NATIONAL RESEARCH UNIVERSITY

Epidemics on networks II

Network Science
Lecture 10

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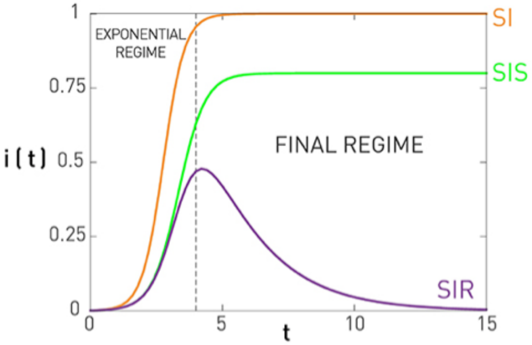
Compartmental models summary



Model	early time	late time	Epidemic threshold
SI	$i_0 e^{\beta_c t}$	1	-
SIS	$(1-\frac{\gamma}{\beta_c})e^{(\beta_c-\gamma)t}$	$1-\frac{\gamma}{\beta_c}; 0$	$\beta_c/\gamma = 1$
SIR	exponential	0	$\beta_c/\gamma = 1$

from Barabasi, 2016

Probabilistic node-level model

- network of potential contacts (adjacency matrix **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 - probably that disease will be transmitted on a contact in time δt (for compartmental model $\beta_c = \beta\langle k\rangle$)
- 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 **A** is symmetric)

Probabilistic model

Two processes:

- Node infection:

$$P_{inf} \approx \beta s_i(t) \sum_{j \in \mathcal{N}(i)} x_j(t) \delta t$$

- Node recovery:

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

SI model

- 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

$$\begin{aligned} \frac{dx_i(t)}{dt} &= \beta s_i(t) \sum_j A_{ij} x_j(t) \\ x_i(t) &+ s_i(t) = 1 \end{aligned}$$

SI model

- System of differential equations

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

- 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

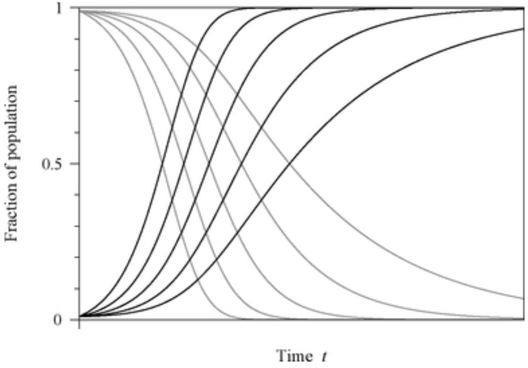
$$\mathbf{x}(t) = \sum_k a_k(0)e^{\lambda_k \beta t}\mathbf{v}_k$$

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

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

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

SI model



Fractions of susceptible and infected vertices of various degrees in the SI model.

The highest values of k give the fastest growth

SI simulation

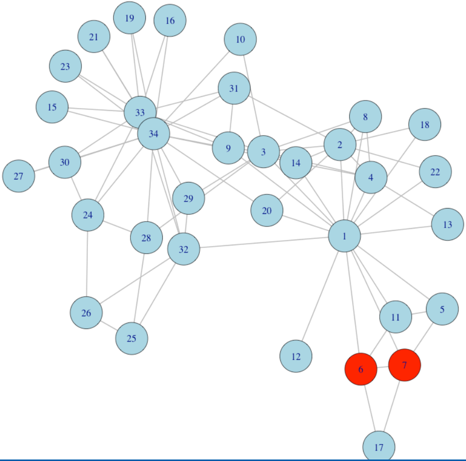
1. Every node at any time step is in one state $\{S, I\}$
2. Initialize c nodes in state I
3. On each time step each I node has a probability β to infect its nearest neighbors (NN), $S \to I$

Model dynamics:

$$I + S \xrightarrow{\beta} 2I$$

SI model simulation

$\beta = 0.5$



SI model simulation

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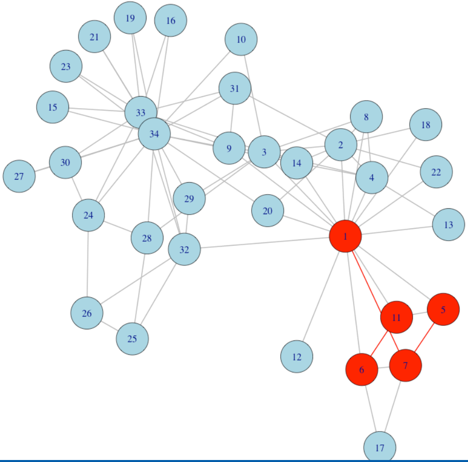
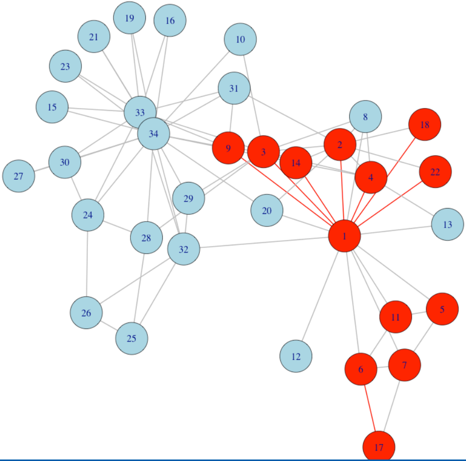


