Agent Based Stochastic SIR Model

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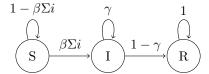
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Introduction

Deterministic models are valid only at the thermodynamic limit: population $n \to \infty$. Stochastic models can more accurately describe outbreaks in their early stages. [1] provides are overview for Markov chain models among other stochastic models. Some other stochastic models: [2], [3]

We present a SIR based stochastic model.

Formulation



where Σi is the number of infected individuals adjacent to an individual. The state space is described by \mathbf{S}, \mathbf{I} both n dimensional vectors with elements 0 or 1, where n is the population size. The conditional probability of \mathbf{S} to \mathbf{I} state transition during a simulation period is $\mathbf{P}_{S \to I} = \beta \mathbf{A}_{\mathbf{n} \times \mathbf{n}} \mathbf{I}.\mathbf{S}$, where \mathbf{A} is the adjacency matrix and \mathbf{S} is an element-wise multiplication, and $\beta \in \mathbb{R}^+$ is the infection standard deviation.

Conditional probability of I to R state transition has mean at $\gamma_m \in \mathbb{Z}^+$ simulation periods after infection with a standard deviation of $\gamma \in (0,1]$. If $\gamma = 1$, recovery will always occur after γ_m periods. $\mathbf{P}_{I \to R} = \gamma(\mathbf{I}_t - \gamma_m).\mathbf{I}$. Number of periods after infection is tracked by vector $\mathbf{I}_t \in \mathbb{Z}^n$ and is updated every cycle as $\mathbf{I}_t = \mathbf{I}_t + \mathbf{I}$.

Both transition probability vectors are compared element wise to a random vector whose elements are in the range [0,1]. If the values are larger than the random number, the state for that person is transitioned. Initial condition is defined as a single infected individual. The susceptible vector is set as the complement of the infected vector. The program is run multiple iterations to show different paths.

```
for k=1:n/10 %number of runs I=zeros(n,1); \ \%infected \ population , \ binary \\ I(2)=1; \ \%initial \ condition \ infected \\ S=~I; \ \%susceptible \ population , \ binary \\ It=I; \ \%time \ a \ person \ has \ been \ infected , \ natural \ number \\ x=zeros(T,1); \ \%plot \ number \ of \ infecteds \ over \ time \\ for \ t=1:T \\ \ \%contraction \ probability \ given \ that \ individual \ is \ susceptible \\ contract = (beta*A*I > rand(n,1)).*S; \\ \ \%recovery \ probability \ given \ that \ individual \ is \ infected \\ recover = (gamma*(It-gamma\_m) > rand(n,1)).*I; \\ S+=-contract; \\ I+= \ contract - \ recover;
```

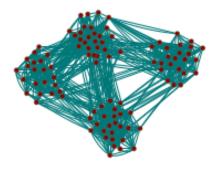


Figure 1: Random Modular Graph

```
It+= I;
    x(t)=sum(I);
end
plot(x)
hold on
end
```

Graph Generation

Contact in a population are best described by "small-world graph" where contacts are clustered.[4] [5] is used to generate the adjacency matrix for a clustered undirected graph. A random graph with 100 nodes clustered into four groups is generated in figure 1. The ratio of inside-module links to outside-module links is set to 5.

```
[A, \tilde{}] = \text{randomModularGraph}(n, 4, 0.1, 5);
```

Result

Using the algorithm and graph described, the number of infected persons are plotted over time. The program is run 10 times to show 10 trajectories. If the inter-modular links are reduced, the trajectories are more divergent run-to-run, see figure 3.

References

[1] L. Allen, An Introduction to Stochastic Epidemic Models, [Online] Available: https://www.math.mun.ca/~zhao/ARRMSschool/StochEpidModels.pdf

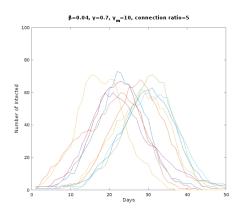


Figure 2: Infected Population, cluster connection ratio 5

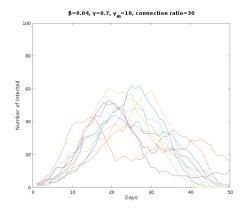


Figure 3: Infected Population, cluster connection ratio 30

- [2] R. Connell, P. Dawson, A. Skvortsov, "Comparison of an Agent-based Model of Disease Propagation with the Generalised SIR Epidemic Model," [Online] Available: https://apps.dtic.mil/dtic/tr/fulltext/u2/a510899.pdf
- [3] EpiModel "Mathematical Modeling of Infectious Disease Dynamics" [Online] Available: http://www.epimodel.org/index.html
- [4] M. Wolf "Differential Equation and Agent-Based Models in Epidemiology" page 36, [Online] Available: https://www.sandia.gov/~mmwolf/presentations/CS591MH_20060215.pdf
- [5] octave-networks-toolbox [Online] Available: https://github.com/aeolianine/octave-networks-toolbox