

Epidemics on networks

Leonid E. Zhukov

School of Data Analysis and Artificial Intelligence
Department of Computer Science
National Research University Higher School of Economics

Network Science



NATIONAL RESEARCH
UNIVERSITY

- 1 Probabilistic model
 - SI model
 - SIS model
 - SIR model
- 2 Simulations
- 3 Experimental results

Probabilistic model

- network of potential contacts (adjacency matrix \mathbf{A})
- probabilistic model (state of a node):
 - $s_i(t)$ - probability that at t node i is susceptible
 - $x_i(t)$ - probability that at t node i is infected
 - $r_i(t)$ - probability that at t node i is recovered
- β - infection rate (probably to get infected on a contact in time δt)
- γ - recovery rate (probability to recover in a unit time δt)
- from deterministic to probabilistic description
- connected component - all nodes reachable
- network is undirected (matrix \mathbf{A} is symmetric)

Probabilistic model

Two processes:

- Node infection:



$$P_{inf} = s_i(t) \left(1 - \prod_{j \in \mathcal{N}(i)} (1 - \beta x_j(t) \delta t) \right) \approx \beta s_i(t) \sum_{j \in \mathcal{N}(i)} x_j(t) \delta t$$

- Node recovery:



$$P_{rec} = \gamma x_i(t) \delta t$$

- SI Model

$$S \longrightarrow I$$

- Probabilities that node i : $s_i(t)$ - susceptible, $x_i(t)$ -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 equations

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

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

- Differential equation

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

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

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

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

- Solution in the basis

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

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

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

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

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

- Solution

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

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

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

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

- late- time approximation, $t \rightarrow \infty$, $x_i(t) \rightarrow \text{const}$

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

Ax $\neq 0$ since $\lambda_{\min} \neq 0$, $1 - x_i(t) \approx 0$

- All nodes in connected component get infected $t \rightarrow \infty$ $x_i(t) \rightarrow 1$
- Connected component structure and distribution. Does initially infected node belong to GCC?

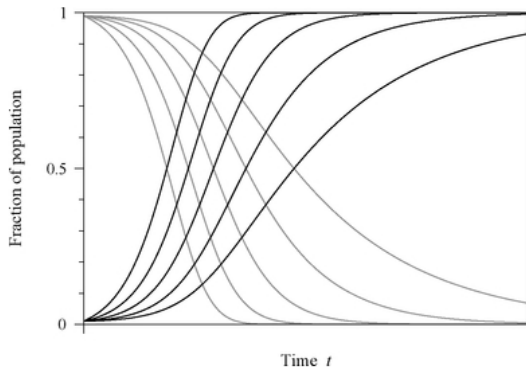
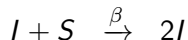


image from M. Newman, 2010

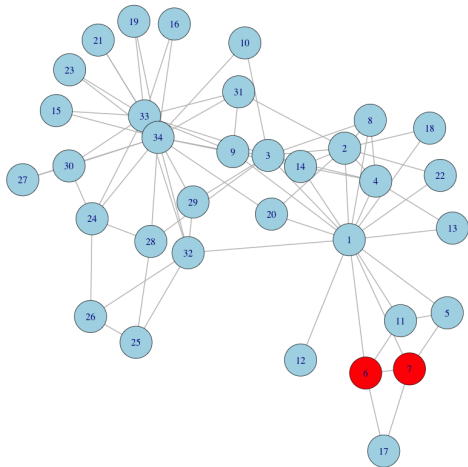
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- 2 Initialize c nodes in state I
- 3 On each time step each I node has a probability β to infect its nearest neighbors (NN), $S \rightarrow I$

Model dynamics:



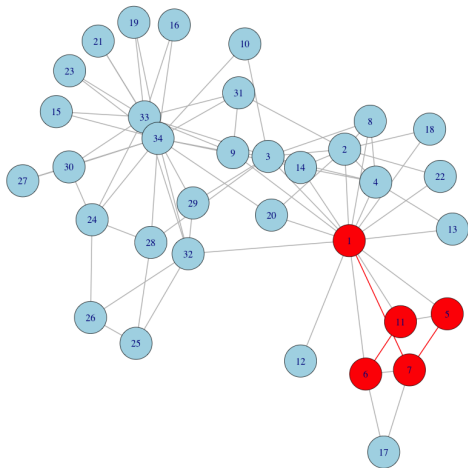
SI model simulation

$$\beta = 0.5$$



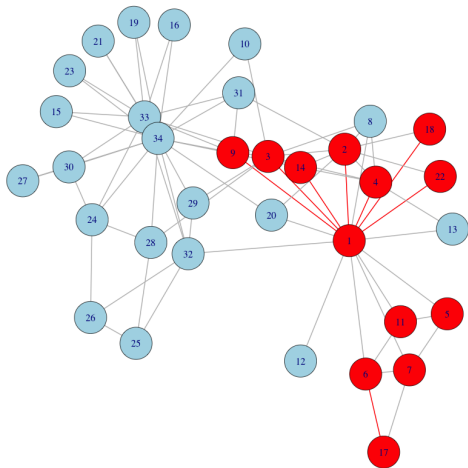
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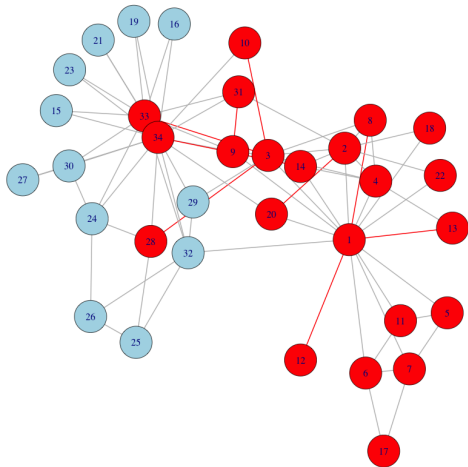
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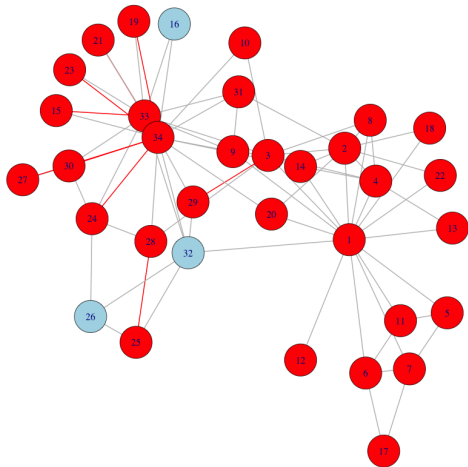
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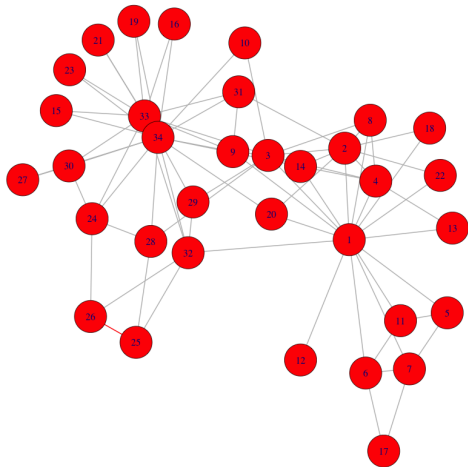
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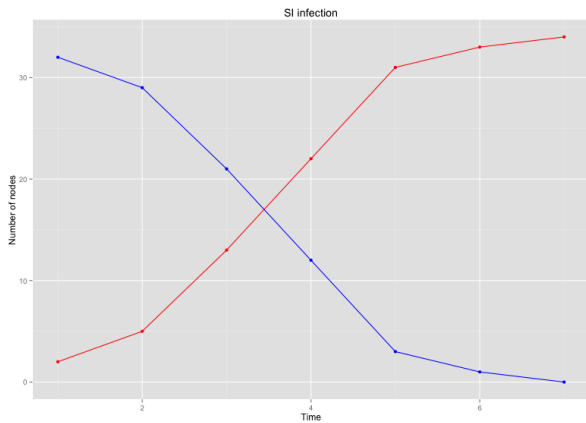


SI model simulation

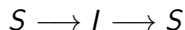
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SI model



- SIS Model



- Probabilities that node i : $s_i(t)$ - susceptible, $x_i(t)$ -infected at t

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

- β - infection rate, γ - recovery rate
- infection equations:

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

- Differential equation

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

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

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

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

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

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

- Eigenvector basis

$$\mathbf{M}\mathbf{v}'_k = \lambda'_k \mathbf{v}'_k, \quad \mathbf{M} = \mathbf{A} - \left(\frac{\gamma}{\beta}\right)\mathbf{I}, \quad \mathbf{A}\mathbf{v}_k = \lambda_k \mathbf{v}_k$$
$$\mathbf{v}'_k = \mathbf{v}_k, \quad \lambda'_k = \lambda_k - \frac{\gamma}{\beta}$$

- 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 $\beta \lambda_1 > \gamma$, $\mathbf{x}(t) \rightarrow \mathbf{v}_1 e^{(\beta \lambda_1 - \gamma)t}$ - growth
 - if $\beta \lambda_1 < \gamma$, $\mathbf{x}(t) \rightarrow 0$ - decay

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:

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

long time $t \rightarrow \infty$:

- $x_i(t) \rightarrow \text{const}$

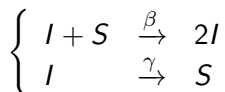
$$\frac{dx_i(t)}{dt} = \beta(1 - x_i) \sum_j A_{ij}x_j - \gamma x_i = 0$$

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

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

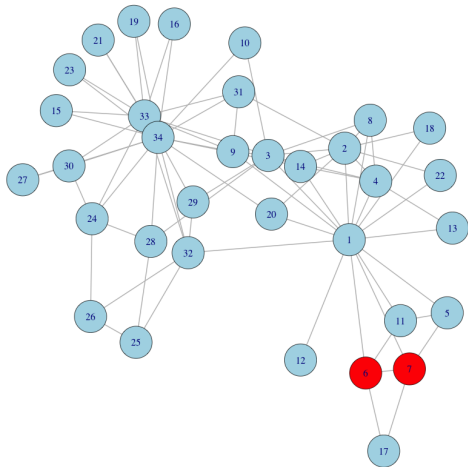
- 1 Every node at any time step is in one state $\{S, I\}$
- 2 Initialize c nodes in state I
- 3 Each node stays infected $\tau_\gamma = \int_0^\infty \tau e^{-\tau\gamma} d\tau = 1/\gamma$ time steps
- 4 On each time step each I node has a probability β to infect its nearest neighbours (NN), $S \rightarrow I$
- 5 After τ_γ time steps node recovers, $I \rightarrow S$

