

# Diffusion and random walks on graphs. Epidemics and COVID-19

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**BigData Academy MADE from Mail.ru Group**

**Network Science**



# Lecture outline

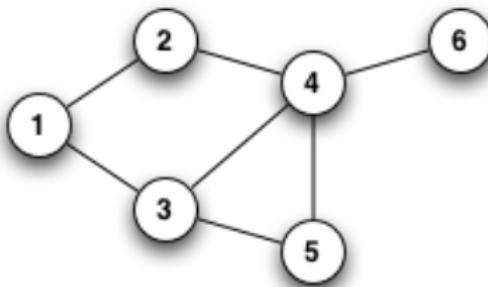
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- 2 Diffusion on graph
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- 5 Branching process as contagion model
- 6 Epidemic modeling
  - SI model
  - SIS model
  - SIR model
- 7 Modeling epidemics on networks

# Random walks on graph

- A random walk on graph  $G$  is a sequence of vertices  $v_0, v_1, \dots, v_t, \dots$ , where each  $v_{t+1}$  is chosen to be a random neighbor of  $v_t$ ,  $\{v_t, v_{t+1}\} \in E(G)$  and probability of the transition is given by

$$P_{ij} = P(x_{t+1} = v_j | x_t = v_i),$$

where  $\sum_i P_{ij} = 1$ , matrix  $P$  - row stochastic



# Random walks on graph

2D grid ( $k=2$  regular graph)

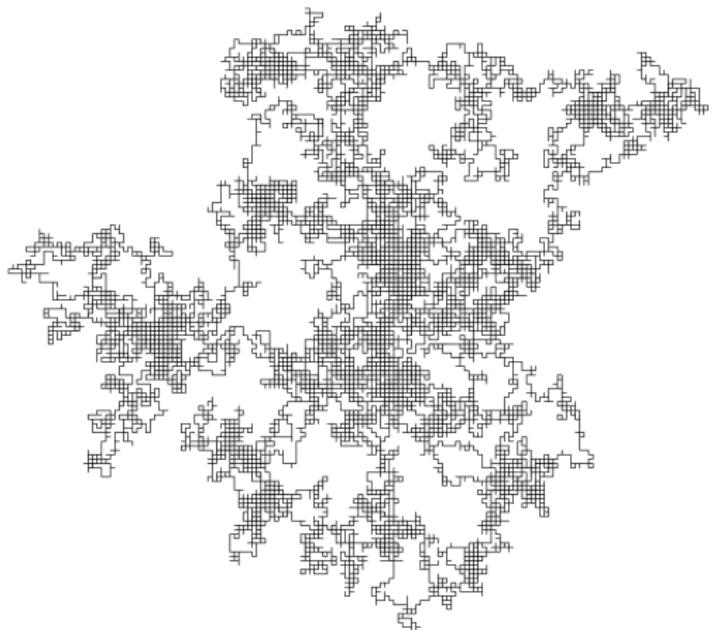
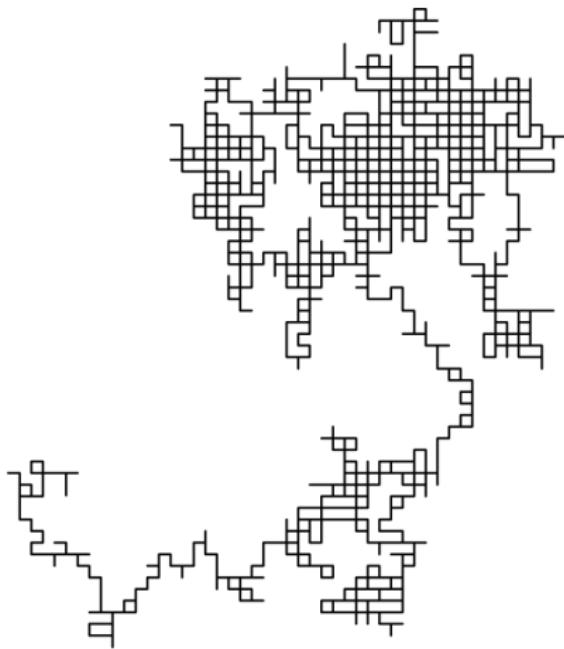


image from wikipedia.org

# Random walks on graph

- We will be considering undirected connected unweighted graphs
- Transition matrix

$$P_{ij} = \begin{cases} 1/d(i), & \text{if } \exists e(i,j), i \text{ and } j \text{ adjacent,} \\ 0 & \text{otherwise} \end{cases}$$

- Using adjacency matrix

$$P_{ij} = \frac{A_{ij}}{d_i} = D_{ii}^{-1} A_{ij}, \text{ where } D_{ij} = d_i \delta_{ij}$$

- Let  $p_i(t)$  - probability, that a walk is at node  $i$  at moment  $t$  (probability distribution vector, value per node)
- Random walk

$$p_j(t+1) = \sum_i P_{ij} p_i(t) = \sum_i \frac{p_i(t)}{d_i} A_{ij}$$

- Matrix form

$$\vec{p}(t+1) = \vec{p}(t)P = \vec{p}(t)(D^{-1}A)$$

# Random walks on graph

- Starting from initial distribution  $\vec{p}(0)$  after  $t$  steps

$$\vec{p}(t) = \vec{p}(0)P^t$$

- Random walk on connected non-bipartite graphs converges to limiting distribution

$$\lim_{t \rightarrow \infty} \vec{p}(t) = \lim_{t \rightarrow \infty} \vec{p}(0)P^t = \vec{\pi}$$

- Limiting distribution = stationary distribution

$$\lim_{t \rightarrow \infty} \vec{p}(t+1) = \lim_{t \rightarrow \infty} \vec{p}(t)P$$

$$\vec{\pi} = \vec{\pi}P$$

- Left eigenvalue corresponding to  $\lambda = 1$  (dominant eigenvalue)

$$\lambda \vec{\pi} = \vec{\pi}P$$

# Perron-Frobenius Theorem

Perron-Frobenius theorem

If real square matrix is

- stochastic (non-negative and rows sum up to one, describes Markov chain)
- irreducible (strongly connected graph)
- aperiodic

then

$$\exists \lim_{t \rightarrow \infty} \vec{p}^t = \vec{\pi}$$

and can be found as a left eigenvector

$$\vec{\pi}P = \lambda\vec{\pi}, \text{ where } ||\vec{\pi}||_1 = 1, \lambda = 1$$

$\vec{\pi}$  - stationary distribution (row vector)

Oscar Perron, 1907, Georg Frobenius, 1912.

