Epidemiology on a Network

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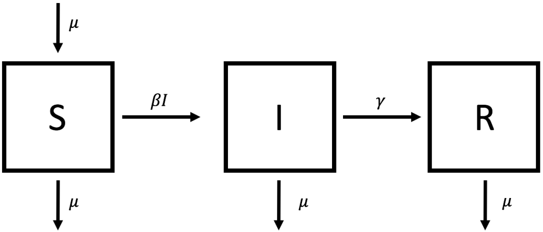
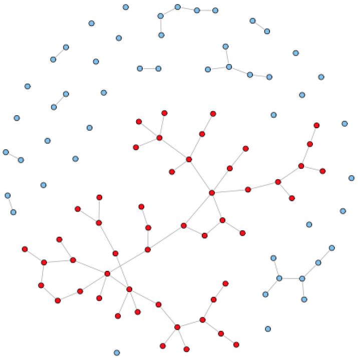
Well mixed approach to SIR Model [JCM13]

- Every individual has an equal chance, per unit time, of coming into contact with every other person



$$\frac{\mathrm{d}S}{\mathrm{d}t} = \mu N - \beta SI - \mu S \qquad \frac{\mathrm{d}I}{\mathrm{d}t} = \beta SI - \gamma I - \mu I \qquad \frac{\mathrm{d}R}{\mathrm{d}t} = \gamma I - \mu R$$

Giant component [Tie16]



Q: How do we know if the infected vertex, X, is in the giant component of a random graph?

A: Degree distribution

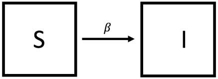
- excess degree distribution
- neighbor degree distribution

Set up [Tie16] I

- **Goal:** A system of ordinary differential equations (ODEs) that describe the probability that a given vertex is in a given state at a given time
  - Simulating networks can be computationally costly, especially for large networks
  - Techniques for approximating the system of ODEs by using a lower dimensional set of ODEs (pair approximation)
  - Underlying process: Stochastic disease model on a network
- Focus only on giant component (n vertices)

Set up [Tie16] II

- Simplify to an S-I model without vital dynamics



Graph properties

- Infection occurs via infected neighbors
- Undirected
- Unweighted
- Simple graph: no self-loops, single edge between neighbors

Notation [Tie16]

$\beta \rightarrow$ disease transmission rate
$\langle s_j \rangle \rightarrow$ probability that vertex j is susceptible at time t
$\langle i_j \rangle \rightarrow$ probability that vertex j is infected at time t
$\langle s_j i_k \rangle \rightarrow$ probability that j is in s and k is in i at time t
$A \rightarrow$ adjacency matrix of the graph

$$A_{jk} = \begin{cases} 0 & \text{j and k not neighbors} \\ 1 & \text{j and k neighbors} \end{cases}$$

Pair approximation [New10] [Tie16] [DFHea11] I

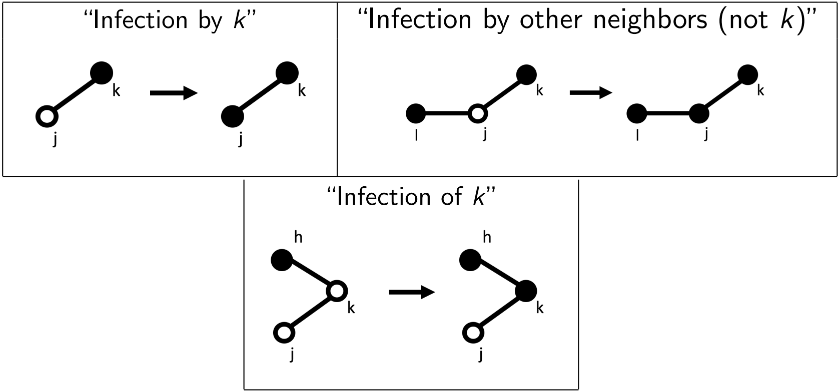
$$\frac{d\langle s_j\rangle}{dt} = -\beta \sum_{k=1}^{n} A_{jk} \langle s_j\rangle (1 - \langle s_k\rangle)$$

$$\frac{d\langle i_j\rangle}{dt} = -\beta \sum_{k=1}^{n} A_{jk} (1 - \langle i_j\rangle) \langle i_k\rangle$$