SI model simulation

$\beta = 0.5$



SI model simulation

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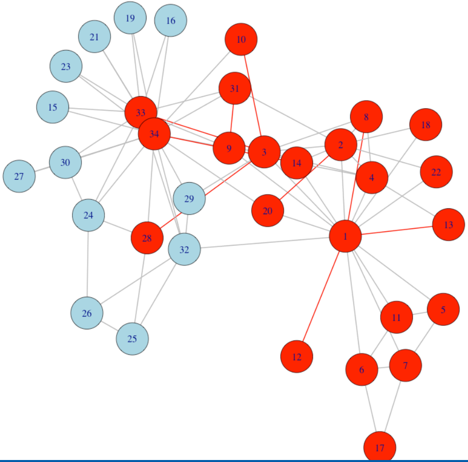

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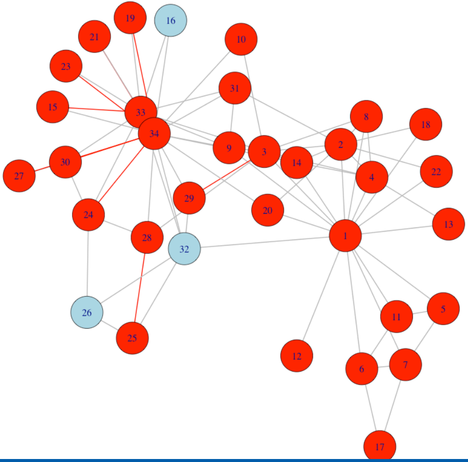

SI model simulation

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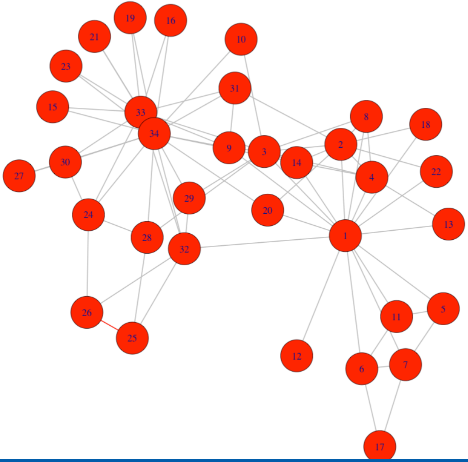
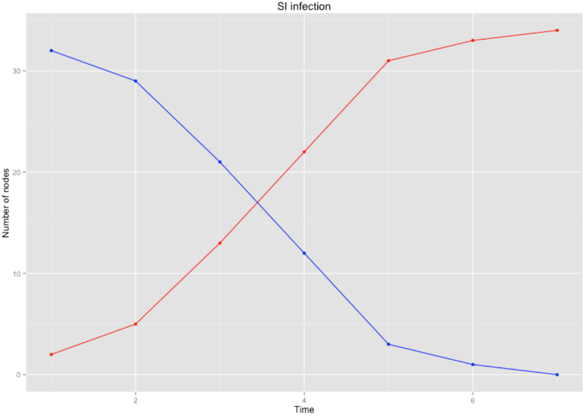


SI model



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
- infection equations:

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

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, $x_i(t) \ll 1$

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

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

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

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

SIS model

- Eigenvector basis

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

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

SIS model

- if $\beta\lambda_1 > \gamma$, infection survives and becomes epidemic
- if $\beta\lambda_1 < \gamma$, infection dies over time

Epidemic threshold:

$$R = \frac{1}{\lambda_1}, \;\; \lambda_1 - \text{largest eigenvalue of the adjacency matrix}$$

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

SIS simulation

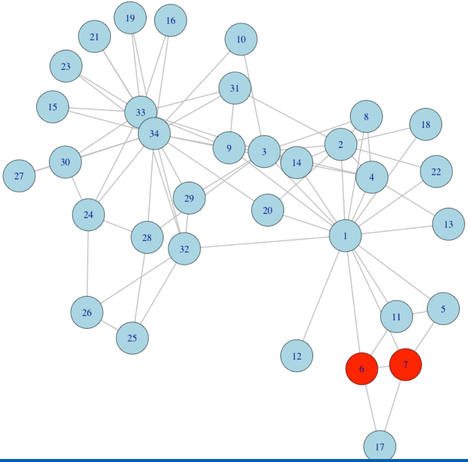
1. Every node at any time step is in one state $\{S, I\}$
2. Initialize c nodes in state I
3. Each node stays infected $\tau_\gamma = \int_0^\infty \tau e^{-\tau\gamma} d\tau = 1/\gamma$ time steps
4. On each time step each I node has a prabability β to infect its nearest neighbours (NN), $S \to I$
5.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

Model dynamics:

$$\begin{cases} I + S & \xrightarrow{\beta} \quad 2I \\ I & \xrightarrow{\gamma} \quad S \end{cases}$$