# Random walks on graph

- Random walk on graph is reversible ( satisfies detailed balance)

$$\pi_i P_{ij} = \pi_j P_{ji}$$

- On undirected graph:

$$\pi_i \frac{A_{ij}}{d_i} = \pi_j \frac{A_{ji}}{d_j}$$

$$\frac{\pi_i}{d_i} = \frac{\pi_j}{d_j} = \text{const}$$

and  $\sum_i \pi_i = 1$

- Stationary (stable) distribution

$$\pi_i = \frac{d_i}{\sum_j d_j} = \frac{d_i}{2|E|}$$

# Random walks on graph

- Lazy random walk

$$p_j(t+1) = \frac{1}{2}p_j(t) + \frac{1}{2} \sum_i \frac{p_i(t)}{d_i} A_{ij}$$

- Matrix form

$$\vec{p}(t+1) = \frac{1}{2}\vec{p}(t)(\mathbf{I} + \mathbf{D}^{-1}\mathbf{A})$$

- Converges (always!) to the same stationary distribution

$$(2\lambda - 1)\vec{\pi} = \vec{\pi}(\mathbf{D}^{-1}\mathbf{A})$$

# Random walks on graph

## Theorem

Let  $\lambda_2$  denote second largest eigenvalue of transition matrix  $P = D^{-1}A$ ,  $p(t)$  probability distribution vector and  $\pi$  stationary distribution. If walk starts from the vertex  $i$ ,  $p_i(0) = 1$ , then after  $t$  steps for every vertex:

$$|p_j(t) - \pi_j| \leq \sqrt{\frac{d_j}{d_i}} \lambda_2^t$$

- For  $P = D^{-1}A$ ,  $\lambda_1 = 1$ ,  $\lambda_2 < 1$
- For  $P' = \frac{1}{2}(I + D^{-1}A)$ ,  $\lambda'_2 = \frac{1}{2}(1 + \lambda_2)$

# Physics of Diffusion

Diffusion is the movement of a substance down a concentration gradient.  
"to diffuse" = "to spread out"

- Let  $\Phi(r, t)$  -concentration
- Fick's Law

$$J = -C \frac{\partial \Phi}{\partial r} = -C \nabla \Phi$$

- Continuity equation (conserved quantity)

$$\frac{\partial \Phi}{\partial t} + \nabla J = 0$$

- Diffusion equation (heat equation)

$$\frac{\partial \Phi(r, t)}{\partial t} = C \Delta \Phi(r, t)$$

$\Delta$  - Laplacian operator

# Diffusion on network

- Some substance that occupy vertices, on each time step diffuses out  $\phi_i(t)$  - quantity per node

$$\phi_i(t+1) = \phi_i(t) + \sum_j A_{ij}(\phi_j(t) - \phi_i(t))C\delta t$$

$$\frac{d\phi_i(t)}{dt} = C \sum_j A_{ij}(\phi_j(t) - \phi_i(t))$$

$$\frac{d\phi_i}{dt} = C \left( \sum_j A_{ij}\phi_j - \sum_j A_{ij}\phi_i \right) = C \left( \sum_j A_{ij}\phi_j - d_i\phi_i \right) = C \sum_j (A_{ij} - \delta_{ij}d_j)\phi_j$$

$$\frac{d\phi_i}{dt} = -C \sum_j L_{ij}\phi_j$$

# Graph Laplacian

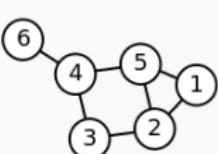
- Graph Laplacian

$$L_{ij} = d_j \delta_{ij} - A_{ij} = D_{ij} - A_{ij}, \quad D_{ij} = d_j \delta_{ij}$$

$$L_{ij} = \begin{cases} d(i) , & \text{if } i = j, \\ -1 , & \text{if } \exists e(i,j) - i \text{ and } j \text{ adjacent,} \\ 0 & \text{otherwise} \end{cases}$$

- Matrix form

$$\mathbf{L} = \mathbf{D} - \mathbf{A}$$

Labeled graph	Degree matrix	Adjacency matrix	Laplacian matrix
	$\begin{pmatrix} 2 & 0 & 0 & 0 & 0 & 0 \\ 0 & 3 & 0 & 0 & 0 & 0 \\ 0 & 0 & 2 & 0 & 0 & 0 \\ 0 & 0 & 0 & 3 & 0 & 0 \\ 0 & 0 & 0 & 0 & 3 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \end{pmatrix}$	$\begin{pmatrix} 0 & 1 & 0 & 0 & 1 & 0 \\ 1 & 0 & 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 & 1 & 1 \\ 1 & 1 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \end{pmatrix}$	$\begin{pmatrix} 2 & -1 & 0 & 0 & -1 & 0 \\ -1 & 3 & -1 & 0 & -1 & 0 \\ 0 & -1 & 2 & -1 & 0 & 0 \\ 0 & 0 & -1 & 3 & -1 & -1 \\ -1 & -1 & 0 & -1 & 3 & 0 \\ 0 & 0 & 0 & -1 & 0 & 1 \end{pmatrix}$

# Laplace matrix

- Spectral properties

$$Lv_i = \lambda v_i$$

- real non-negative eigenvalues  $\lambda_i \geq 0$  and orthogonal eigenvectors  $v_i$
- smallest eigenvalue always  $\lambda_1 = 0$  for  $v_1 = e = [1, 1, 1\dots 1]^T$

$$Le = (D - A)e = 0$$

- Number of zero eigenvalues  $\lambda_i = 0$  equal to the number of connected components
- In a connected graph  $\lambda_2 \neq 0$  - algebraic connectivity of a graph (spectral gap),  $v_2$  - Fiedler vector
- $\lambda_2 = 0$  - disconnected graph,  $\lambda_2 = n$  - totally connected

# Diffusion on Graph

- Diffusion equation

$$\frac{d\phi}{dt} + C\mathbf{L}\phi = 0$$

- Eigenvector basis

$$\phi(t) = \sum_k a_k(t) \mathbf{v}_k, \quad a_k(t) = \phi(t)^T \mathbf{v}_k; \quad \mathbf{L}\mathbf{v}_k = \lambda \mathbf{v}_k$$