- Does not take into account the correlation between j and k
- Assumes $\langle s_j i_k\rangle = \langle s_j\rangle \langle i_k\rangle$

Pair approximation [New10] [Tie16] [DFHea11] II

Taking correlation of j, k into account $\langle s_j i_k \rangle$:



Pair approximation [New10] [Tie16] [DFHea11] III

$$\frac{d\langle s_j i_k\rangle}{dt} = -\beta\langle s_j i_k\rangle - \beta\sum_{l\neq k} A_{jl}\langle s_j i_k i_l\rangle + \beta\sum_{h\neq j} A_{kh}\langle s_j s_k i_h\rangle$$

Can use pair approximation on the triples

- Only a good approximation if there are not a lot of triangles in the network

With Bayes Theorem, P(A ∩ B) = P(A—B)P(B), we obtain

$$\langle s_j s_k i_h\rangle \approx \frac{\langle s_k i_h\rangle\langle s_j s_k\rangle}{\langle s_k\rangle} \qquad \langle s_j i_k i_l\rangle \approx \frac{\langle s_j i_k\rangle\langle i_k i_l\rangle}{\langle i_k\rangle}$$

Pair approximation [New10] [Tie16] [DFHea11] IV

Substituting the results obtained using Bayes Theorem into the original equation gives

$$\frac{d\langle s_j i_k\rangle}{dt} = -\beta\langle s_j i_k\rangle - \beta\sum_{l\neq k} A_{jl}\frac{\langle s_j i_k\rangle\langle i_k i_l\rangle}{\langle i_k\rangle} + \beta\sum_{h\neq j} A_{kh}\frac{\langle s_k i_h\rangle\langle s_j s_k\rangle}{\langle s_k\rangle}.$$

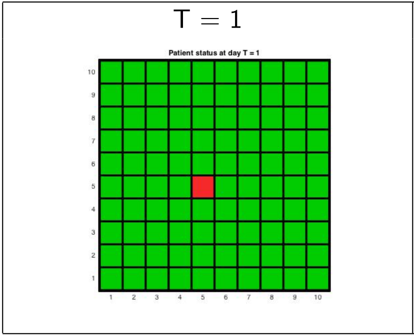
Rewrite $\langle s_j s_k\rangle = \langle s_j(1-i_k)\rangle = \langle s_j\rangle - \langle s_j i_k\rangle$ and let p_{jk} be the conditional probability that k is infected given that j is not.

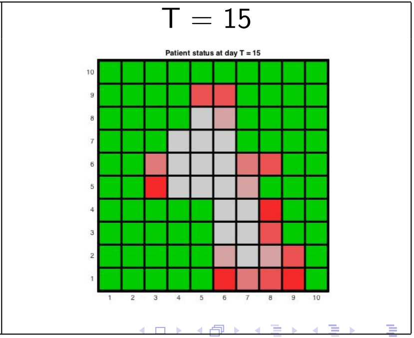
$$\frac{dp_{jk}}{dt} = \beta(1-p_{jk})\left[-p_{jk} + \sum_{h\neq j} A_{kh}p_{kh}\right]$$

Simulation 1 [Coo13] I

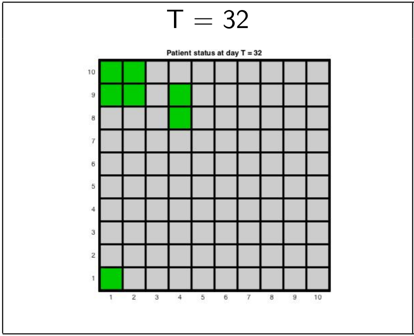
Parameters:

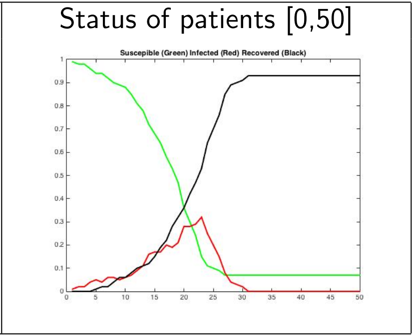
- one infected patient in middle
- t-max = 50





Simulation 1 [Coo13] II



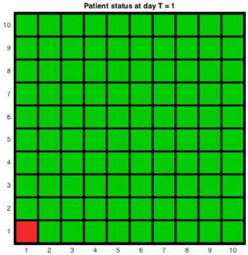


Simulation 2 [Coo13] I

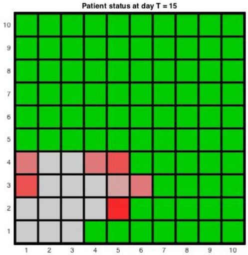
Parameters:

- one infected patient in corner
- t-max = 50

T = 1

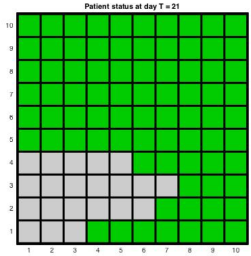


T = 15

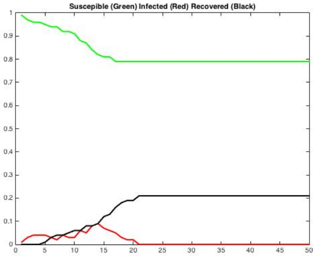


Simulation 2 [Coo13] II

T = 21



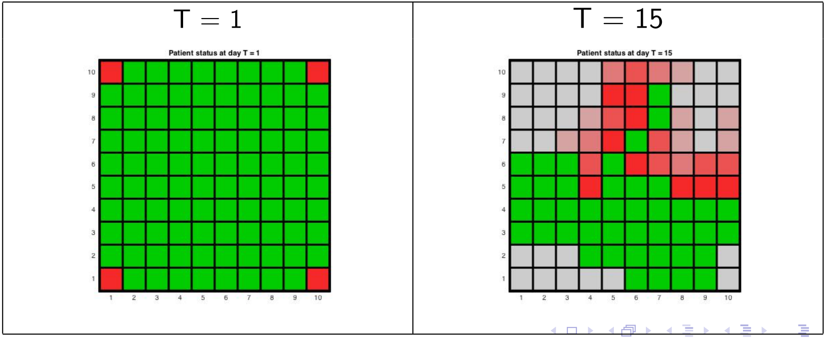
Status of patients [0,50]



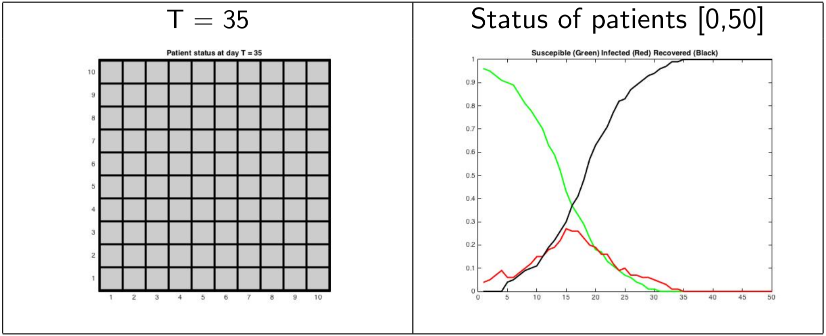
Simulation 3 [Coo13] I

Parameters:

- one infected patient in corner
- t-max = 50



Simulation 3 [Coo13] II



NetLogo Simulations [SW09] [Wil08]

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