Epidemics on networks

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Lecture outline

1. Compartmental epidemic models
   - SI model
   - SIS model
   - SIR model
2. Probabilistic network models
   - SI model
   - SIS model
   - SIR model
3. Simulations

Epidemics models

- Mathematical epidemiology
- W. O. Kermack and A. G. McKendrick, 1927
- Deterministic compartmental model (population classes) $\{S, I, T\}$
- $S(t)$ - susceptible, number of individuals not yet infected with the disease at time t
- $I(t)$ - infected, number of individuals who have been infected with the disease and are capable of spreading the disease.
- $R(t)$ - recovered, number of individuals who have been infected and then recovered from the disease, can't be infected again or to transmit the infection to others.
- Fully-mixing model
- Closed population (no birth, death, migration)
- Models: SI, SIS, SIR, SIRS,..

SI model

- $S(t)$ -susceptible , $I(t)$ - infected

$$S \longrightarrow I$$

$$S(t) + I(t) = N$$

- β - infection/contact rate, number of contacts per unit time
- Infection equation:

$$I(t + \delta t) = I(t) + \beta \frac{S(t)}{N} I(t) \delta t$$

$$\frac{dI(t)}{dt} = \beta \frac{S(t)}{N} I(t)$$

SI model

- Fractions: $i(t) = I(t)/N$, $s(t) = S(t)/N$
- Equations

$$\begin{aligned} \frac{di(t)}{dt} &= \beta s(t) i(t) \\ \frac{ds(t)}{dt} &= -\beta s(t) i(t) \end{aligned}$$

$$s(t) + i(t) = 1$$

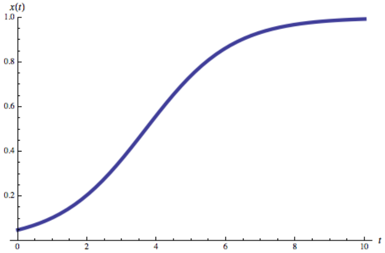
- Differential equation, $i(t = 0) = i_0$

$$\frac{di(t)}{dt} = \beta (1 - i(t)) i(t)$$

Logistic growth function

- Solution:

$$i(t) = \frac{i_0}{i_0 + (1 - i_0)e^{-\beta t}}$$



- Limit $t \to \infty$

$$i(t) \to 1$$
$$s(t) \to 0$$

in image $i_0 = 0.05$, $\beta = 0.8$

SIS model

- $S(t)$ -susceptable , $I(t)$ - infected,

$$S \longrightarrow I \longrightarrow S$$

$$S(t) + I(t) = N$$

- β - infection rate (on contact), γ - recovery rate
- Infection equations:

$$\begin{aligned} \frac{ds}{dt} &= -\beta si + \gamma i \\ \frac{di}{dt} &= \beta si - \gamma i \end{aligned}$$

$$s + i = 1$$

- Differential equation, $i(t = 0) = i_0$

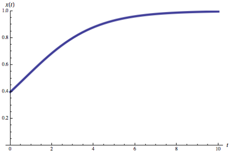
$$\frac{di}{dt} = (\beta - \gamma - i)i$$

Logistic function

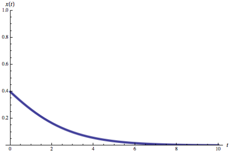
- Solution

$$i(t) = (1 - \frac{\gamma}{\beta})\frac{C}{C + e^{-(\beta-\gamma)t}}, \quad C = \frac{\beta i_0}{\beta - \gamma - \beta i_0}$$

- $\beta > \gamma, \lim t \to \infty : i(t) \to (1 - \frac{\gamma}{\beta})$



- $\beta < \gamma, \lim t \to \infty : i(t) = i_0 e^{(\beta-\gamma)t} \to 0$



SIR model

- $S(t)$ -susceptable , $I(t)$ - infected, $R(t)$ - recovered

$$S \longrightarrow I \longrightarrow R$$

$$S(t) + I(t) + R(t) = N$$

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

$$\begin{aligned} \frac{ds}{dt} &= -\beta si \\ \frac{di}{dt} &= \beta si - \gamma i \\ \frac{dr}{dt} &= \gamma i \end{aligned}$$

$$s + i + r = 1$$

SIR model

- Equation

$$\frac{ds}{dt} = -\beta s \frac{dr}{dt}\frac{1}{\gamma}$$

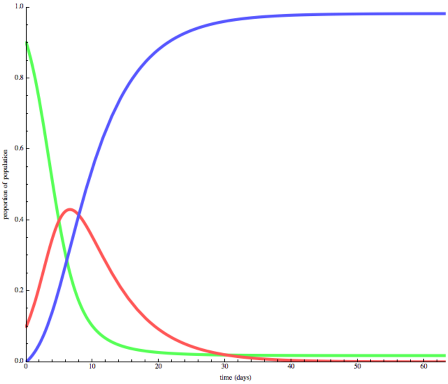
$$s = s_0 e^{-\frac{\beta}{\gamma} r}$$

$$\frac{dr}{dt} = \gamma(1 - r - s_0 e^{-\frac{\beta}{\gamma} r})$$

- Solution

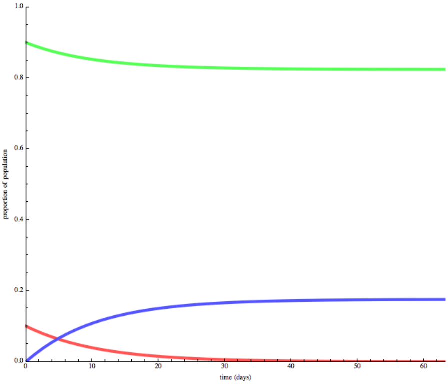
$$t = \frac{1}{\gamma}\int_0^r \frac{dr}{1 - r - s_0 e^{-\frac{\beta}{\gamma} r}}$$