- ODE

$$\sum_k \left( \frac{da_k(t)}{dt} + C\lambda_k a_k(t) \right) \mathbf{v}_k = 0$$

$$\frac{da_k(t)}{dt} + C\lambda_k a_k(t) = 0$$

$$a_k(t) = a_k(0) e^{-C\lambda_k t}$$

- Solution

$$\phi(t) = \sum_k a_k(0) \mathbf{v}_k e^{-C\lambda_k t}$$

# Diffusion on Graph

- Solution

$$\phi(t) = \sum_k a_k(0) v_k e^{-C\lambda_k t}$$

- all  $\lambda_i > 0$  for  $i > 1$ ,  $\lambda_1 = 0$ :

$$\lim_{t \rightarrow \infty} \phi(t) = a_1(0) v_1$$

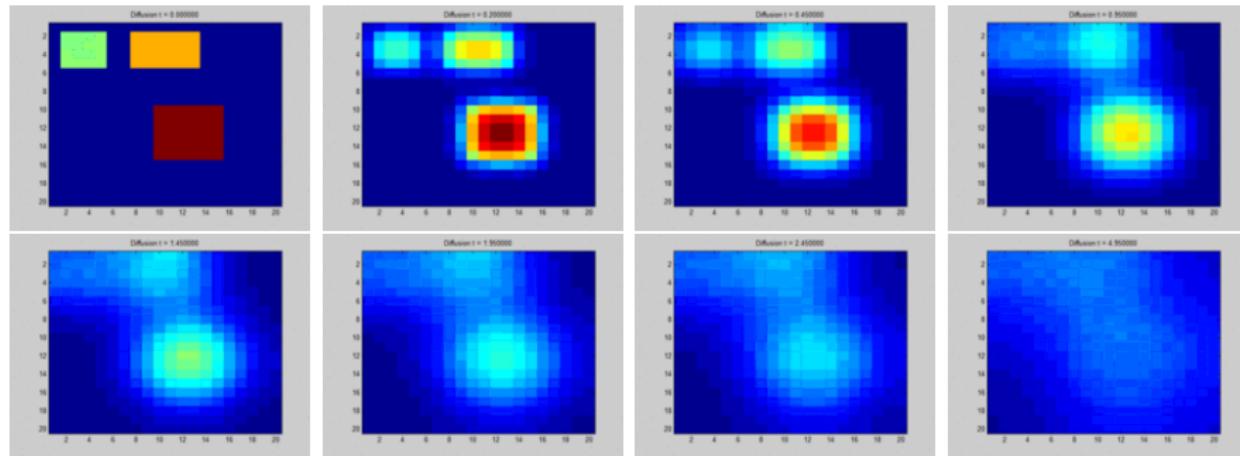
- Normalized solution  $v_1 = \frac{1}{\sqrt{N}} e$

$$a_1(0) = \phi(0)^T v_1 = \frac{1}{\sqrt{N}} \sum_j \phi_j(0)$$

- Steady state

$$\lim_{t \rightarrow \infty} \phi(t) = \left( \frac{1}{N} \sum_j \phi_j(0) \right) e = const$$

# Diffusion on Graph



# Smoothing operator

- $L$  - symmetric positive semidefinite

$$\phi^T L \phi = \sum_{ij} L_{ij} \phi_i \phi_j = \sum_{ij} (d_i \delta_{ij} - A_{ij}) \phi_i \phi_j = \frac{1}{2} \sum_{ij} A_{ij} (\phi_i - \phi_j)^2$$

- Smoothing operator

$$L\phi_i = \sum_j (D_{ij} - A_{ij}) \phi_j = \sum_j (d_i \delta_{ij} \phi_j - A_{ij} \phi_j) = d_i \left( \phi_i - \frac{1}{d_i} \sum_j A_{ij} \phi_j \right)$$

- Laplace equation  $\nabla \phi = 0$ ,  $(L\phi)_i = 0$ , solution - harmonic function

$$\phi_i = \frac{1}{d_i} \sum_j A_{ij} \phi_j$$

- Regression on graphs

# Normalized Laplacian

- Normalized Laplacian

$$\mathcal{L} = D^{-1/2} L D^{-1/2}$$

$$\mathcal{L}_{ij} = \begin{cases} 1 & , \text{ if } i = j, \\ -\frac{1}{\sqrt{d_i d_j}} & , \text{ if } \exists e(i,j) - i \text{ and } j \text{ adjacent,} \\ 0 & , \text{ otherwise} \end{cases}$$

- Connection to random walks:

$$P = D^{-1} A = D^{-1/2} (I - \mathcal{L}) D^{1/2}$$

Similar matrices represents the same linear transformations in different basis and share properties of represented linear operators, i.e. eigenvalues:  $\lambda_{max}(P) = 1$ ,  $\lambda_1(\mathcal{L}) = 0$ .

# Normalized Laplacian

- Conductance of a vertex set  $S$

$$\phi(S) = \frac{cut(S, V \setminus S)}{\min(vol(S), vol(V \setminus S))}$$

where  $vol(S) = \sum_{i \in S} k_i$  - sum of all node degrees in the set

- Cheeger's inequality

$$\lambda_2(\mathcal{L})/2 \leq \min_S \phi(S) \leq \sqrt{2\lambda_2(\mathcal{L})}$$

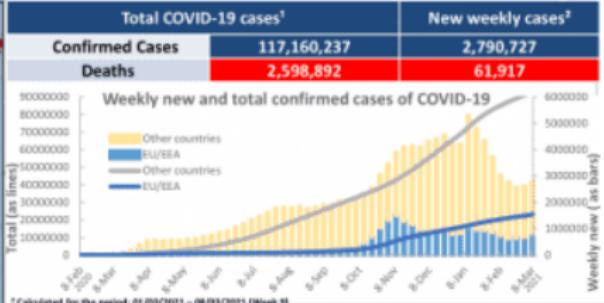
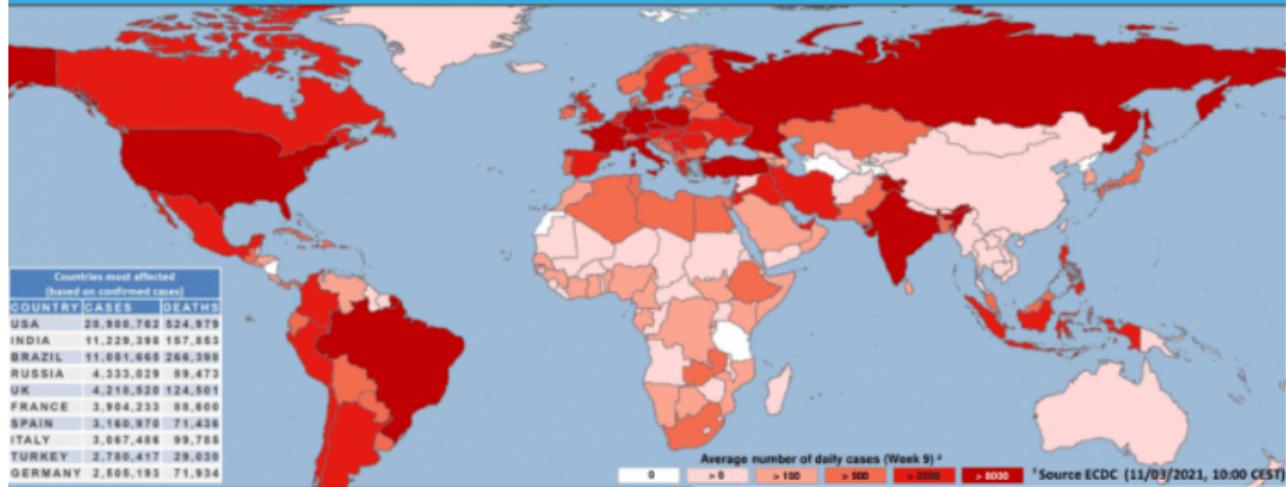
- $\lambda_1 = 0$ ,  $0 \leq \lambda_i \leq 2$
- $0 \leq \lambda_2 \leq \frac{n}{n-1}$   
 $\lambda_2 = 0$ , disconnected graph  
 $\lambda_2 = \frac{n}{n-1}$ , completely connected graph