SIS model simulation

$\beta = 0.5, \tau = 2$



SIS model simulation

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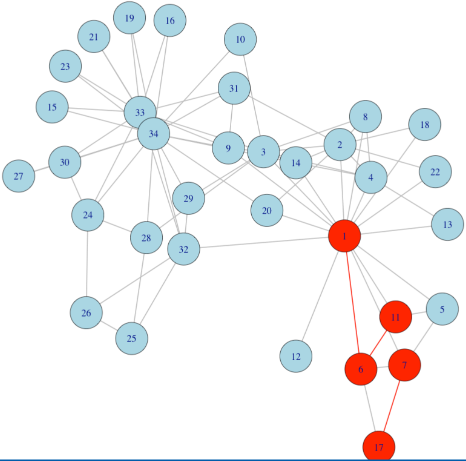

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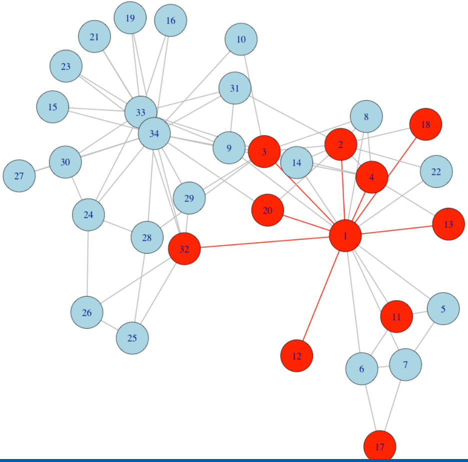

SIS model simulation

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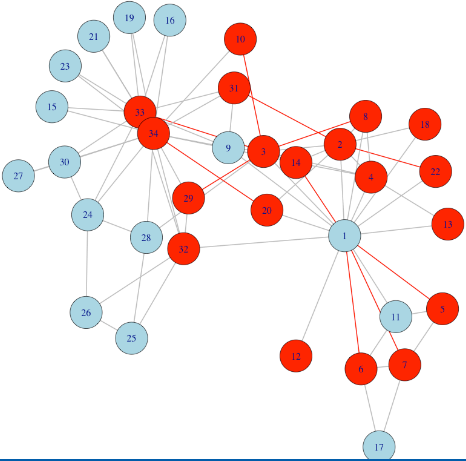

SIS model simulation

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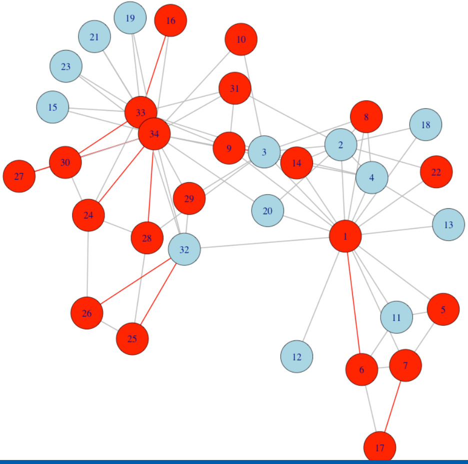

SIS model simulation

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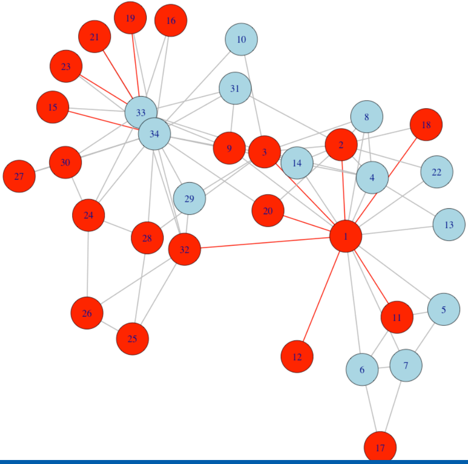

SIS model simulation

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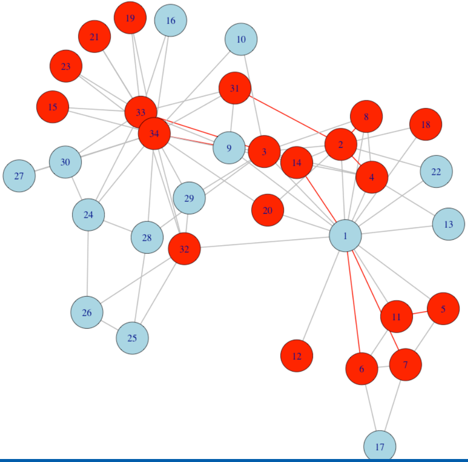
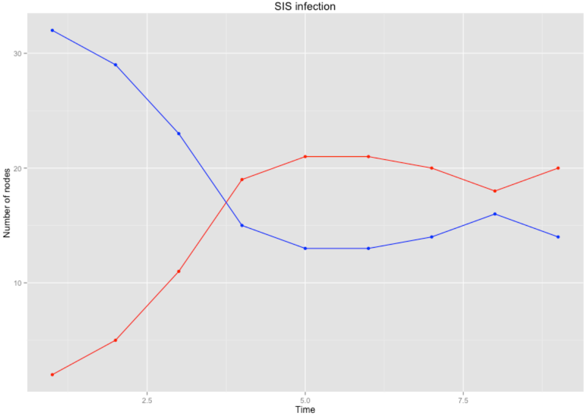
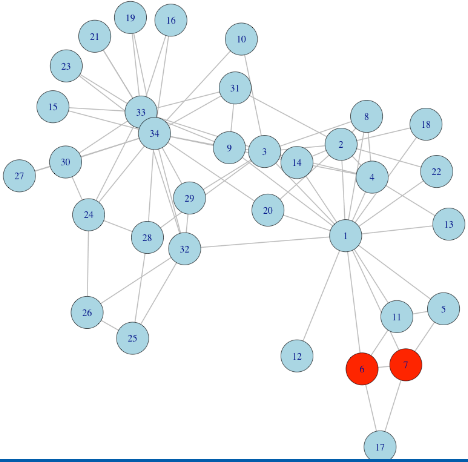