SIR model



- $\frac{\beta}{\gamma} = 4$
- $i_0 = 0.1$

SIR model



- $\frac{\beta}{\gamma} = 0.5$
- $i_0 = 0.1$

SIR model

- Equation

$$\frac{dr}{dt} = \gamma(1 - r - s_0 e^{-\frac{\beta}{\gamma} r})$$

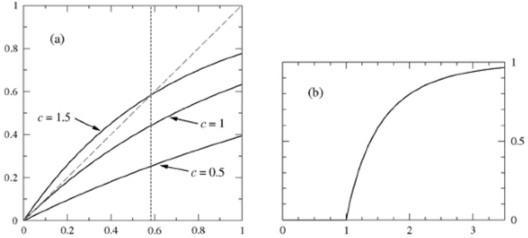
- Limits: $t \to \infty$, $\frac{dr}{dt} = 0$, $r_\infty = const$,

$$1 - r_\infty = s_0 e^{-\frac{\beta}{\gamma} r_\infty}$$

- Initial conditions: $r(0) = 0$, $i(0) = c/N$, $s(0) = 1 - c/N \approx 1$

$$1 - r_\infty = e^{-\frac{\beta}{\gamma} r_\infty}$$

SIR model



$$r_\infty = 1 - e^{-R_0 r_\infty}, \quad R_0 = \frac{\beta}{\gamma}$$

$$(r_\infty)'|_{r_\infty=0} = (1 - e^{-R_0 r_\infty})'|_{r_\infty=0},$$

critical point: $R_0 = 1$

SIR model

- Basic reproduction number

$$R_0 = \frac{\beta}{\gamma}$$

β - infection rate, γ - recovery rate

- Epidemic threshold $R_0 = 1$, (r_∞ - the total size of the outbreak)

$$R_0 > 1, \quad (\beta > \gamma) \quad \text{: epidemics}, \quad r_\infty = const > 0$$
$$R_0 < 1, \quad (\beta < \gamma) \quad \text{: no epidemics}, \quad r_\infty \to 0$$

- Recovery is a Poisson process (independent events at a constant rate)
  Average number of people infected by a person before his recovery

$$\beta E[\tau] = \beta \int_0^\infty \tau \gamma e^{-\gamma \tau} d\tau = \frac{\beta}{\gamma} = R_0$$

Probabilistic 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 - 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 **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

- 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

- Differential equation

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

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

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

- Solution

$$x_i(t) = \sum_k a_k(0) e^{\lambda_k \beta t} v_{k,i}; \quad a_k(0) = \sum_i v_{k,i} x_i(0); \quad \mathbf{A}\mathbf{v}_k = \lambda_k \mathbf{v}_k$$

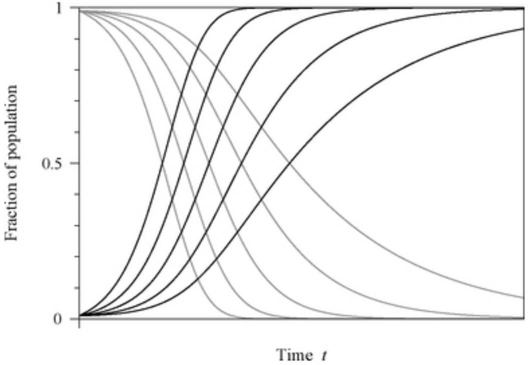
- At $t \to 0$, $\lambda_{max} = \lambda_1 > \lambda_k$

$$x_i(t) = v_{1,i} e^{\lambda_1 \beta t}$$

  – growth rate of infections depends on λ_1

  – probability of infection of nodes depends on $\mathbf{v}_1$,

SI model



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

image from M. Newman, 2010

SI simulation

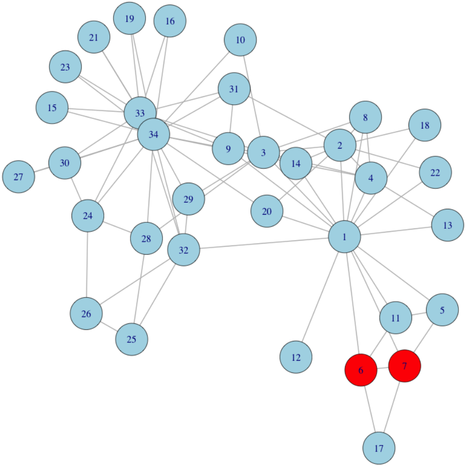
1. Every node at any time step is in one state $\{S, I\}$
2. Initialize c nodes in state I
3. On each time step each I node has a probability β to infect its nearest neighbors (NN), $S \to I$

Model dynamics:

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

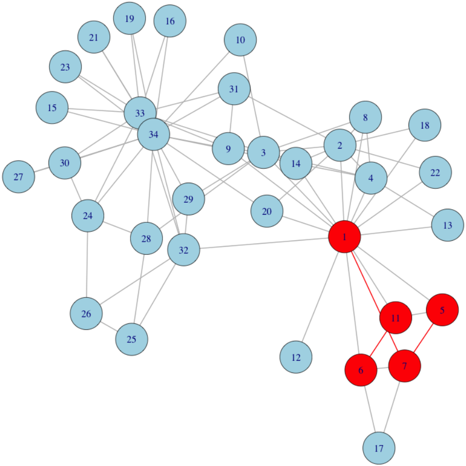
SI model simulation

$\beta = 0.5$



SI model simulation

$\beta = 0.5$



SI model simulation

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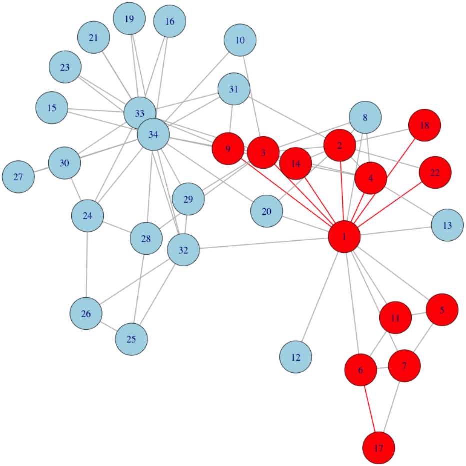

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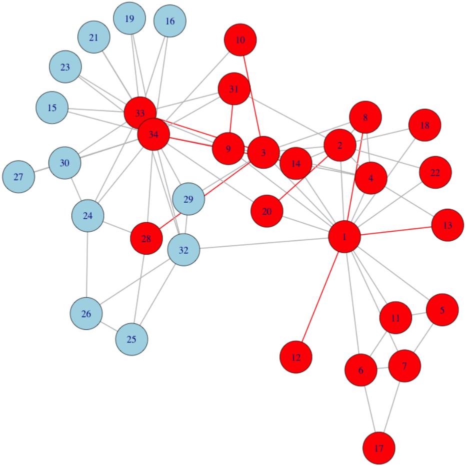

SI model simulation

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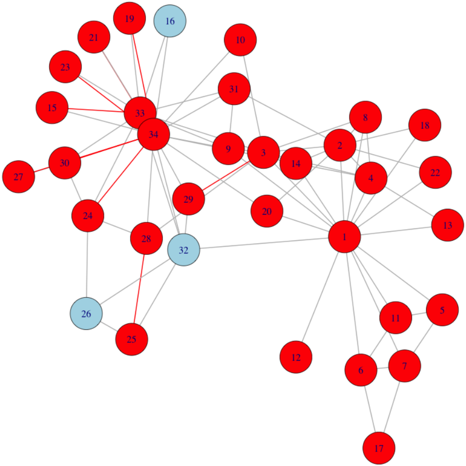

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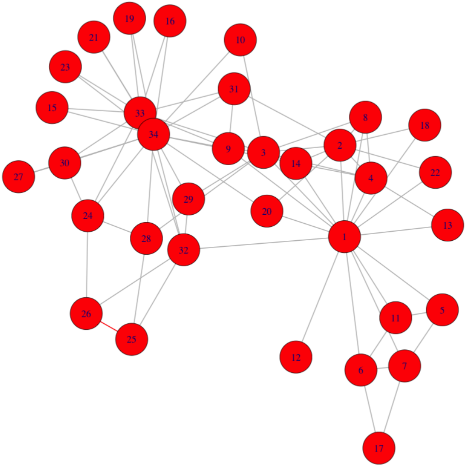
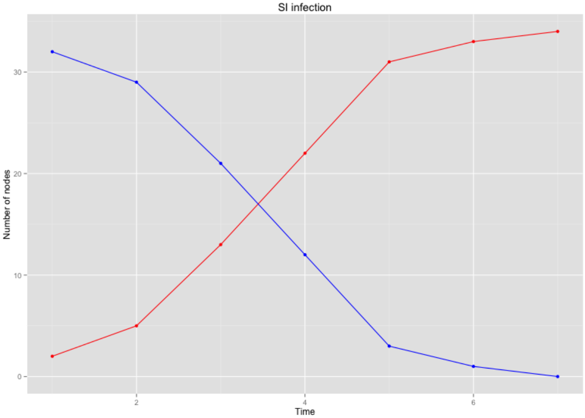


SI model



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, $x_i(t) \ll 1$

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

- Solution

$$x_i(t) = \sum_k a_k(0) e^{\beta\lambda_k - \gamma} v_{k,i}; \quad a_k(0) = \sum_i v_{k,i} x_i(0); \quad \mathbf{A}\mathbf{v}_k = \lambda_k \mathbf{v}_k$$

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

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 simulation

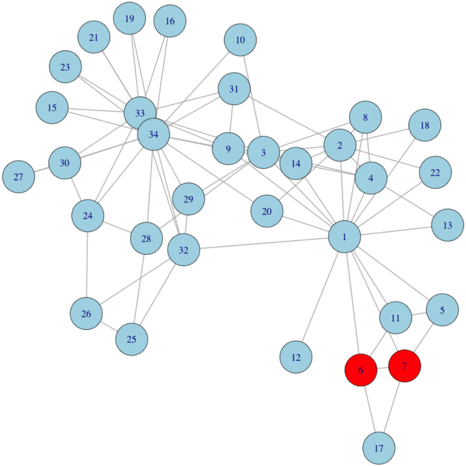
1. Every node at any time step is in one state $\{S, I\}$
2. Initialize c nodes in state I
3. Each node stays infected $\tau_\gamma = \int_0^\infty \tau e^{-\tau\gamma} d\tau = 1/\gamma$ time steps
4. On each time step each I node has a prabability β to infect its nearest neighbours (NN), $S \to I$
5.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