# Lecture outline

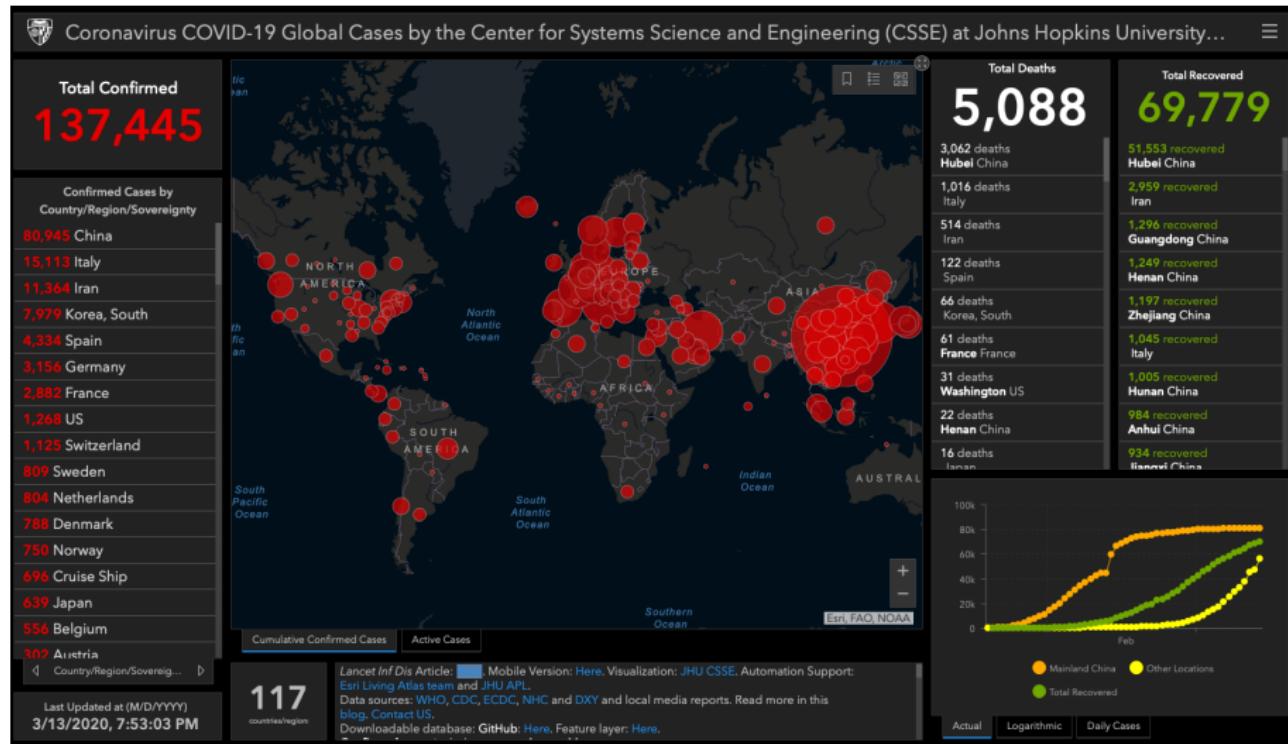
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# Coronavirus COVID-19

Emergency Response Coordination Centre (ERCC) | DG ECHO Daily Map | 12/03/2021  
COVID-19 pandemic | 11/03/2021

