Epidemics on networks

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14.04.2014

Epidemic models on networks

- network of potential contacts (adjacency matrix **A**)
- probabilistic model (state of a node):
  $s_i(t)$ - probability that at t node i is susceptable
  $x_i(t)$ - probability that at t node i is infected
  $r_i(t)$ - probability that at t node i is recovered
- from determenistic to probabilistic description
- connected component - all nodes reachable
- network is undirected (matrix **A** is symmetric)

SI model

- SI Model

$$S \longrightarrow I$$

- Probabilites that node i: $s_i(t)$ - susceptable, $x_i(t)$ -infected at t

$$x_i(t) + s_i(t) = 1$$

- β - infection rate, probability to get infected in a unit time

$$x_i(t+\delta t) = x_i(t) + \beta s_i \sum_j A_{ij} x_j \delta t$$

- infection equation

$$\begin{aligned}
\frac{dx_i(t)}{dt} &= \beta s_i(t) \sum_j A_{ij} x_j(t) \\
\frac{ds_i(t)}{dt} &= -\beta s_i(t) \sum_j A_{ij} x_j(t)
\end{aligned}$$

SI model

- Differential equation

$$\frac{dx_i(t)}{dt} = \beta(1 - x_i(t)) \sum_j A_{ij} x_j$$

- early time approximation, $t \to 0, \;\; x_i(t) \ll 1$

$$\frac{dx_i(t)}{dt} = \beta \sum_j A_{ij} x_j$$

$$\frac{d\mathbf{x}(t)}{dt} = \beta \mathbf{A}\mathbf{x}(t)$$

- Solution in the basis

$$\mathbf{A}\mathbf{v}_k = \lambda_k \mathbf{v}_k$$

$$\mathbf{x}(t) = \sum_k a_k(t) \mathbf{v}_k$$

SI model

$$\sum_k \frac{da_k}{dt}\mathbf{v}_k = \beta \sum_k \mathbf{A} a_k(t)\mathbf{v}_k = \beta \sum_k a_k(t)\lambda_k \mathbf{v}_k$$

$$\frac{da_k(t)}{dt} = \beta\lambda_k a_k(t)$$

$$a_k(t) = a_k(0)e^{\beta\lambda_k t}, \quad a_k(0) = \mathbf{v}_k^T\mathbf{x}(0)$$

- Solution

$$\mathbf{x}(t) = \sum_k a_k(0)e^{\lambda_k\beta t}\mathbf{v}_k$$

- $t \to 0$, $\lambda_{max} = \lambda_1 > \lambda_k$

$$\mathbf{x}(t) = \mathbf{v}_1 e^{\lambda_1\beta t}$$

1. growth rate of infections depends on λ_1
2. probability of infection of nodes depends on $\mathbf{v}_1$, i.e v_{1i}

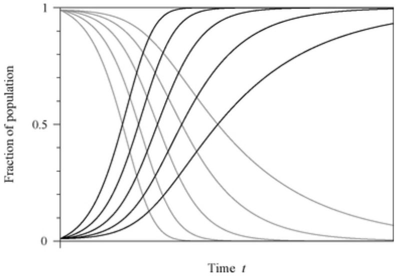
SI model

- late- time approximation, $t \to \infty$, $x_i(t) \to const$

$$\frac{dx_i(t)}{dt} = \beta(1 - x_i(t)) \sum_j A_{ij} x_j = 0$$

  $\mathbf{Ax} \neq 0$ since $\lambda_{min} \neq 0$, $1 - x_i(t) \approx 0$
- All nodes in connected component get infected $t \to \infty \quad x_i(t) \to 1$
- Connected component structure and distribution. Does initially infected node belong to GCC?

SI model



SIS model

- SIS Model

$$S \longrightarrow I \longrightarrow S$$

- Probabilites that node i: $s_i(t)$ - susceptable, $x_i(t)$ -infected at t

$$x_i(t) + s_i(t) = 1$$

- β - infection rate, γ - recovery rate

$$\begin{aligned}
\frac{dx_i(t)}{dt} &= \beta s_i(t) \sum_j A_{ij} x_j(t) - \gamma x_i \\
\frac{ds_i(t)}{dt} &= -\beta s_i(t) \sum_j A_{ij} x_j(t) + \gamma x_i
\end{aligned}$$

SIS model

- Differential equation

$$\frac{dx_i(t)}{dt} = \beta(1 - x_i(t)) \sum_j A_{ij} x_j - \gamma x_i$$

- early time approximation, $x_i(t) \ll 1$

$$\frac{dx_i(t)}{dt} = \beta \sum_j A_{ij} x_j - \gamma x_i$$

$$\frac{dx_i(t)}{dt} = \beta \sum_j (A_{ij} - \frac{\gamma}{\beta} \delta_{ij}) x_j$$

$$\frac{d\mathbf{x}(t)}{dt} = \beta(\mathbf{A} - (\frac{\gamma}{\beta})\mathbf{I})\mathbf{x}(t)$$

$$\frac{d\mathbf{x}(t)}{dt} = \beta \mathbf{M}\mathbf{x}(t), \quad \mathbf{M} = \mathbf{A} - (\frac{\gamma}{\beta})\mathbf{I}$$