Model dynamics:

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

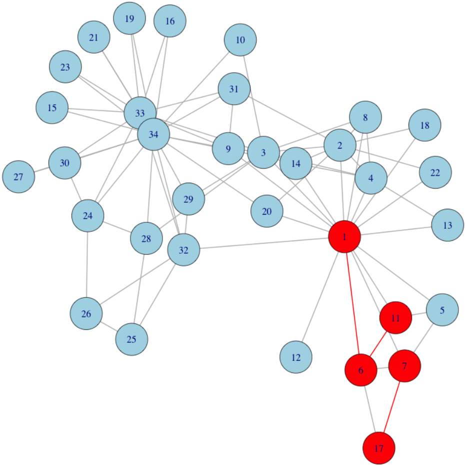
SIS model simulation

$\beta = 0.5, \tau = 2$



SIS model simulation

$\beta = 0.5, \tau = 2$



SIS model simulation

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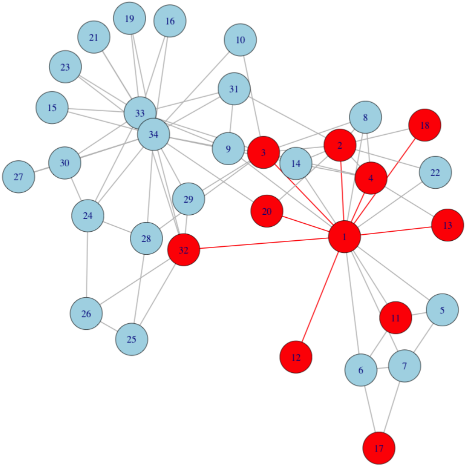

SIS model simulation

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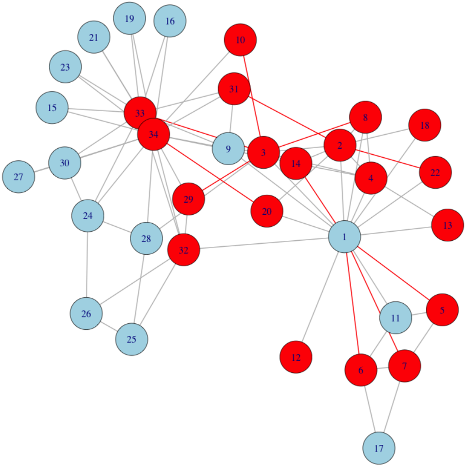

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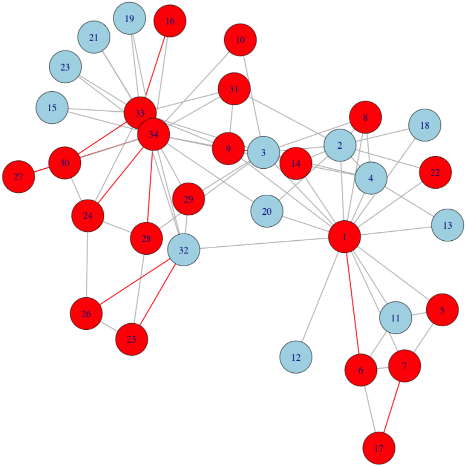

SIS model simulation

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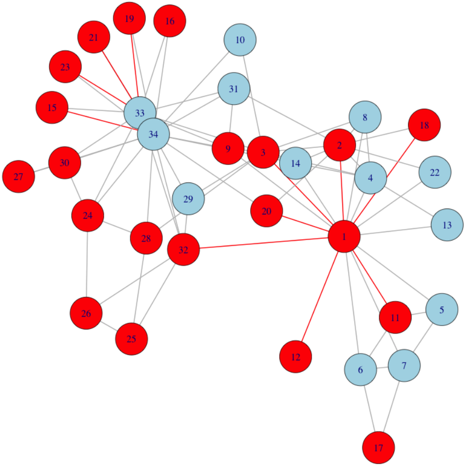