Model dynamics:



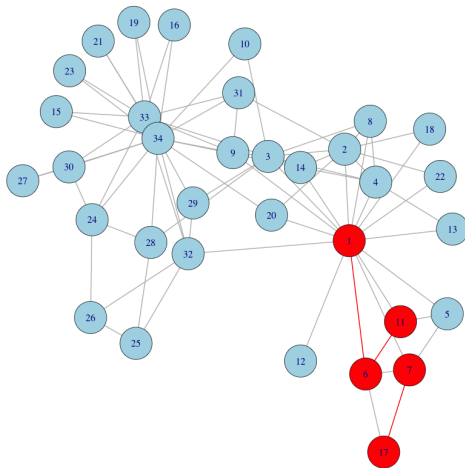
SIS model simulation

$$\beta = 0.5, \tau = 2$$



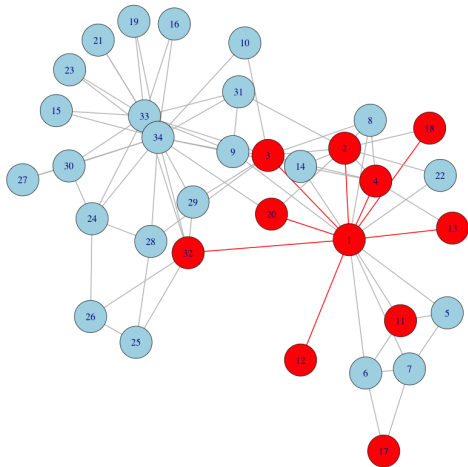
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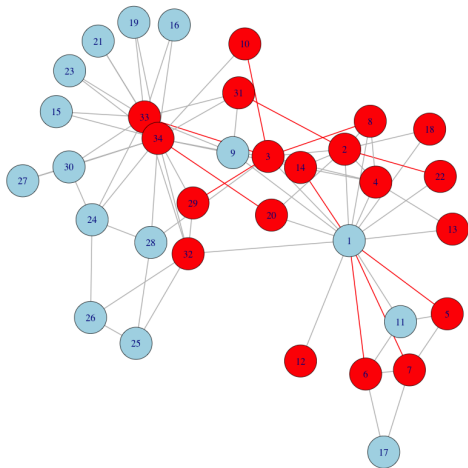
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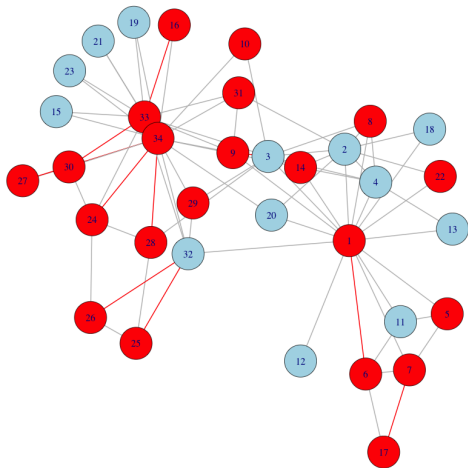
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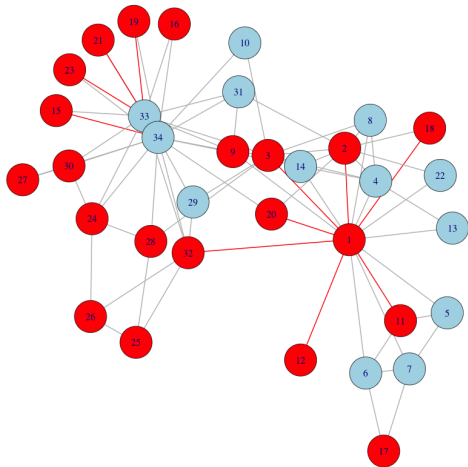
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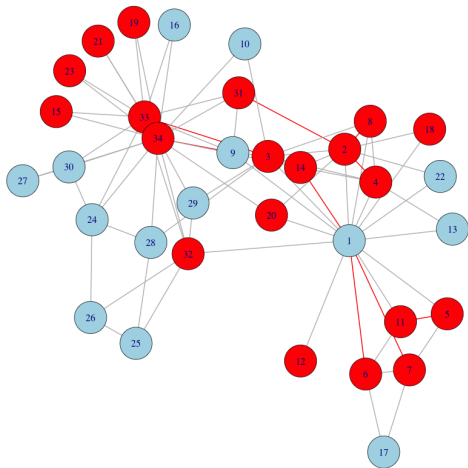
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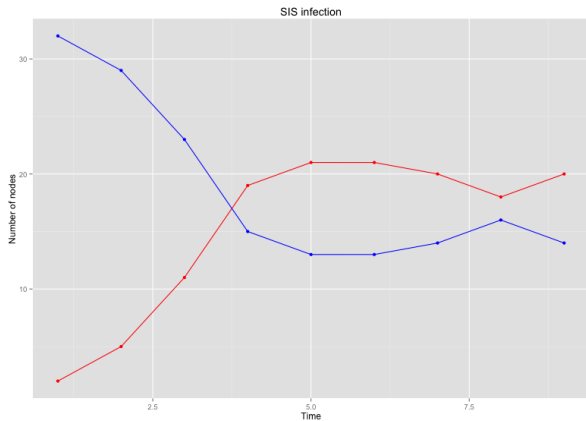