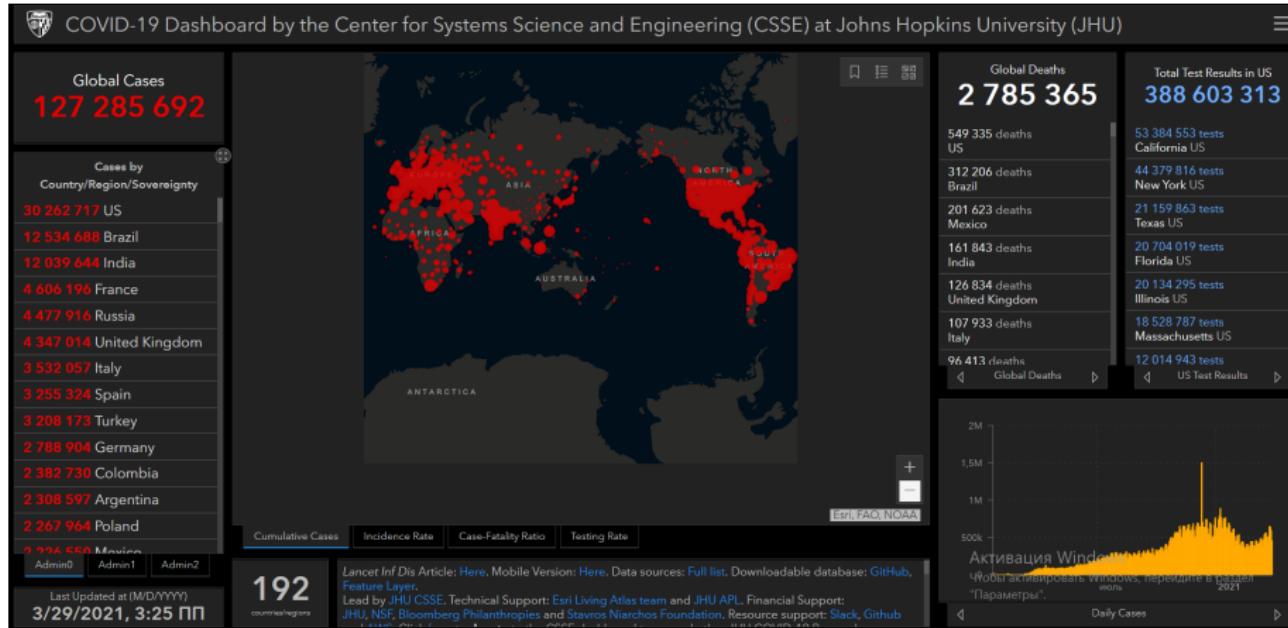


# Coronavirus COVID-19



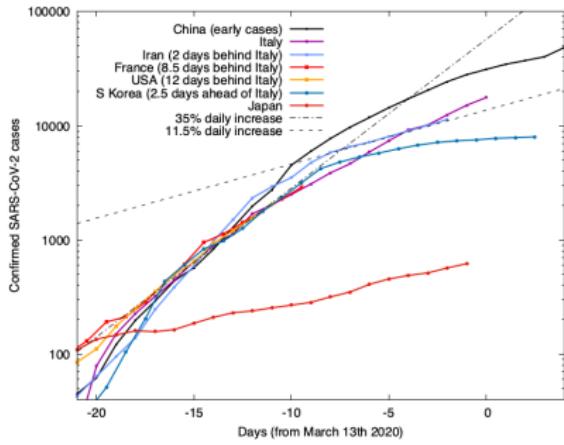
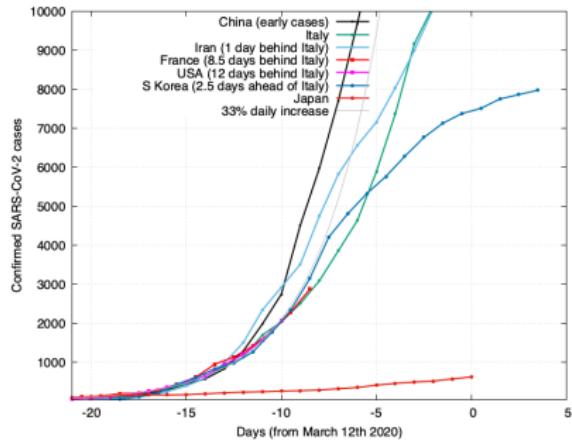
Dashboard from Johns Hopkins University, <https://coronavirus.jhu.edu/map.html>

# Coronavirus COVID-19



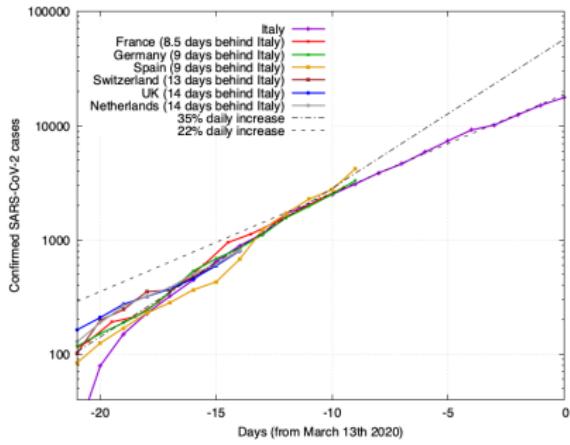
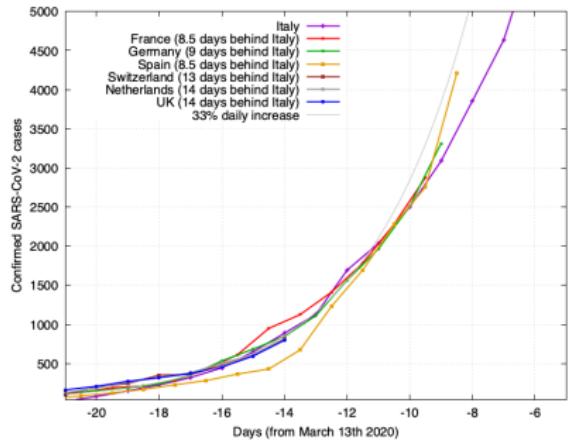
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# Coronavirus COVID-19