SIS model

- Eigenvector basis

$$\begin{aligned} \mathbf{M}\mathbf{v}'_k &= \lambda'_k \mathbf{v}'_k, \quad \mathbf{M} = \mathbf{A} - (\frac{\gamma}{\beta})\mathbf{I}, \quad \mathbf{A}\mathbf{v}_k = \lambda_k \mathbf{v}_k \\ \mathbf{v}'_k &= \mathbf{v}_k, \quad \lambda'_k = \lambda_k - \frac{\gamma}{\beta} \end{aligned}$$

- Solution

$$\mathbf{x}(t) = \sum_k a_k(t)\mathbf{v}'_k = \sum_k a_k(0)\mathbf{v}'_k e^{\lambda'_k \beta t} = \sum_k a_k(0)\mathbf{v}_k e^{(\beta\lambda_k - \gamma)t}$$

- $\lambda_1 \geq \lambda_k$, critical: $\beta\lambda_1 = \gamma$
  -if $\beta\lambda_1 > \gamma, \quad \mathbf{x}(t) \to \mathbf{v}_1 e^{(\beta\lambda_1 - \gamma)t}$ - growth
  -if $\beta\lambda_1 < \gamma, \quad \mathbf{x}(t) \to 0$ - decay

SIS model

Epidemic threshold R_0:

- if $\frac{\beta}{\gamma} < R_0$ - infection dies over time
- if $\frac{\beta}{\gamma} > R_0$ - infection survives and becomes epidemic

In SIS model:

$$R_0 = \frac{1}{\lambda_1}, \quad \mathbf{A}\mathbf{v}_1 = \lambda_1 \mathbf{v}_1$$

SIS model

long time $t \to \infty$:

- $x_i(t) \to const$

$$\frac{dx_i(t)}{dt} = \beta(1 - x_i)\sum_j A_{ij}x_j - \gamma x_i = 0$$

$$x_i = \frac{\sum_j A_{ij}x_j}{\frac{\gamma}{\beta} + \sum_j A_{ij}x_j}$$

- Above the epidemic threshold ($\beta/\gamma > R_0$)
  - if $\beta \gg \gamma$, $x_i(t) \to 1$
  - if $\beta \sim \gamma$, $x_i \frac{\gamma}{\beta} = \sum_j A_{ij}x_j$, then $\lambda_1 = \frac{\gamma}{\beta}$, $\quad x_i(t) \to (v_1)_i$

SIR model

- SIR Model

$$S \longrightarrow I \longrightarrow R$$

- probabilities $s_i(t)$ -susceptable , $x_i(t)$ - infected, $r_i(t)$ - recovered

$$s_i(t) + x_i(t) + r_i(t) = 1$$

- β - infection rate, γ - recovery rate
- Infection equation:

$$\begin{aligned}
\frac{ds_i}{dt} &= -\beta s_i \sum_j A_{ij} x_j \\
\frac{dx_i}{dt} &= \beta s_i \sum_j A_{ij} x_j - \gamma x_i \\
\frac{dr_i}{dt} &= \gamma x_i
\end{aligned}$$

SIR model

- Differential equation

$$\frac{dx_i(t)}{dt} = \beta(1 - r_i - x_i)\sum_j A_{ij}x_j - \gamma x_i$$

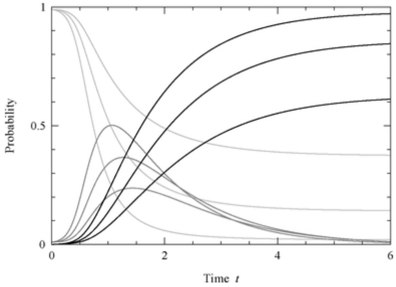
- early time, $t \to 0$, $r_i \sim 0$, SIS = SIR

$$\frac{dx_i(t)}{dt} = \beta(1 - x_i)\sum_j A_{ij}x_j - \gamma x_i$$

- Solution

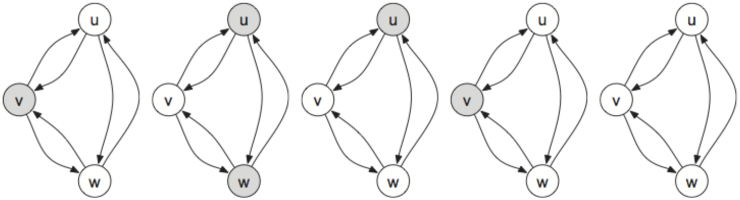
$$\mathbf{x}(t) \sim \mathbf{v}_1 e^{(\beta\lambda_1 - \gamma)t}$$