SIS model simulation

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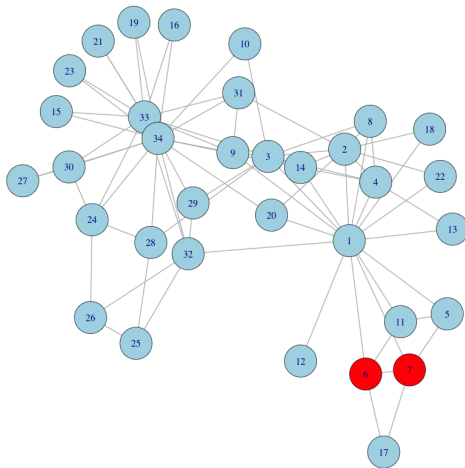


SIS model



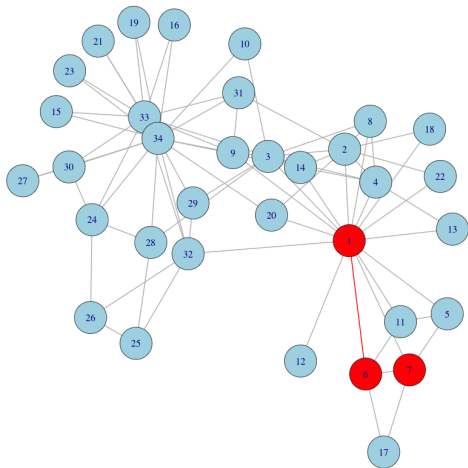
SIS model simulation

$$\beta = 0.2, \tau = 2$$



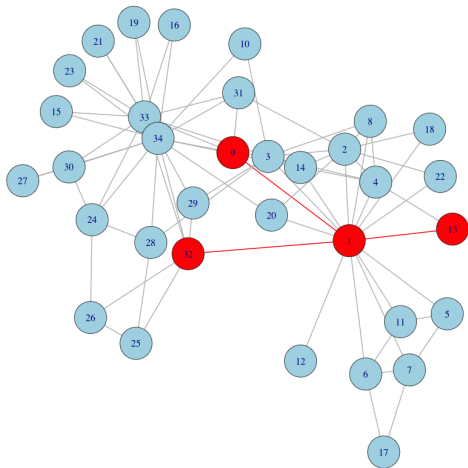
SIS model simulation

$$\beta = 0.2, \tau = 2$$



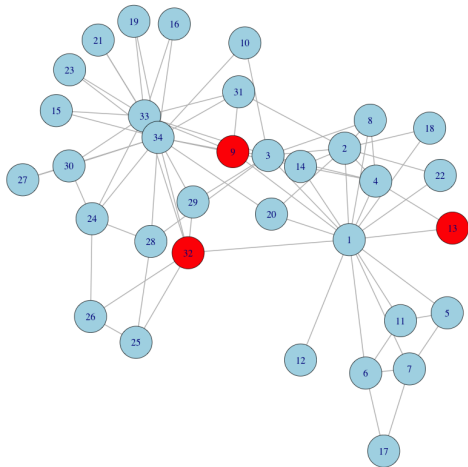
SIS model simulation

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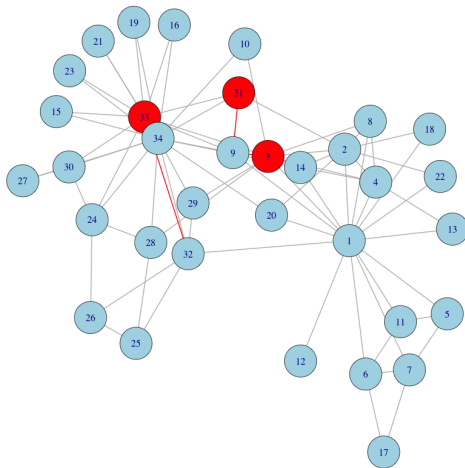
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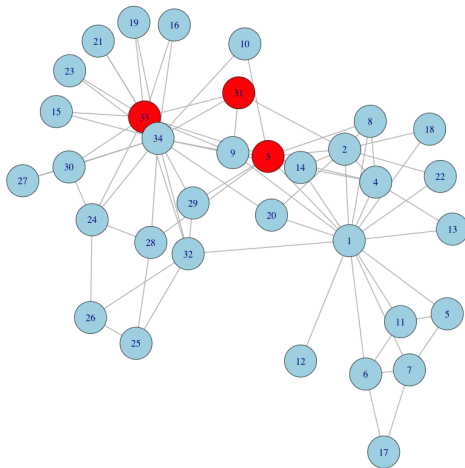
SIS model simulation

