A generalized SIR and an approach to network

Efforts of a newbie

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Chapter 1: Preliminaries and model

An informal definition of network

As long as we are concerned, a network is a set of agents in which the behaviour (transition rates/probabilities) of a single individual is affected by the state of some other agents, called neighbours.
It can easily be represented by an adjacency matrix A_{ij} and a set of rates.
Here the topology of the networks is fixed (no scale-free networks).

The model

Generalised SIR: Unified approach for disease and rumor spreading.Here we will only look at contact processes.[1]

$$
\begin{aligned}
Y + X &\xrightarrow{\lambda\eta} Y + Y, \\
Y + X &\xrightarrow{\lambda(1-\eta)} Y + Z, \\
Y + Y &\xrightarrow{\alpha} Z + Y, \\
Y + Z &\xrightarrow{\alpha} Z + Z, \\
Z + X &\xrightarrow{\beta} Y + X, \\
Y &\xrightarrow{\delta_1} X, \\
Y &\xrightarrow{\delta_2} Z, \\
Z &\xrightarrow{\gamma} X,
\end{aligned}
$$

[1] *Ferraz De Arruda,Rodrigues,Cozzo,Moreno and Rodriguez*, Unifying Markov Chain Approach for Disease and Rumour Spreading in Complex Networks

Problems of a DTMC approach

- Synchronous networks
- Finalization $\rightarrow$ node ordering as agent/node "speed".

We prevent these factors by using a CTMC approach. All the above parameters are now rates, except from η.

Chapter 2: CTMC network and node-based method

Simulation approaches

How to update the system? Variation of Gillespie Algorithm:

- Rule-based model: total rate of a transition is match(Pattern,Graph)*single_rate. Avoided: searching for multiple occurrences of multiple patterns in a graph can be expensive.
- Node-based method[2]: the update starts from a node sampled with probability proportional to its total rate.

[2] *St-Onge,Young,Dube'*, Efficient Sampling of spreading processes on complex networks using a composition and rejection algorithm

Node-based method with rejection sampling

The article analyzes the SIS model and define:

- ω_i= total rate of interaction of node i
- $W = \sum_{i=1}^{N} \omega_i$

ω_i in a network depends on state of node i, rates of transitions and from $k_{i,s}$=number of neighbours of i in state s.
i.e. for node(i) in state Z in our model we have $\omega_i = \gamma + k_{i,X} * \beta$

Node-based method, part 2

Rejection sampling is used: at every iteration the starting node j is sampled uniformly between the neighboours of i and accepted iff $rand < \omega_j / W$. Otherwise, a new node is sampled until acceptance. Let $spont_j$ be the rate of spontaneous transition of node j, let i be the accepted node, the iteration will be a spontaneous process with probability $(spont_i/\omega_i)$.

Otherwise an interaction is performed, contacting a neighbour of i with uniform probability.

Chapter 3: Generalization and attempted improvements

only Y contagion, uniform neighbour distribution

$\lambda = \eta = 1$, all the other rates are 0, so only contact from a Y nodes should be permitted.

Actually the uniform neighbour sampling allows a node in state Y to contact a neighbour!=X independently of the rates, so that Y+Y→ Z+Y is allowed ∀ rate. Z instead has no possible transition.
Using

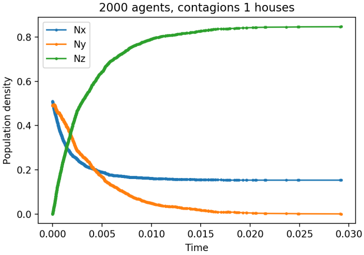
$$E[N_x(it+1)] = \frac{N_x(it)}{N-1}(N_x(it)-1) + \frac{N-1-N_x(it)}{N-1}N_x(it)$$

we get

$$N_x(it) = N_x(0) * (1 - \frac{1}{N-1})^{it}$$

The recursion for N_y is more complicated and has been solved numerically.

only Y contagion, uniform neighbour distribution 2



Using equations from previous slides and confronting with simulated data, the relative error is $< 0.05\%$

Attempted improvements to node-based method

- Generalization for multiple non spontaneous transitions.
- Avoid rejection sampling and directly select node using probabilities (ω_i / W): execution times are reduced by 40%.
- Select neighbours according to rates of interaction: this also prevent the problem of independence by rate encountered in previous slides.