SIR model



Modeling SIS

1. Every node at any time step is in one state $\{S, I\}$
2. Initialize c nodes in state I
3. Each node stay infected $\tau_\gamma = 1/\gamma$ time steps
4. On each time step each I node has a prabability β to infect its nearest neighbours (NN), $S \to I$
5. After τ_γ time steps node recovers, $I \to S$

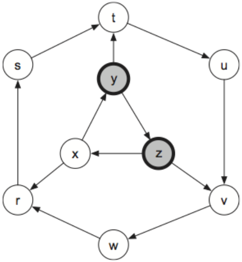


(a) (b) (c) (d) (e)

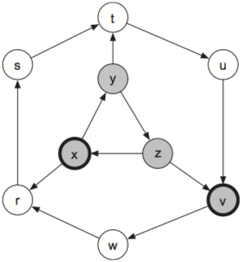
Modeling SIR

1. Every node at any time step is in one state $\{S, I, R\}$
2. Initialize c nodes in state I
3. Each node stay infected $\tau_\gamma = 1/\gamma$ time steps
4. On each time step each I node has a prabability β to infect its nearest neighbours (NN), $S \rightarrow I$
5. After τ_γ time steps node recovers, $I \rightarrow R$
6. Nodes R do not participate in infection propagation

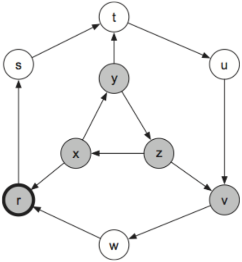
Modeling SIR



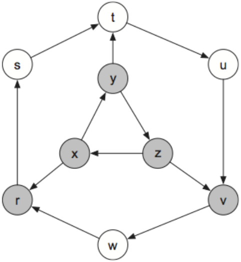
(a)



(b)

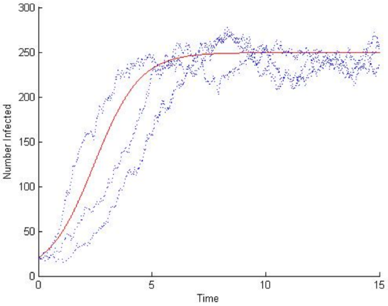


(c)

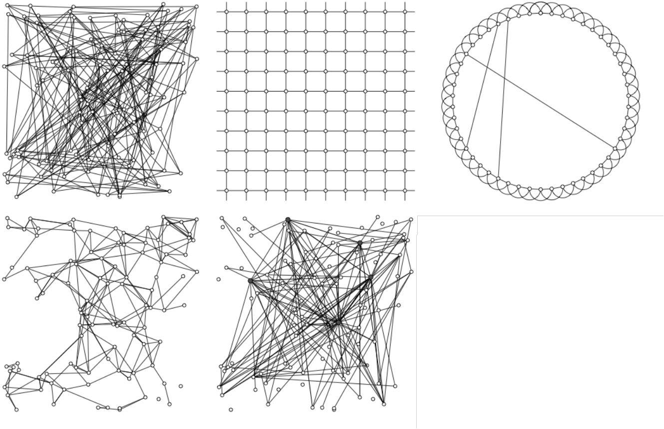


(d)

Stochastic modeling

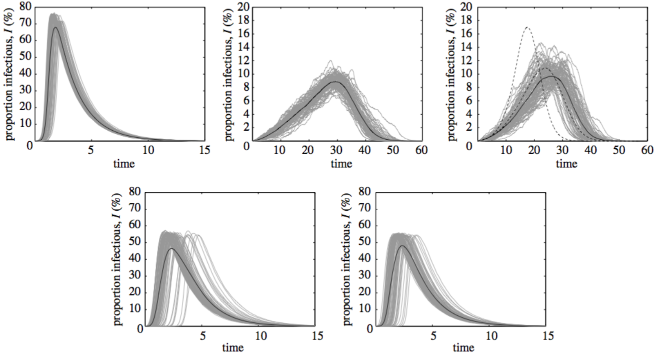


5 Networks, SIR



Networks: random, lettice, small world, spatial, scale-free

Keeling et al, 2005



Networks: random, lettice, small world, spatial, scale-free

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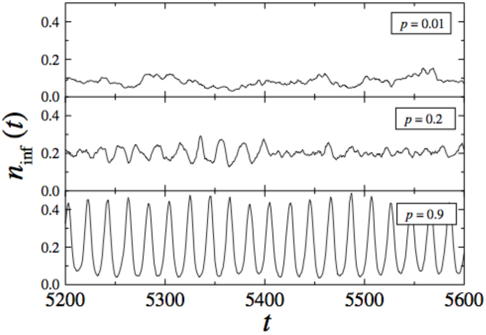

Small-world network at different values of disorder parameter p

Kuperman et al, 2001

References

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- Small World Effect in an Epidemiological Model. M. Kuperman and G. Abramson, Phys. Rev. Lett., Vol 86, No 13, pp 2909-2912, 2001