SIS model simulation

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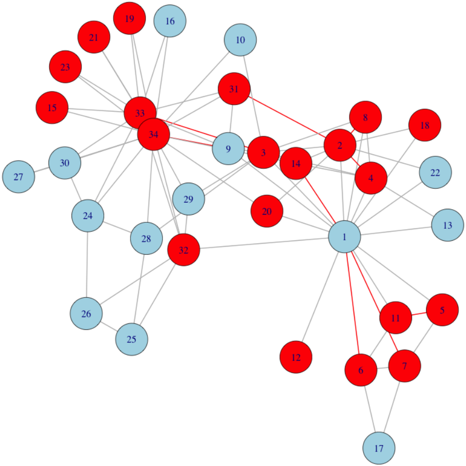
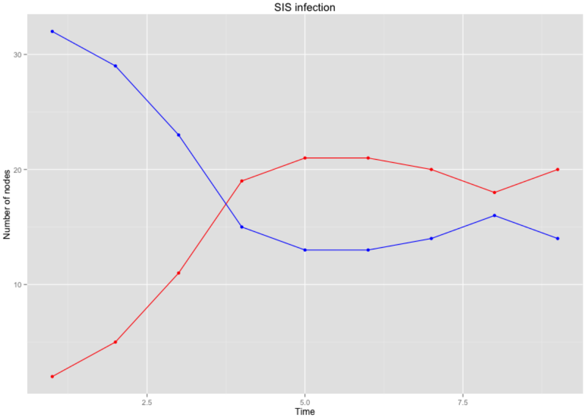
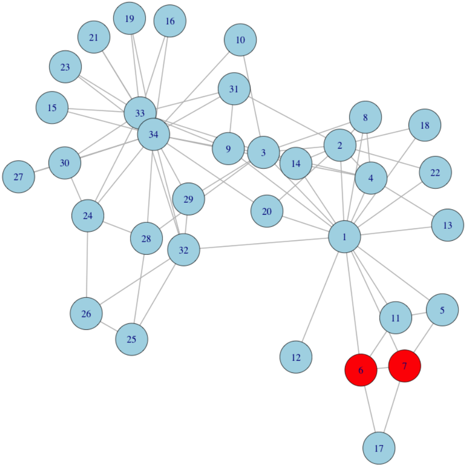


SIS model



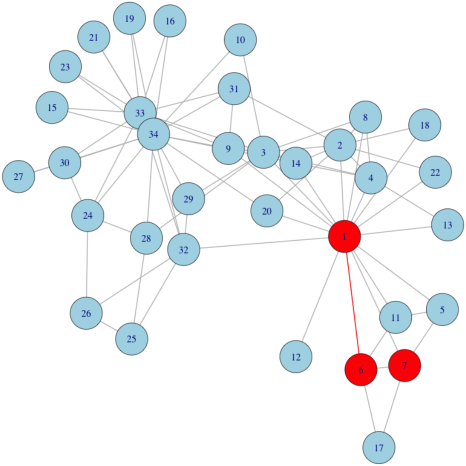
SIS model simulation

$\beta = 0.2, \tau = 2$



SIS model simulation

$\beta = 0.2, \tau = 2$



SIS model simulation

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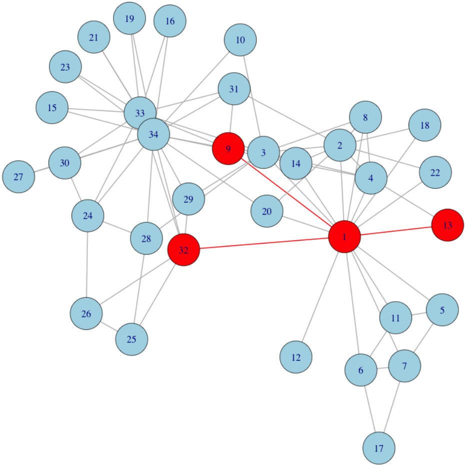
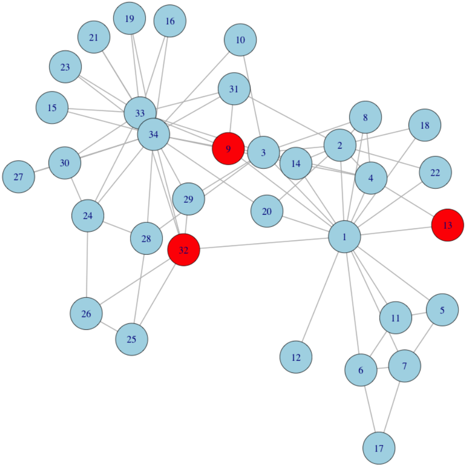


SIS model simulation

$\beta = 0.2, \tau = 2$



SIS model simulation

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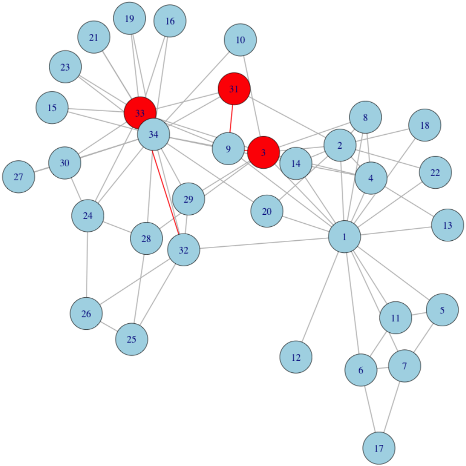