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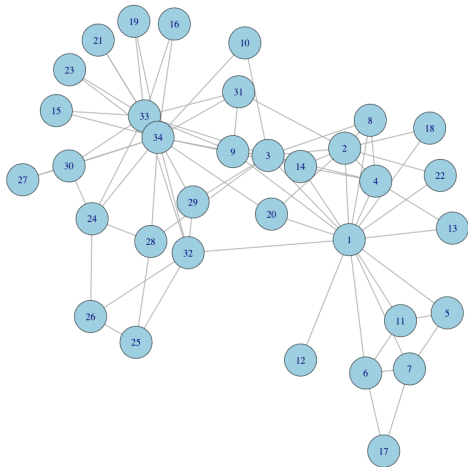
SIS model simulation

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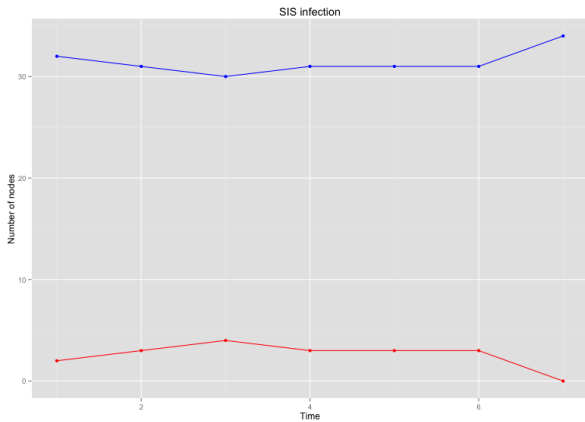


SIS model simulation

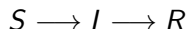
$$\beta = 0.2, \tau = 2$$



SIS model



- SIR Model



- 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:

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

$$\frac{dr_i}{dt} = \gamma x_i$$

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

- Differential equation

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

- early time, $t \rightarrow 0$, $r_i \sim 0$, 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

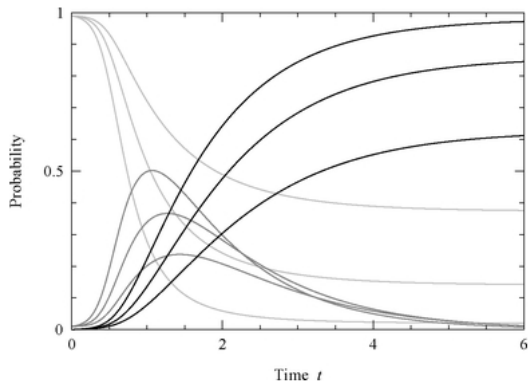
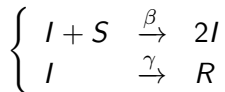


image from M. Newman, 2010

SIR simulation

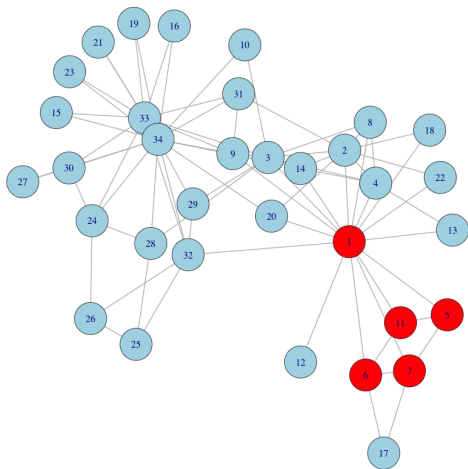
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- 2 Initialize c nodes in state I
- 3 Each node stays infected $\tau_\gamma = 1/\gamma$ time steps
- 4 On each time step each I node has a probability β to infect its nearest neighbours (NN), $S \rightarrow I$
- 5 After τ_γ time steps node recovers, $I \rightarrow R$
- 6 Nodes R do not participate in further infection propagation

Model dynamics:



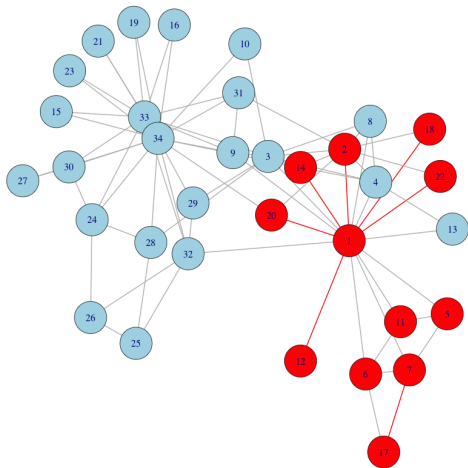
SIR model

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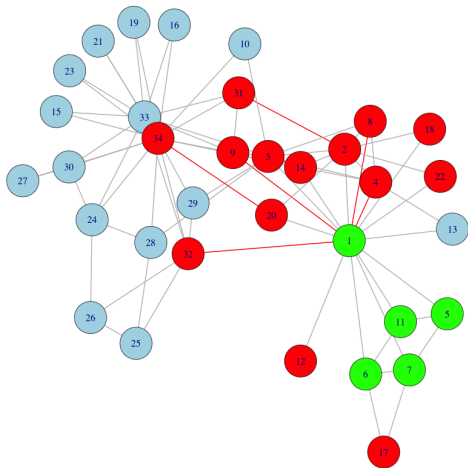
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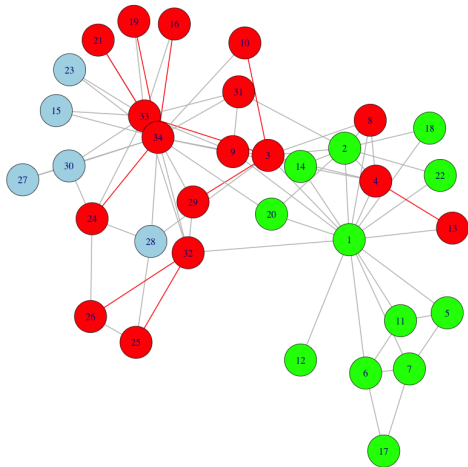
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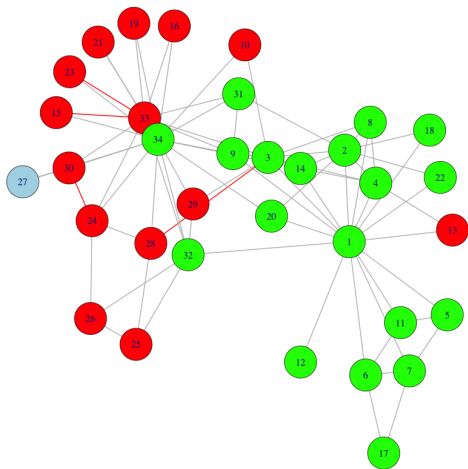
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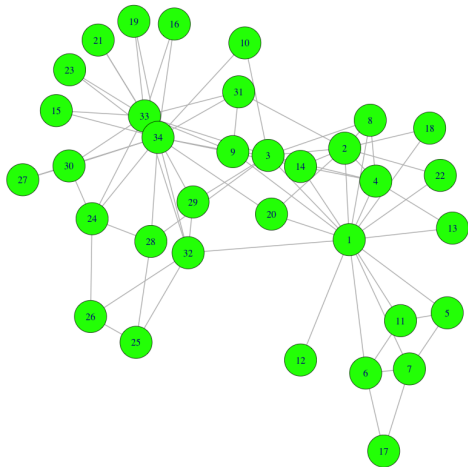
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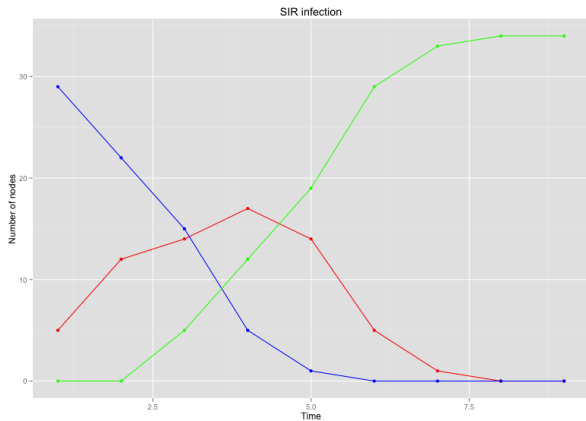


SIR model

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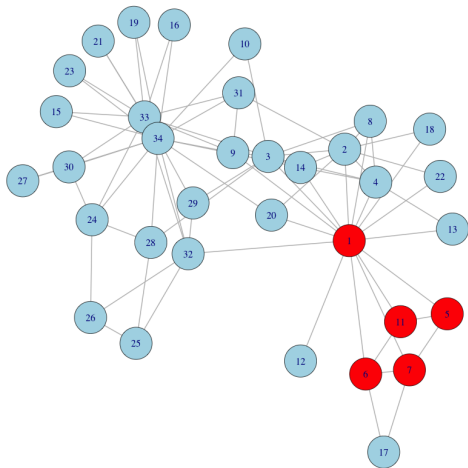