SIS model



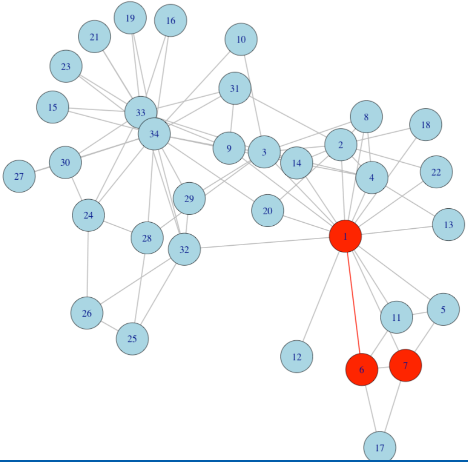
SIS model simulation

$\beta = 0.2, \tau = 2$



SIS model simulation

$\beta = 0.2, \tau = 2$



SIS model simulation

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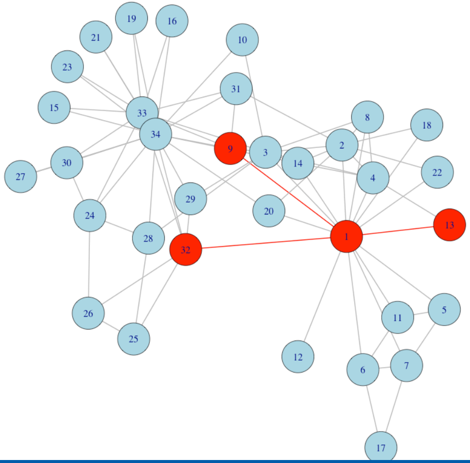

SIS model simulation

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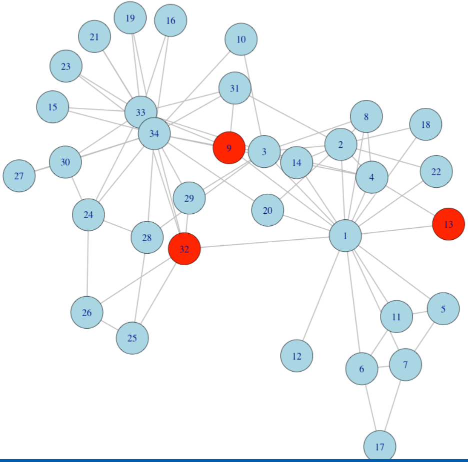

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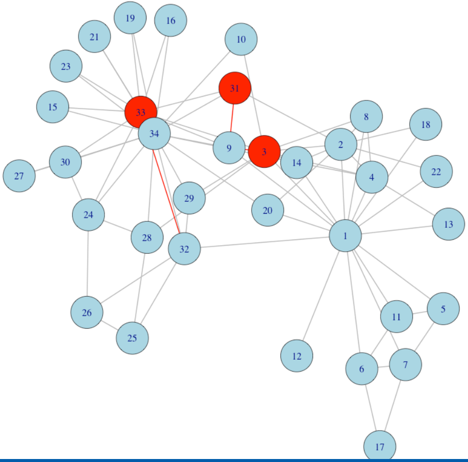

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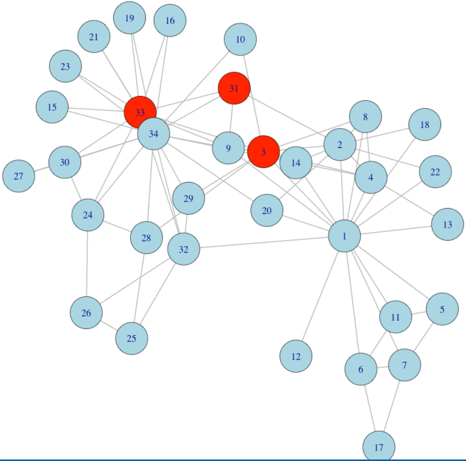
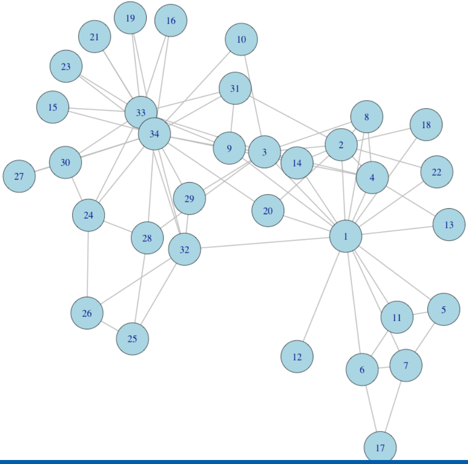
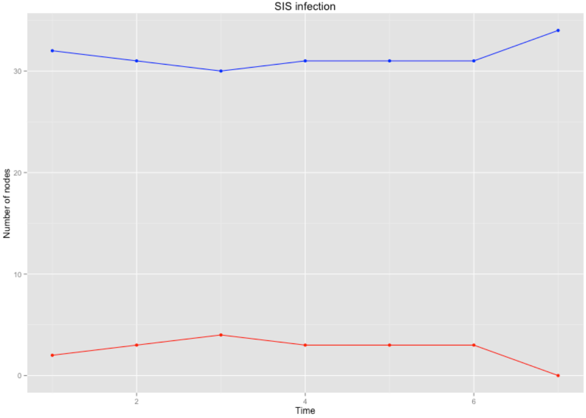