SIS model simulation

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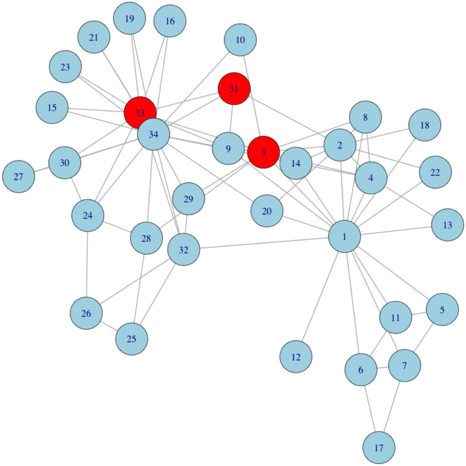
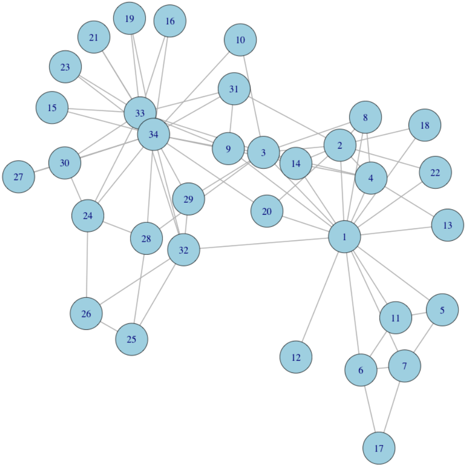
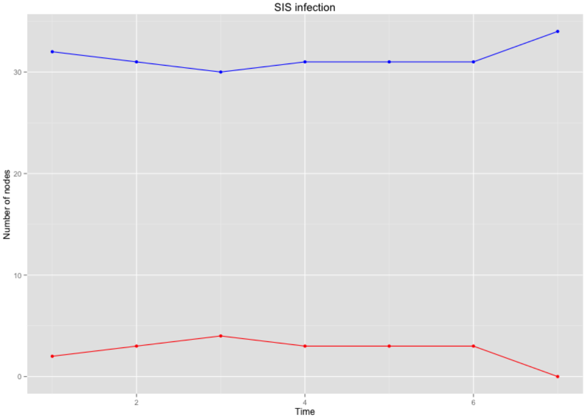


SIS model simulation

$\beta = 0.2, \tau = 2$



SIS model



SIR model

- 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

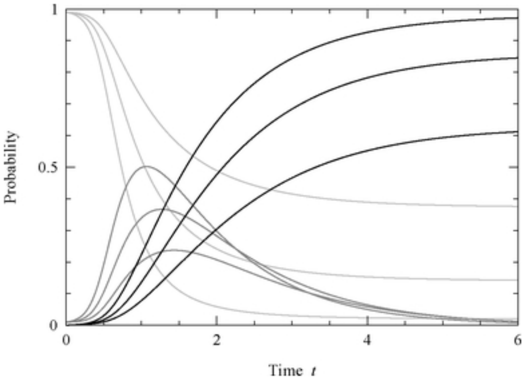


image from M. Newman, 2010

SIR simulation

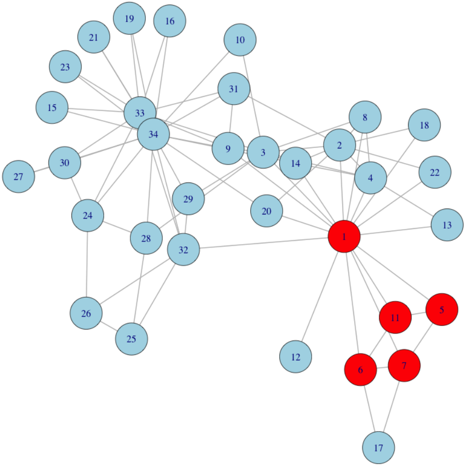
1. Every node at any time step is in one state $\{S, I, R\}$
2. Initialize c nodes in state I
3. Each node stays infected $\tau_\gamma = 1/\gamma$ time steps
4. On each time step each I node has a prabability β to infect its nearest neighbours (NN), $S \to I$
5. After τ_γ time steps node recovers, $I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

Model dynamics:

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

SIR model

$\beta = 0.5, \tau = 2$



SIR model

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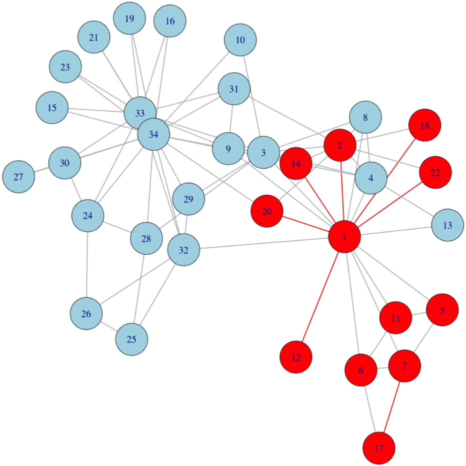

SIR model

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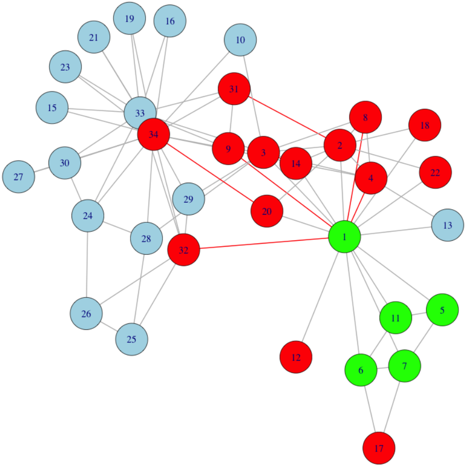

SIR model

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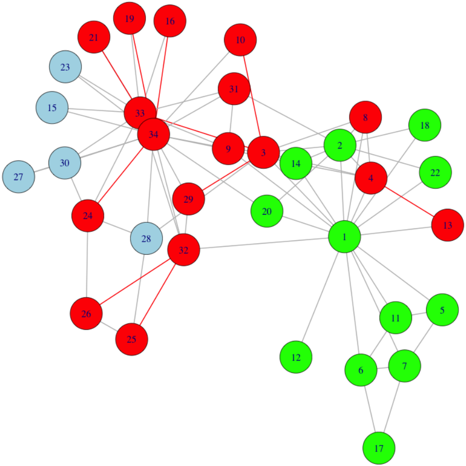