Chapter 4: Verification with fluid approximation and results

Fluid approximation equations (population model)

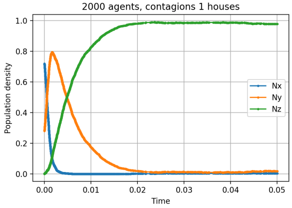
$$\frac{d\rho_x}{dt} = \gamma\,\rho_z + \delta_1\,\rho_y - \langle k \rangle\ \lambda * \rho_y * \rho_x$$

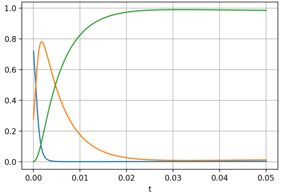
$$\frac{d\rho_y}{dt} = -(\delta_1 + \delta_2)\rho_y + \langle k \rangle\,[\beta \rho_z \rho_x - \alpha \rho_y (1 - \rho_x) + \lambda \eta \rho_y \rho_x]$$

$$\frac{d\rho_z}{dt} = \delta_2 \rho_y - \gamma \rho_z + \langle k \rangle\,[\alpha \rho_y (1 - \rho_x) - \beta \rho_z \rho_x + \lambda (1 - \eta) \rho_y \rho_x]$$

with $\langle k \rangle = (house\_size - 1) + \frac{houses - 1}{houses}$ average degree of all nodes in the graph. It's a good approximation for $house\_size >> houses$

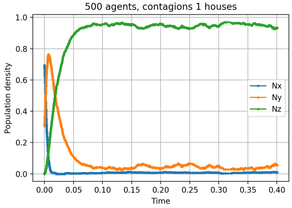
Results: complete graph

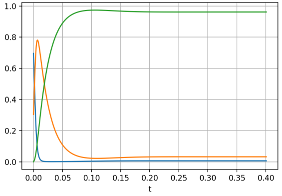




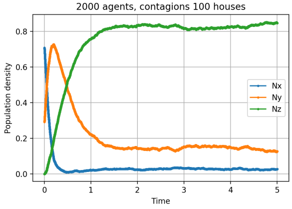
Simulations

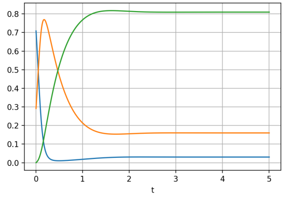
Approximations





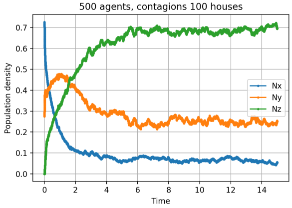
Results: 100 houses

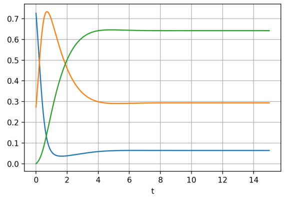




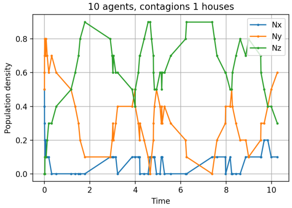
Simulations

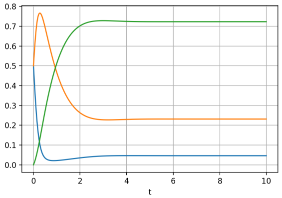
Approximations





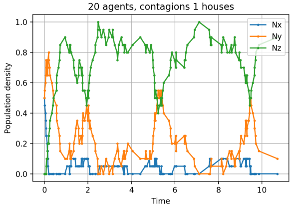
Limits of the approximation: complete graph on little N

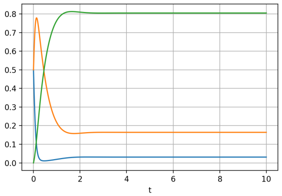




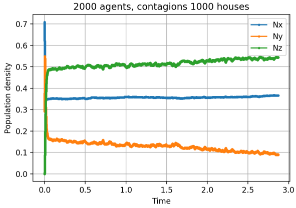
Simulations

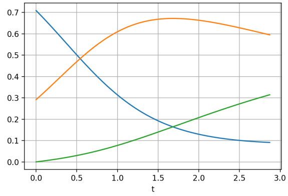
Approximations





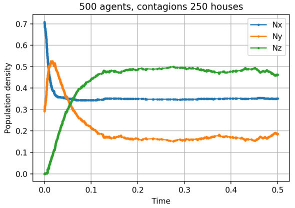
Limits of the approximation: 2 nodes each house

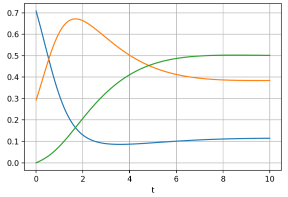




Simulations

Approximations





The End

This has been just an introduction. There's a lot more out there.

Thank you for your attention