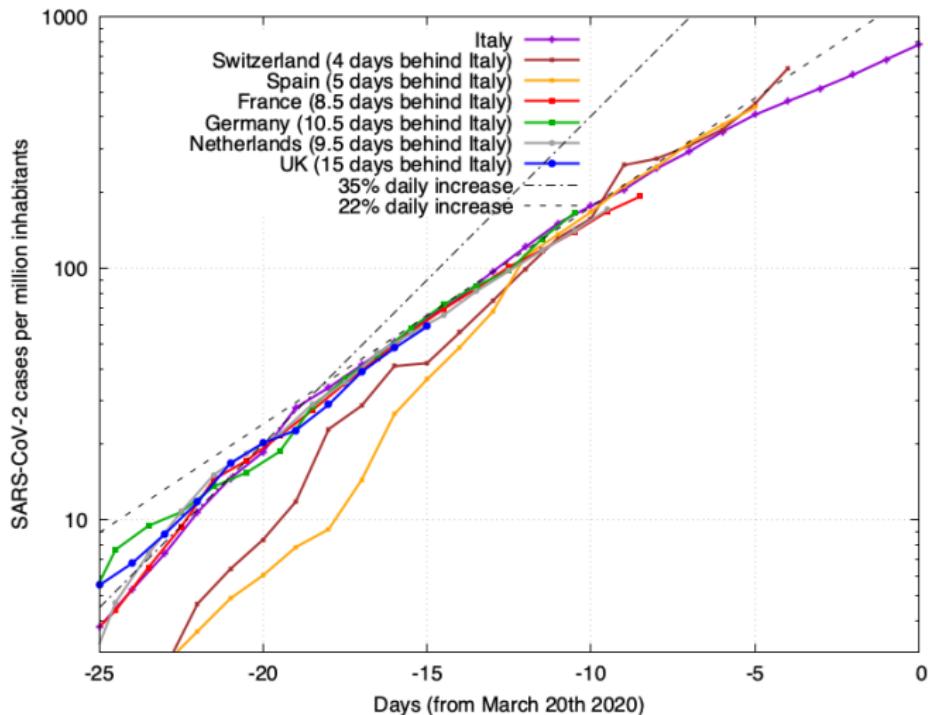
from Mark Handley, UCL

# Coronavirus COVID-19



from Mark Handley, UCL

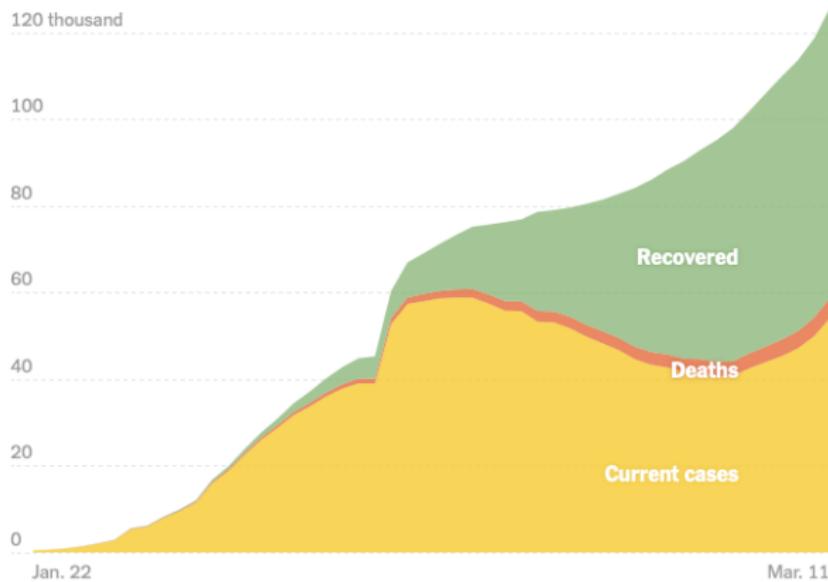
# Coronavirus COVID-19



from Mark Handley, UCL

# Coronavirus COVID-19

How many people have recovered or died



Source: Center for Systems Science and Engineering at Johns Hopkins University.

from the NYT

# Simple model of contagion

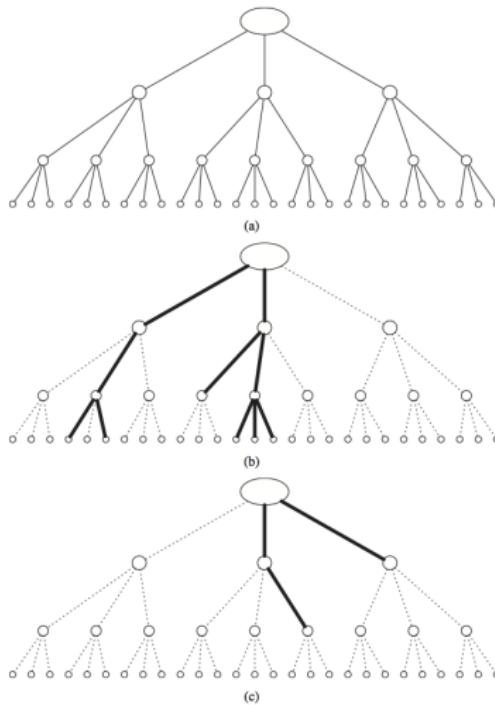
## Simple model of contagion (decease transmission)

- 1st-wave: first infected person enters the population and transmits to each person he meets with probability  $p$ . Suppose he meets  $\langle k \rangle$  people while contagious
- 2nd-wave: Each infected person from 1st wave meets  $\langle k \rangle$  new people and independently transmits infection with probability  $p$
- 3rd-wave: ....

Population is organized as a tree

This is Galton-Watson branching stochastic process

# Branching process



$p \cdot \langle k \rangle$  - average number of secondary infections from one node

image from David Easley, Jon Kleinberg, 2010

# Branching process

- $R_0 = p\langle k \rangle$  - the average number of new infected nodes/people on every step
- On the  $n$  step, the average number of infected people  $R_0^n = (p\langle k \rangle)^n$
- if  $R_0 > 1$ , the average grows geometrically as  $R_0^n$
- if  $R_0 < 1$ , the average shrinks geometrically as  $R_0^n$
- when  $n \rightarrow t$ , geometric growth  $\rightarrow$  exponential growth

$R_0$  - basic reproduction number, is the average number of secondary infections produced when one infected individual is introduced into a host population where everyone is susceptible

$R_0 = 1$  - is the threshold that determines when an infection can invade and persist in a new host population.

# Basic reproductive number

Disease	Transmission	$R_0$
Measles	Airborne	12-18
Pertussis	Airborne droplet	12-17
Diphtheria	Saliva	6-7
Smallpox	Social contact	5-7
Polio	Fecal-oral route	5-7
Rubella	Airborne droplet	5-7
Mumps	Airborne droplet	4-7
HIV/AIDS	Sexual contact	2-5
SARS	Airborne droplet	2-5
Influenza (1918 strain)	Airborne droplet	2-3

from Barabasi, 2016

# Compartmental models in epidemiology

- Mathematical epidemiology
- W. O. Kermack and A. G. McKendrick, 1927
- Deterministic compartmental model (population classes)  $\{S, I, R\}$
- $S(t)$  - 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, SEIR,

# SI model

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

$$S \longrightarrow I$$

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

- $\beta$  - transmission/infection rate, number of transmitting contacts per unit time;  $T_c = 1/\beta$  - time between transmitting contact
- 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

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

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

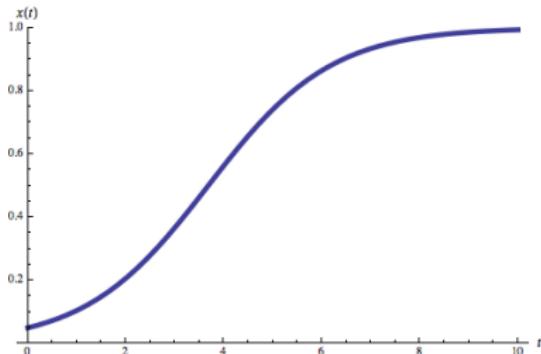
- Differential equation,  $i(t = 0) = i_0$

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

# Logistic growth function

- Solution:

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



- Limit  $t \rightarrow \infty$

$$\begin{aligned}i(t) &\rightarrow 1 \\s(t) &\rightarrow 0\end{aligned}$$

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

# SIS model

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

$$S \longrightarrow I \longrightarrow S$$

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

- $\beta$  - infection rate (on contact),  $\gamma$  - recovery rate;  $T_r = 1/\gamma$  - average time to recovery
- 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,  $i(t = 0) = i_0$