SIR model

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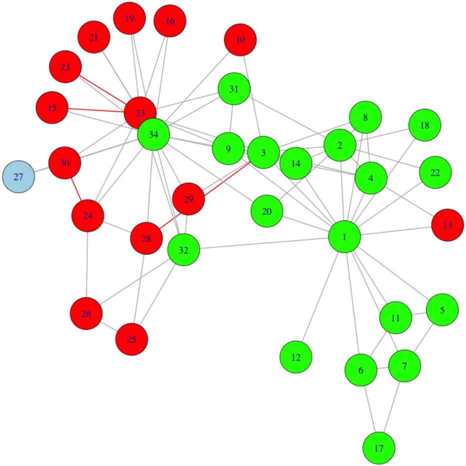
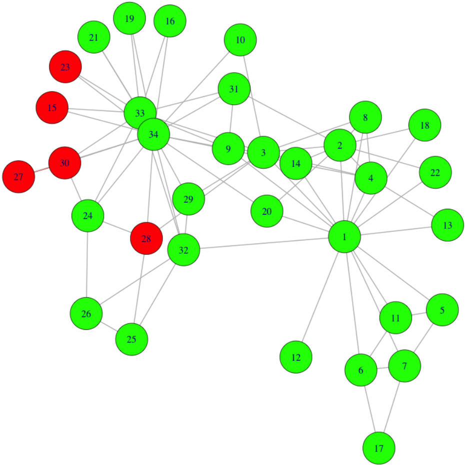