SIR model



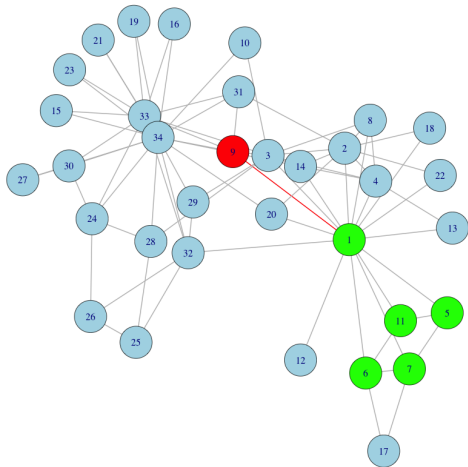
SIR model

$$\beta = 0.2, \tau = 2$$



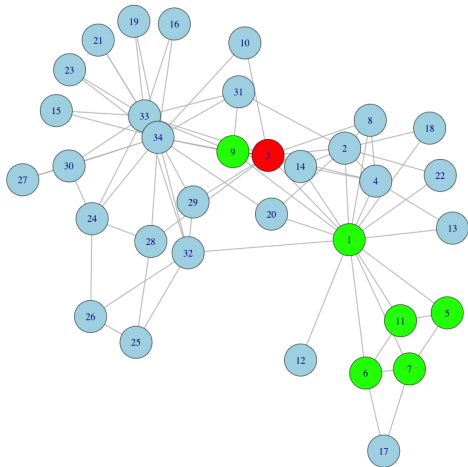
SIR model

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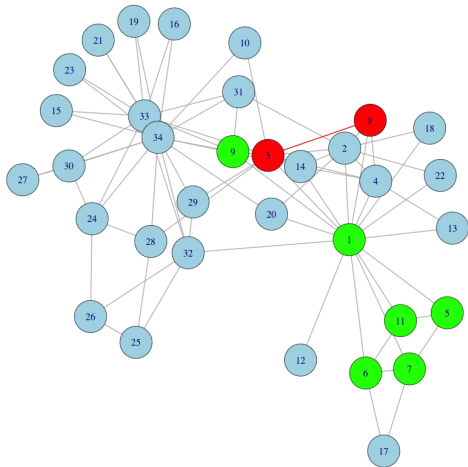
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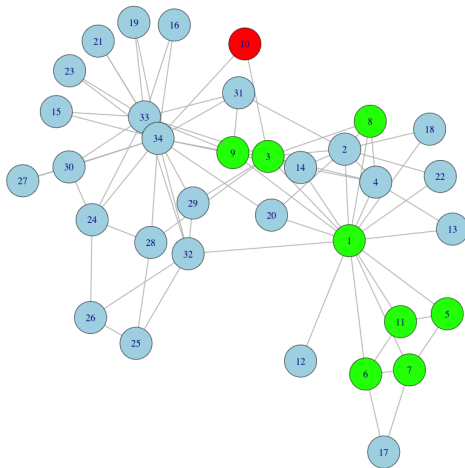
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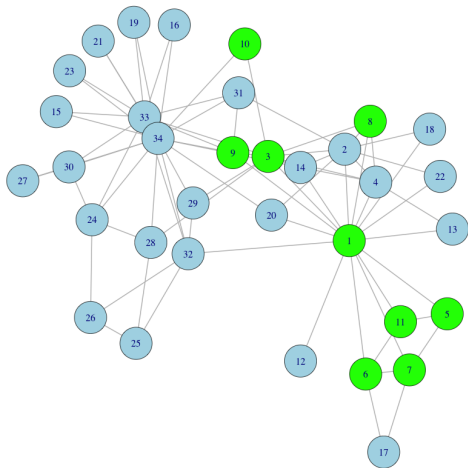
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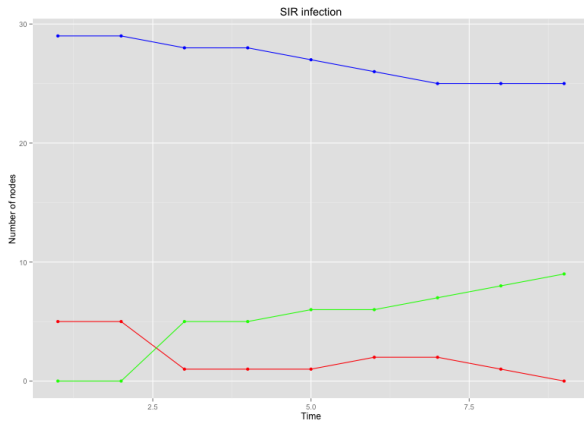


SIR model

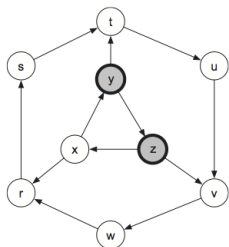
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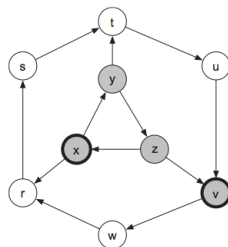
SIR model



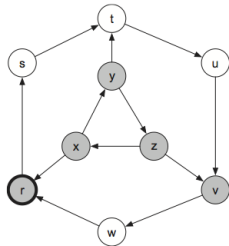
SIR epidemics as percolation



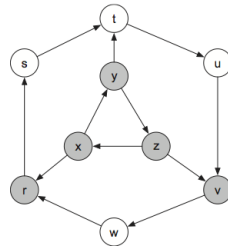
(a)



(b)

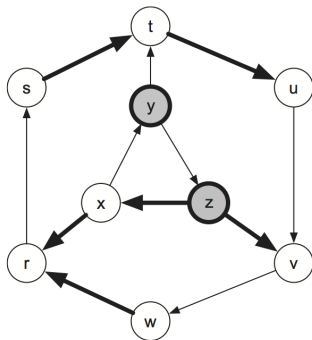


(c)