SIS model simulation

$\beta = 0.2, \tau = 2$



SIS model



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:

$$\begin{aligned} \frac{dx_i}{dt} &= \beta s_i \sum_j A_{ij} x_j - \gamma x_i \\ \frac{dr_i}{dt} &= \gamma x_i \\ x_i(t) &+ s_i(t) + r_i(t) = 1 \end{aligned}$$

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

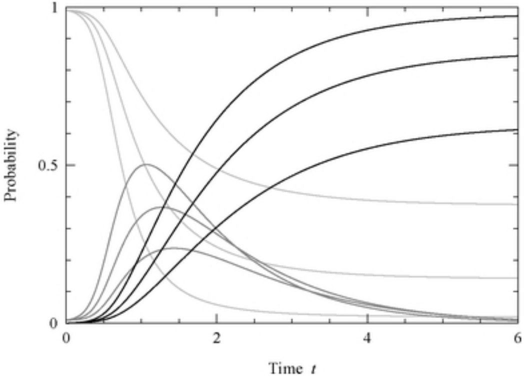


image from M. Newman, 2010

SIR simulation

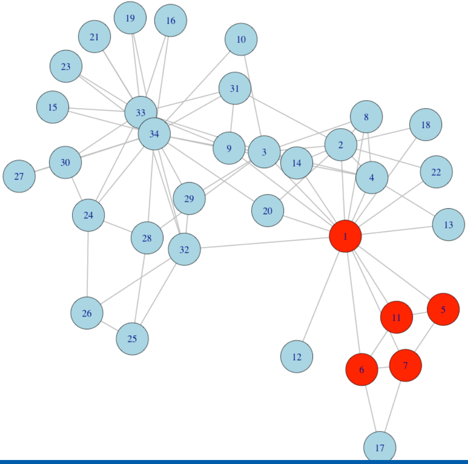
1. Every node at any time step is in one state $\{S, I, R\}$
2. Initialize c nodes in state I
3. Each node stays infected $\tau_\gamma = 1/\gamma$ time steps
4. On each time step each I node has a prabability β to infect its nearest neighbours (NN), $S \to I$
5. After τ_γ time steps node recovers, $I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

Model dynamics:

$$\begin{cases} I + S & \xrightarrow{\beta} & 2I \\ I & \xrightarrow{\gamma} & R \end{cases}$$

SIR model

$\beta = 0.5, \tau = 2$



SIR model

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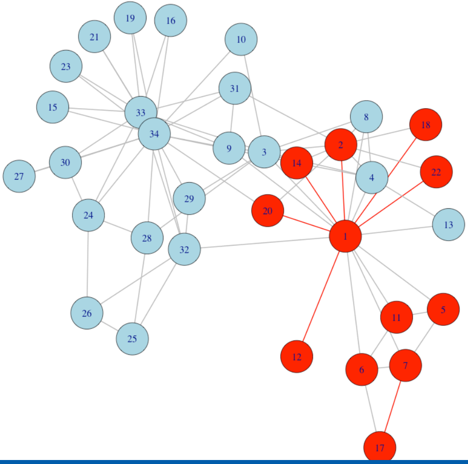

SIR model

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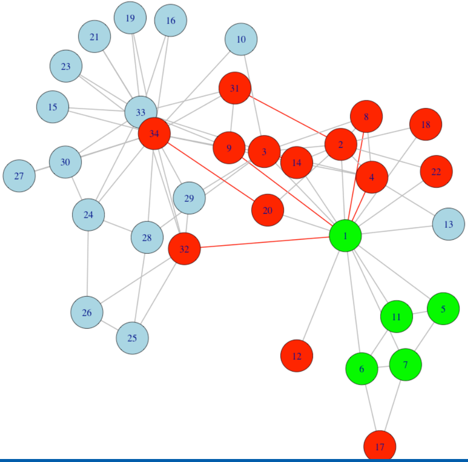

SIR model

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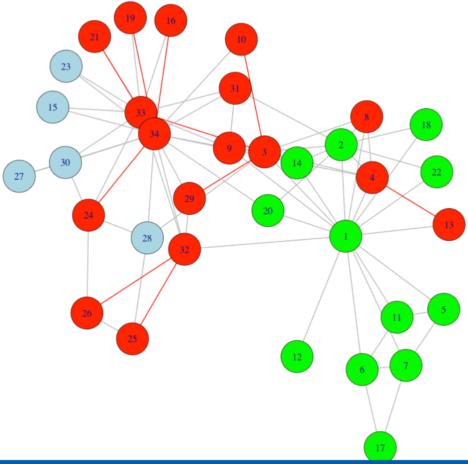