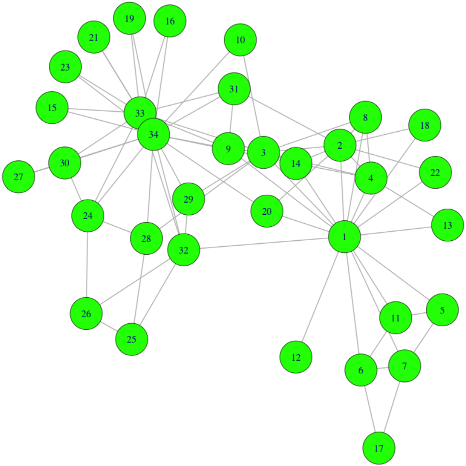
SIR model

$\beta = 0.5, \tau = 2$

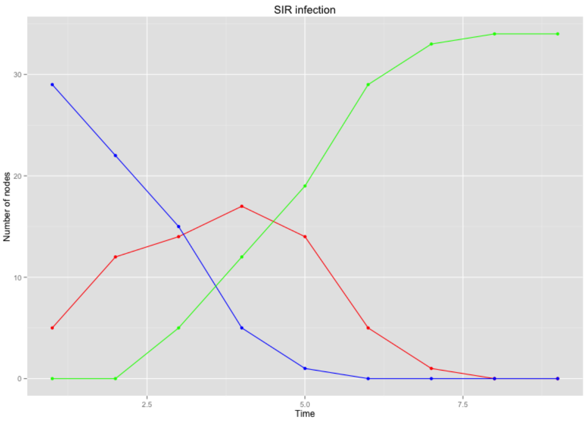


SIR model

$\beta = 0.5, \tau = 2$

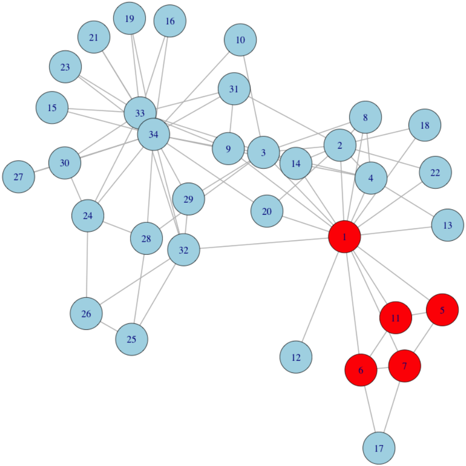


SIR model



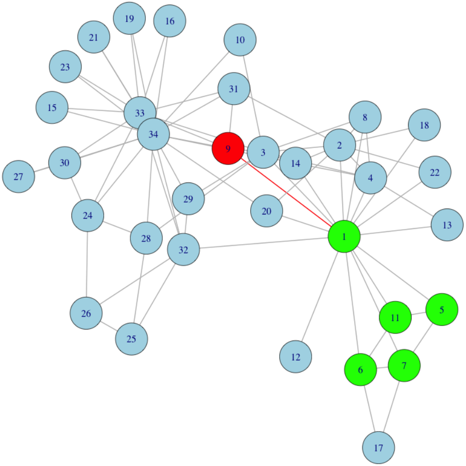
SIR model

$\beta = 0.2, \tau = 2$



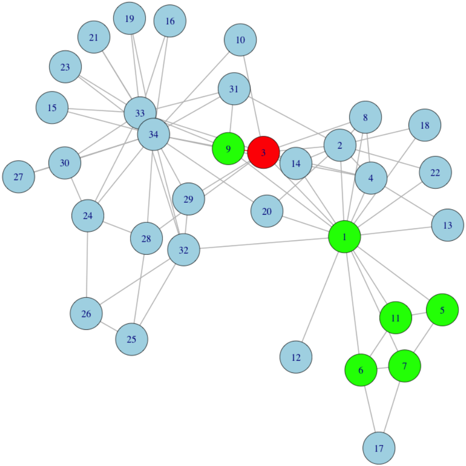
SIR model

$\beta = 0.2, \tau = 2$



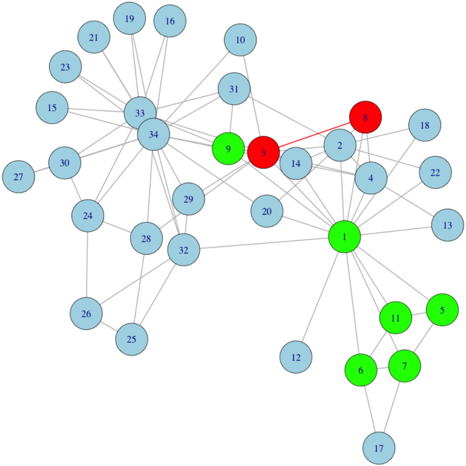
SIR model

$\beta = 0.2, \tau = 2$



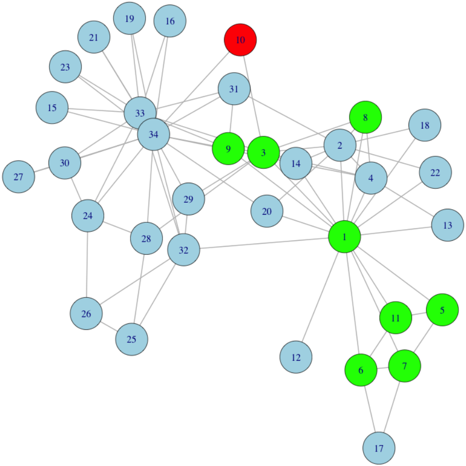
SIR model

$\beta = 0.2, \tau = 2$



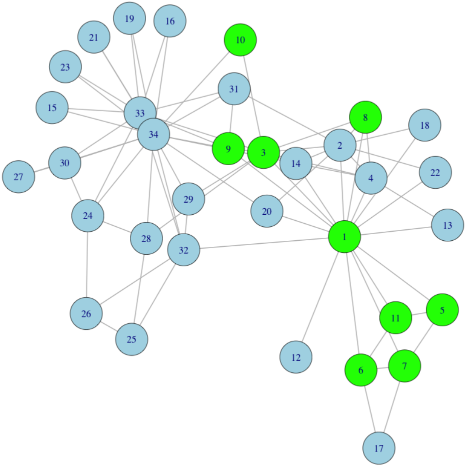
SIR model

$\beta = 0.2, \tau = 2$

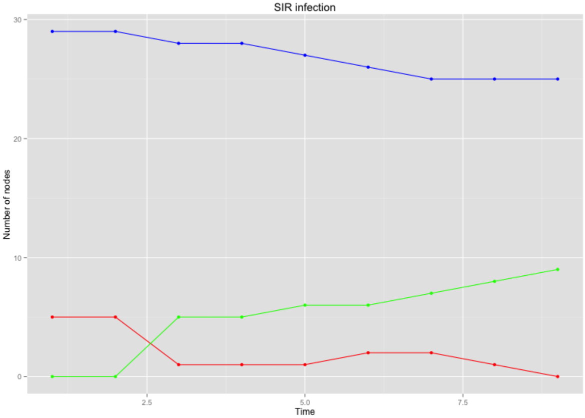


SIR model

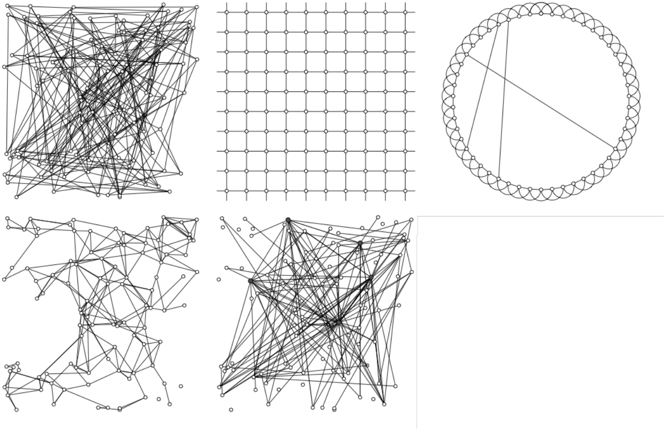
$\beta = 0.2, \tau = 2$



SIR model



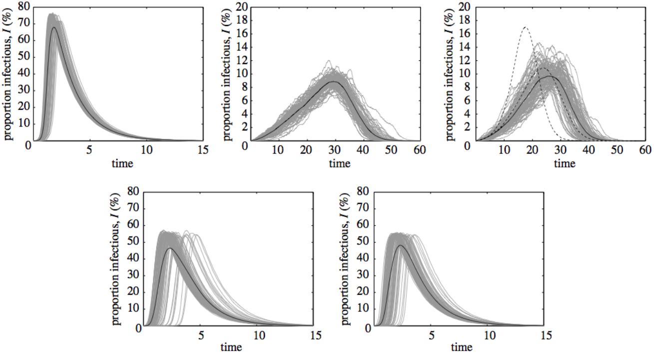
5 Networks, SIR



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

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