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

# SIS model

- Solution

$$i(t) = \left(1 - \frac{\gamma}{\beta}\right) \frac{C}{C + e^{-(\beta-\gamma)t}}$$

where

$$C = \frac{\beta i_0}{\beta - \gamma - \beta i_0}$$

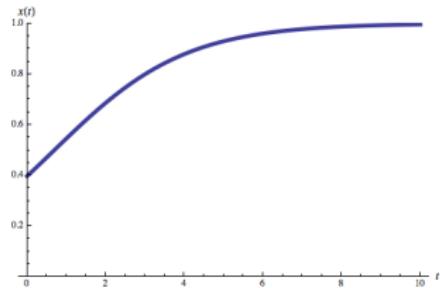
- Limit  $t \rightarrow \infty$

$$\beta > \gamma \quad , \quad i(t) \rightarrow \left(1 - \frac{\gamma}{\beta}\right)$$

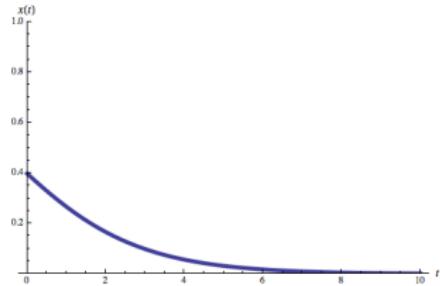
$$\beta < \gamma \quad , \quad i(t) = i_0 e^{(\beta-\gamma)t} \rightarrow 0$$

# Logistic function

- $\beta > \gamma$ ,  $i(t) \rightarrow (1 - \frac{\gamma}{\beta})$



- $\beta < \gamma$ ,  $i(t) = i_0 e^{(\beta - \gamma)t} \rightarrow 0$



# SIR model

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

$$S \longrightarrow I \longrightarrow R$$

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

- $\beta$  - infection rate,  $\gamma$  - 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

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

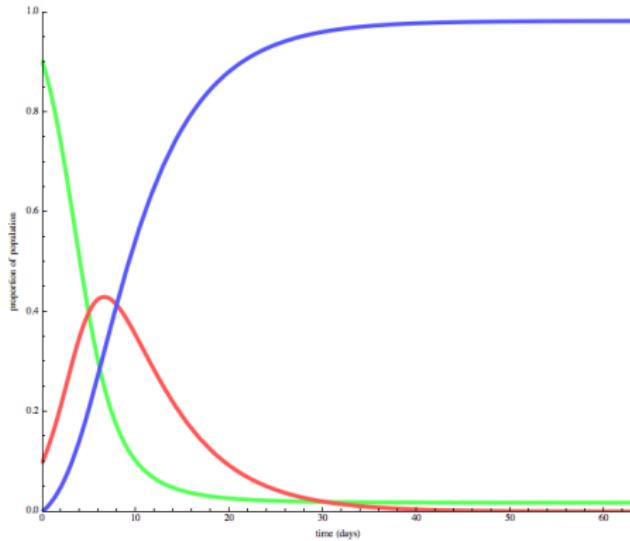
$$s = s_0 e^{-\frac{\beta}{\gamma} r}$$

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

- Solution

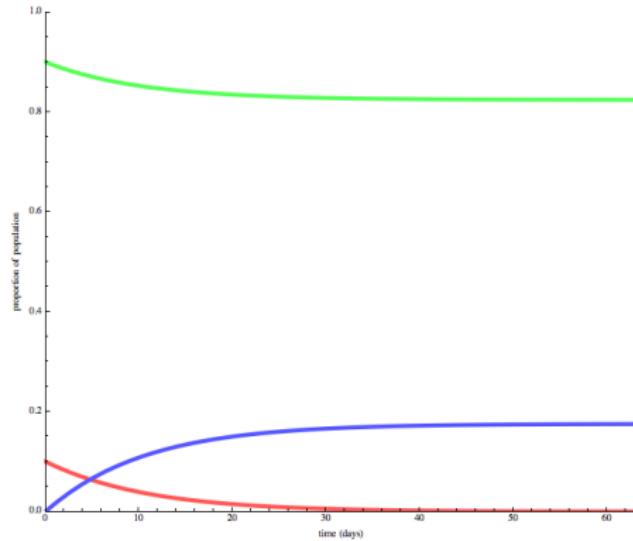
$$t = \frac{1}{\gamma} \int_0^r \frac{dr}{1 - r - s_0 e^{-\frac{\beta}{\gamma} r}}$$

# SIR model



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

# SIR model



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

# SIR model

- Equation

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

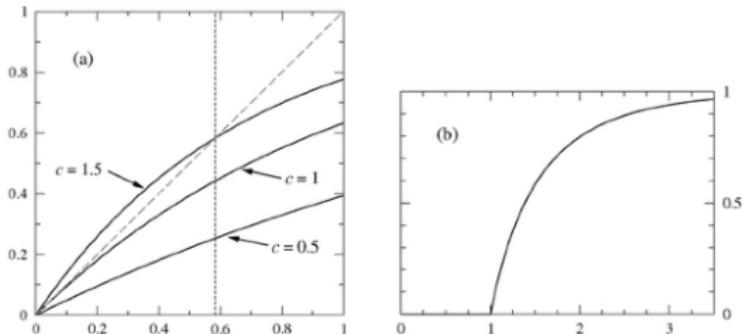
- Limits:  $t \rightarrow \infty$ ,  $\frac{dr}{dt} = 0$ ,  $r_\infty = \text{const}$ ,

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

- 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

- $r_\infty$  - the total size of the outbreak
- Epidemic threshold

Epidemics:  $R_0 > 1, \beta > \gamma, r_\infty = \text{const} > 0$

No epidemics:  $R_0 < 1, \beta < \gamma, r_\infty \rightarrow 0$

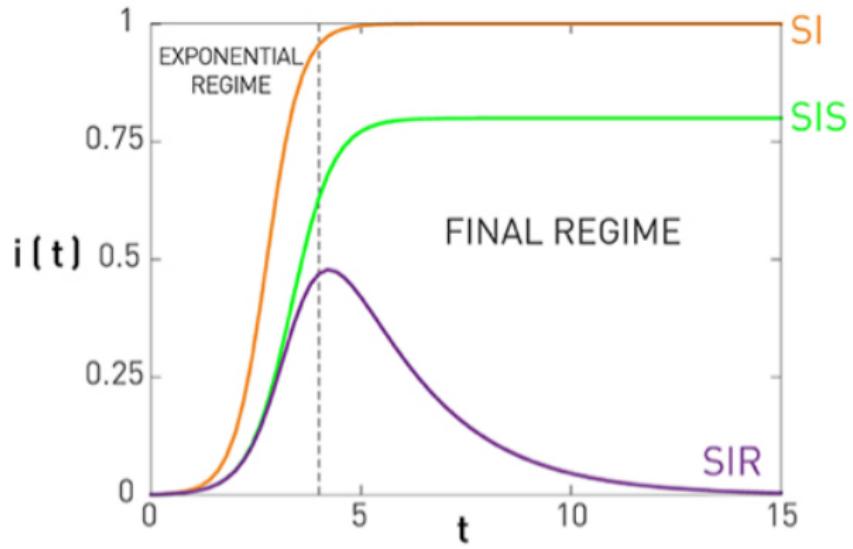
- $\beta$  - infection rate,  $\gamma$  - recovery rate  $\rightarrow$
- Basic reproduction number