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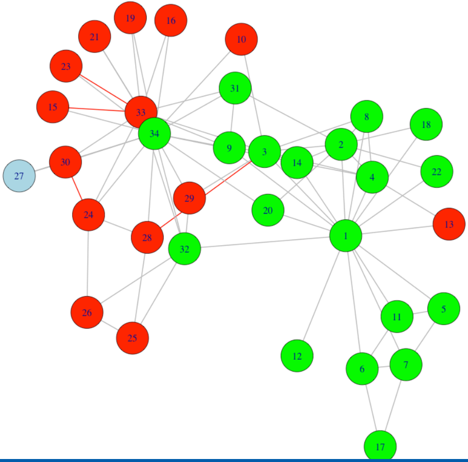

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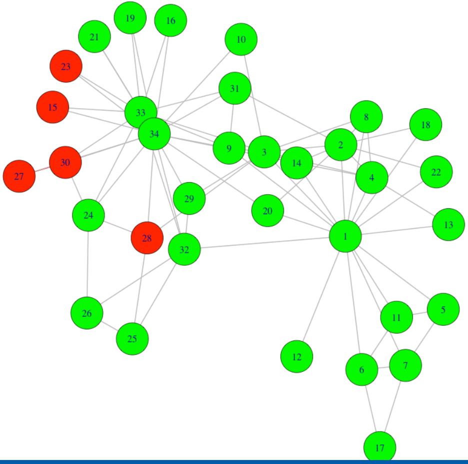

SIR model

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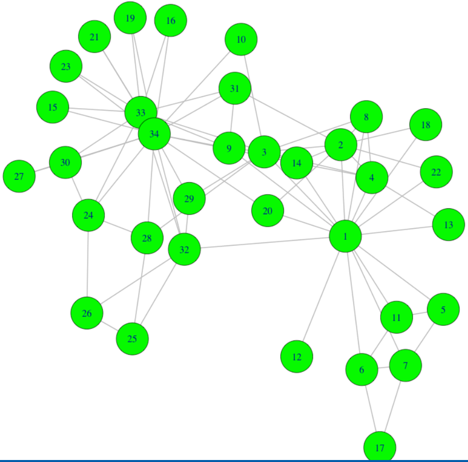
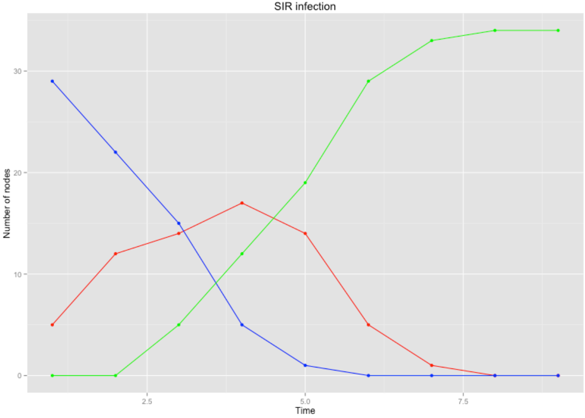
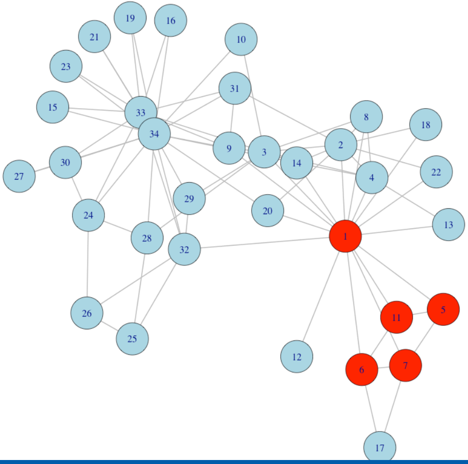


SIR model



SIR model

$\beta = 0.2, \tau = 2$



SIR model

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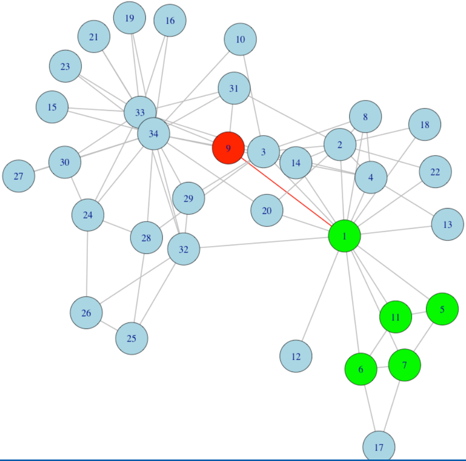

