defence. If a node is not cured even after administering a 3rd level of antibiotic, it is marked as antibiotic resistant.

The model assumes that every successive level of antibiotic has greater effectiveness and increases the odds of recovery.

The infection

The possibility of being infected differs node to node, also an infection is ‘run’ on a node as long as its infected neighbors are present; which increases the odds of being infected for a node surrounded by infected nodes implicitly.

The infection has certain characteristics. ***The infection cannot be contracted if the node has been healed by antibiotic administration. A node which has developed antibiotic resistant strain of the disease cannot spread it to other nodes.*** This assumption is based on my opinion that nodes which have failed the last line of antibiotics will be quarantined.

The mainstream model : SIR model

An SIR model is an epidemiological model that computes the theoretical number of people infected with a contagious illness in a closed population over time. It is best explained and visualized in a resource by ASU : http://www.public.asu.edu/~hnesse/classes/sir.html

The key concepts borrowed from the SIR model for this model are:

Beta	The parameter controlling how often a susceptible-infected contact results in a new infection.
Gamma	The rate an infected recovers and moves into the resistant phase.

Popular implementations of SIR solve differential equations to arrive at absolute numbers, hence there is little randomization involved. Doing a stochastic simulation is grounds for an extended Monte-Carlo simulation that may arrive at similar numbers. This model does what is essentially a single run of a Monte-Carlo for a fixed population.

The SIR also depends on having a homogenous population with the same beta and gamma values. This does not reflect real life, this model tries to implement the variation in beta and gamma values like a real population distribution.

Node Composition

The nodes are described by the following characteristics in the system.

1. **TYPE** : Adult, Child or Old person.
2. **INFECTED_FLAG**: To mark an infected node.
3. **RECOVERED_FLAG**: To mark a node that has recovered.
4. **STAGE_FLAG**: Identify what stage antibiotic was applied to the node.
5. **AB_RESISTANT_FLAG**: To mark a node as antibiotic resistant.
6. **BETA**: Susceptibility for given node.
7. **GAMMA**: Probability of recovery for node.

Gamma and Beta values for different types

The gamma and beta values for different nodes are as follows:

	Adult	**Child**	**Old person**
Gamma:	0.2	0.5	0.7
Beta:	0.6	0.4	0.2

The model assumes these values for our simulation, I chose them to best reflect reality and they are not based upon any empirical analysis. Let's assume them to be true.

Antibiotic trial and its effect on gamma values

Building upon the assumption that each successive antibiotic stage is more effective than the last, every trial boosts the gamma value for the node. When stage 1 antibiotics are administered, the healing trial is conducted using the present/native gamma values of the node.

This model assume that stage 2 and stage 3 antibiotics each boost the gamma values for a node by an addition of 0.1 and 0.2 on its existing gamma value. Thus improving the likelihood of the node recovery.

Population composition

The population is limited by a control variable **'totalPopulation'**, node types are randomly selected to belong to either of the three groups. The selection is unbiased and random. This may lead to situations where a certain group outnumbers another etc.

Node-node relationships

Node-node relationships are also randomly determined. For every node, a random number of connections **(*k*)** is selected with an upper bound defined by control variable '**connectionLimit**', which has been set to 2 for this simulation.

Once ***(k)*** is determined for a node, that many other nodes are randomly selected.

Infection trial on a node

An infection trial is initiated upon a node by its infected neighbor. The infection trial can be summarized as the following steps:

1. Do not infect if node is already infected or has recovered.
2. Random variable ***R*** where [***0 < R < 1***]. For a fair random number implying a continuous bounded uniform distribution ***Unif(0,1)***, ***P(0 < R < BETA) = BETA***.
3. If the random variable is less than the ***BETA*** value, mark the node as infected.
4. If the random variable is above the ***BETA*** value, the node is not infected.

Recovery trial on a node

A recovery trial is initiated by the system on each node after the infection cycle is complete. It has the following steps:

1. Do not heal if node has already recovered.
2. If node's ***STAGE_FLAG*** = 3, that means node has gone through 3 levels of antibiotic administration already and failed. This node must be marked as antibiotic resistant.
3. Random variable ***R*** where [***0 < R < 1***]. For a fair random number implying a continuous bounded uniform distribution ***Unif(0,1)***, ***P(0 < R < GAMMA) = GAMMA***.
4. If the random variable is less than the ***GAMMA*** value, mark the node as recovered.

5. If the random variable is above ***GAMMA***, the node is not recovered. We will move the node to next stage antibiotic and boost its ***GAMMA*** value by o.1 in preparation of the next recovery cycle.

Simulation algorithm

The simulation algorithm runs infinitely in circles! It is characterized by 2 repeating stages called 'infection cycle' and 'recovery cycle' which are executed repeatedly one after another.

Infection Cycle

1. Go over each node-node relationship.
2. If both nodes are infected or either one is recovered, ignore that relationship.
3. If node 1 is infected, then run infection trial on node 2.
4. Else if node 2 is the infected one, run infection trial on node 1.

Recovery Cycle

1. Go over each node.
2. If the node is not infected, ignore the node.
3. If node is infected, run a recovery trial on the node.

Equilibrium conditions of the system

The system comes to an equilibrium state when no new nodes can be healed or infected. Because we are running the simulation infinitely, the system keeps spinning its wheels even when it has reached its equilibrium stage.

What can be inferred from the simulation

The simulation is meant to be an education tool to understand the spread of epidemics in a close knit community. By looking at the visualizations we understand that the composition of a population will greatly affect the outcomes, this model might generate numbers that are irrelevant to simulating such an epidemic in an old-age home.

Also, the model describes the role of chance in the spread of epidemic and the importance of drug administration. We see infected nodes arrested by surrounding recovered nodes that are now immune to the disease.

This model also advocates for the judicious use of antibiotics in such cases, especially when we have a count of members of this community who have developed antibiotic resistant strains of the disease.

The visualization

The visualization is live and available at the following address :
http://she1991.github.io/InfIntGat/index.html