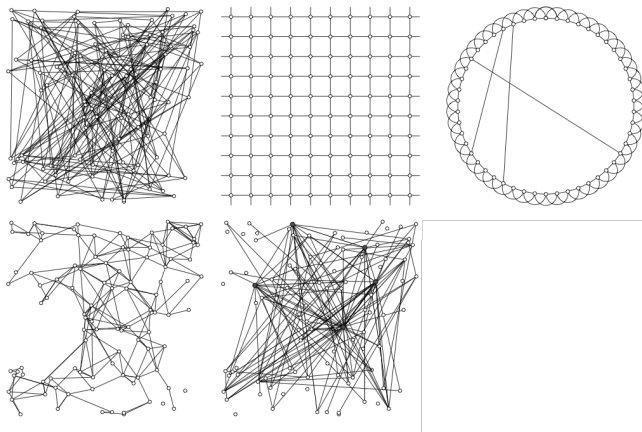
(d)

SIR epidemics as percolation



Bond percolation: only those nodes that are on a percolation path with infected node will get infected

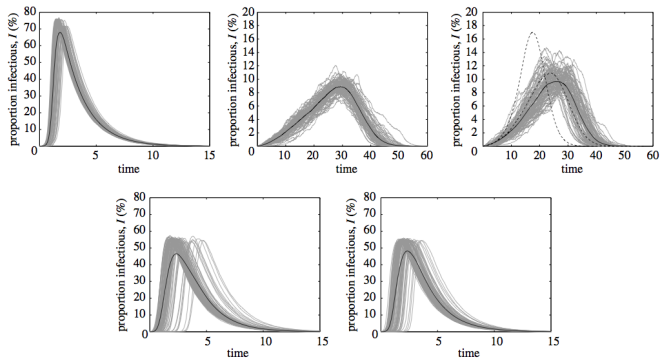
5 Networks, SIR



Networks: 1) random, 2) lattice, 3) small world, 4) spatial, 5) scale-free

image from Keeling et al, 2005

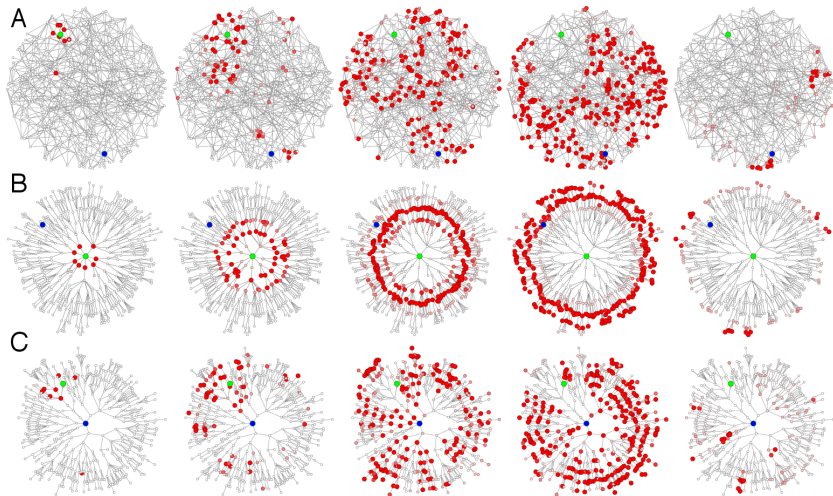
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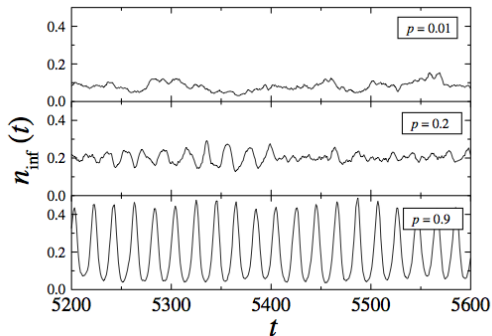
Keeling et al, 2005

Effective distance



J. Manitz, et.al. 2014, D. Brockman, D. Helbing, 2013

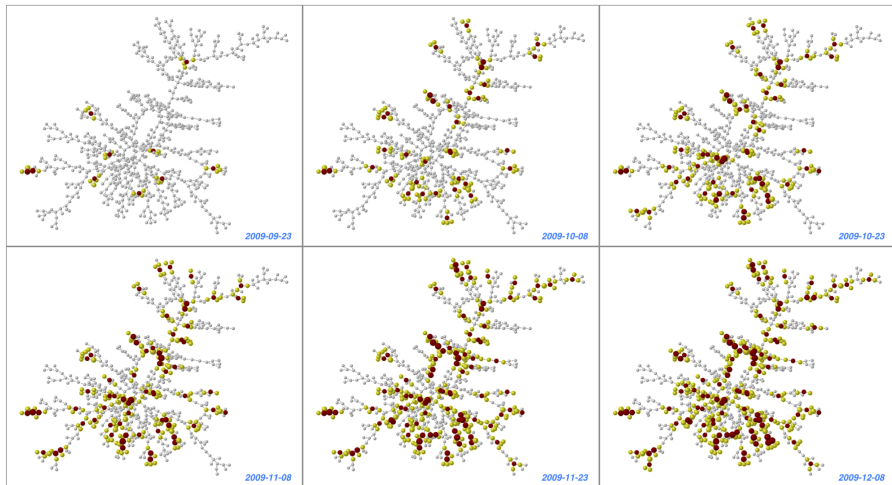
Network synchronization, SIRS



Small-world network at different values of disorder parameter p

Kuperman et al, 2001

Flu contagion



Infected - red, friends of infected - yellow

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