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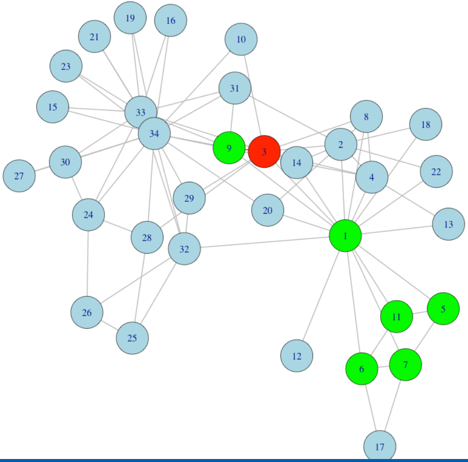

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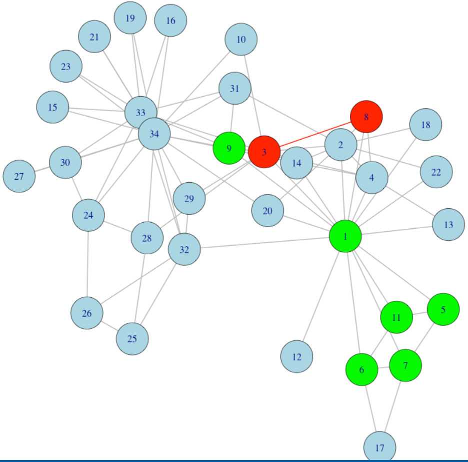

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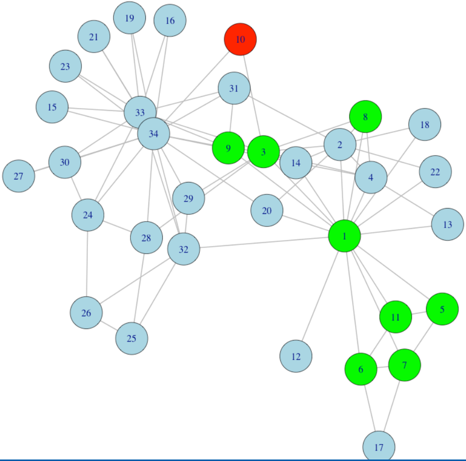

SIR model

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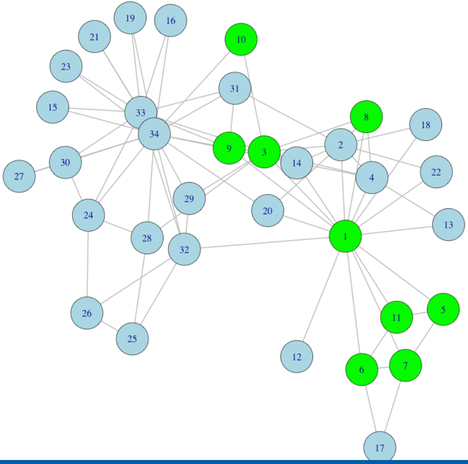
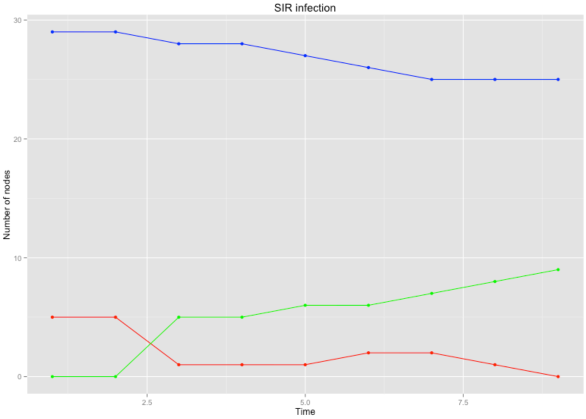
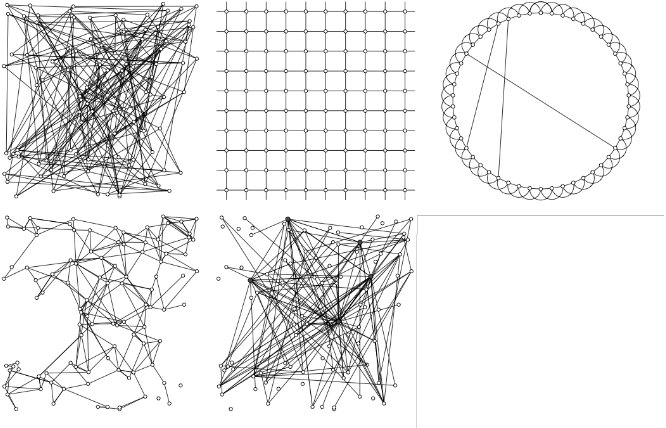


SIR model



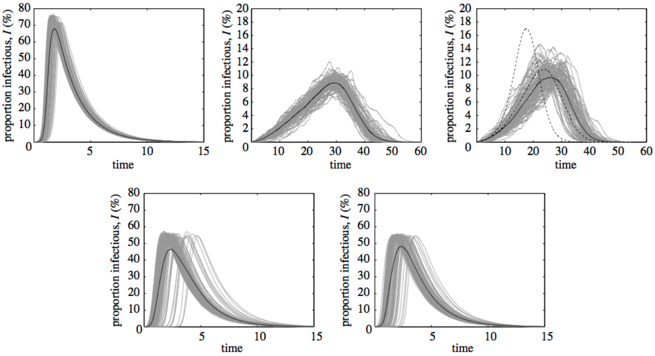
5 Networks, SIR



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

image from Keeling et al, 2005

5 Networks, SIR

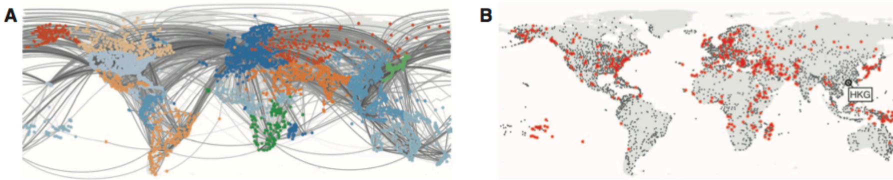


Networks: 1) random, 2) lattice, 3) small world, 4) spatial, 5) scale-free

Keeling et al, 2005

Modeling SARS outbreak

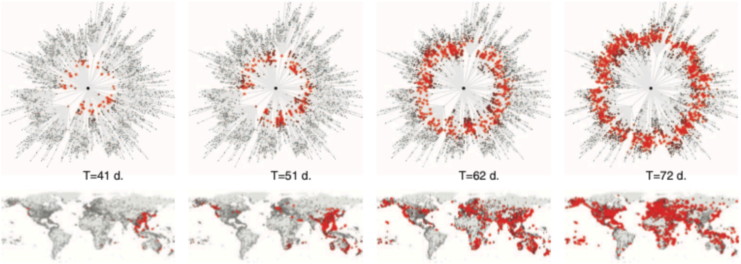
SARS 2003: $> 8,000$ cases, 37 countries



Simulated SIR model:gray lines - passenger flow, red symbols epidemics location

D. Brockmann, D. Helbing, 2013

Modeling SARS outbreak



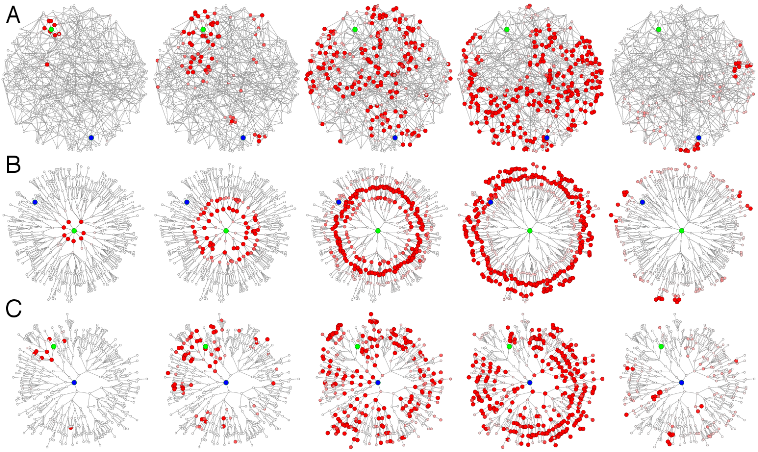
Shortest path tree from Hong Kong, effective distance

$d_{ij} = 1 - \log p_{ij}$, p_{ij} - fraction of travellers leaving node i to node j

$T_a = \frac{d_{eff}}{V_{eff}}; \frac{T_a(j/i)}{T_a(l/i)} = \frac{d_{eff}(j/i)}{d_{eff}(l/i)}$

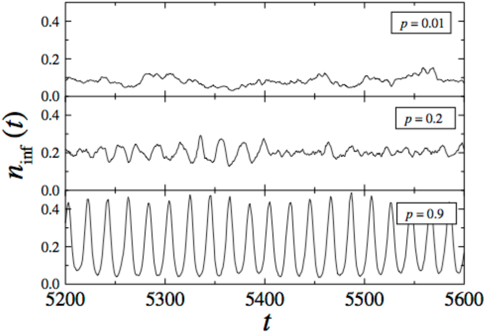
D. Brockmann, D. Helbing, 2013

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

Epidemic threshold

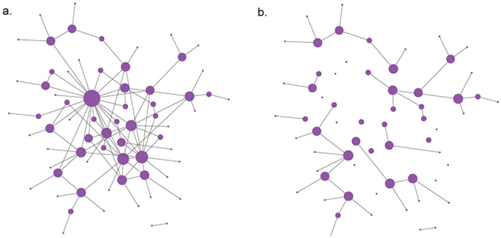
One can show that epidemic threshold depends on network homogeneity $\sigma_k^2 = \langle k^2 \rangle - \langle k \rangle^2$

$$R = \frac{\langle k \rangle}{\langle k^2 \rangle}$$

- in random network $\langle k^2 \rangle = \langle k \rangle(\langle k \rangle + 1): \quad R = 1/\langle k \rangle > 0$
- in scale-free networks $P(k) \sim k^{-\gamma}$,
  when $2 < \gamma \leq 3$ snd $N \to \infty$: $\quad \langle k^2 \rangle \to \infty$, $\ R \to 0$
  NO EPIDEMIC THRESHOLD!

Vaccination strategies

- random vaccination.
- hub vaccination, $k > k_{min}$
- following random edge $kP(k)$ degree probability
- random friend vaccination ("friendship paradox")



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