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

It is average number of people infected by a person before his recovery

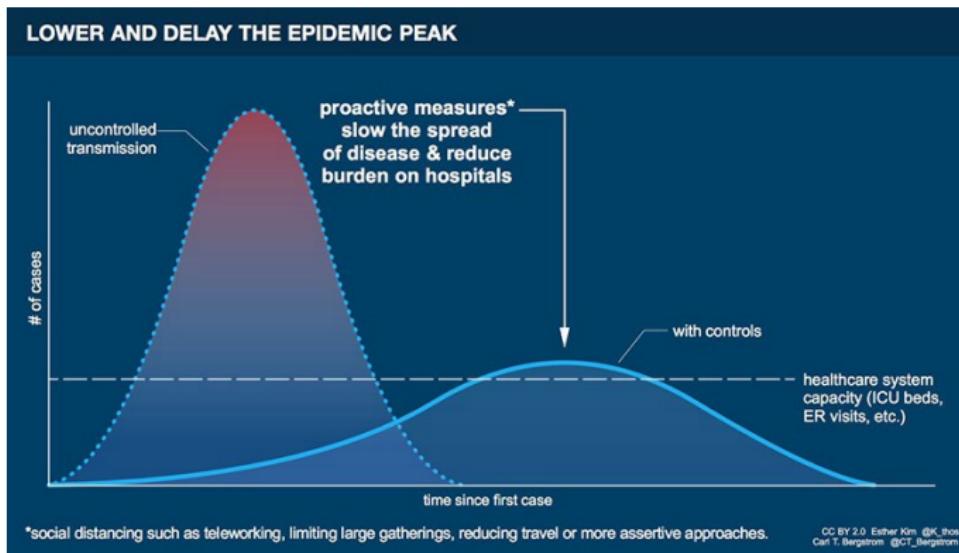
$$R_0 = E[\beta\tau] = \beta \int_0^\infty \gamma\tau e^{-\gamma\tau} d\tau = \frac{\beta}{\gamma}$$

# Compartmental models summary

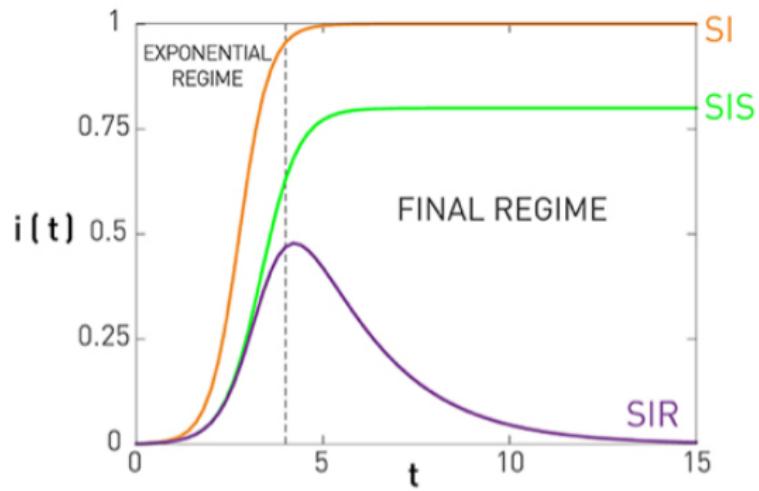


from Barabasi, 2016

# Flatten the curve!



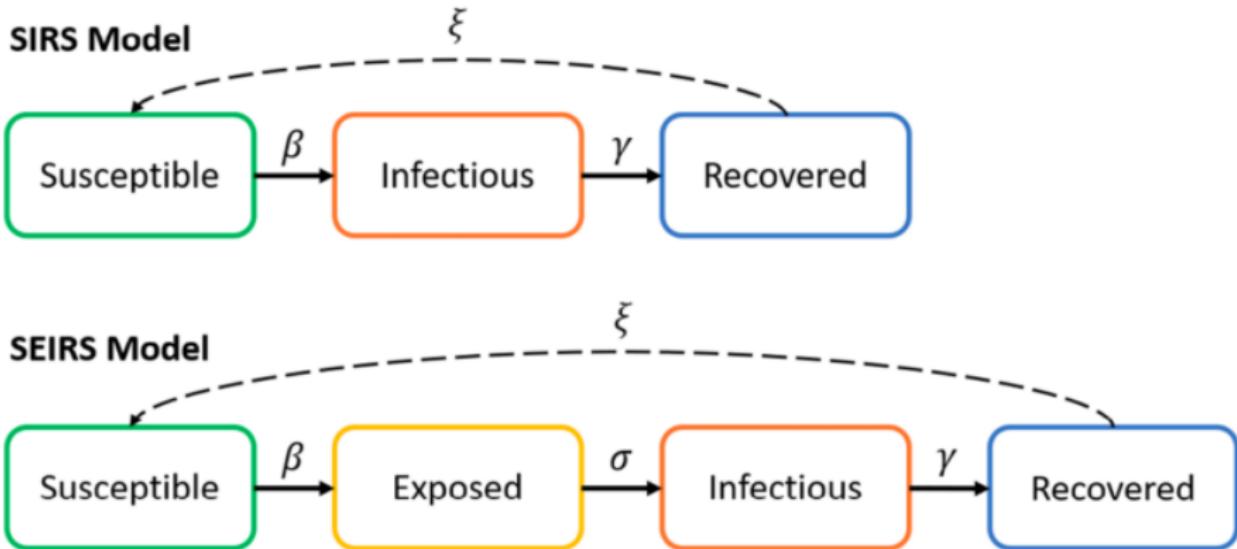
# Compartmental models summary



Model	early time	late time	Epidemic threshold
SI	$i_0 e^{\beta t}$	1	-
SIS	$(1 - \frac{\gamma}{\beta}) e^{(\beta - \gamma)t}$	$1 - \frac{\gamma}{\beta}; 0$	$R_0 = 1$
SIR	exponential	0	$R_0 = 1$

from Barabasi, 2016

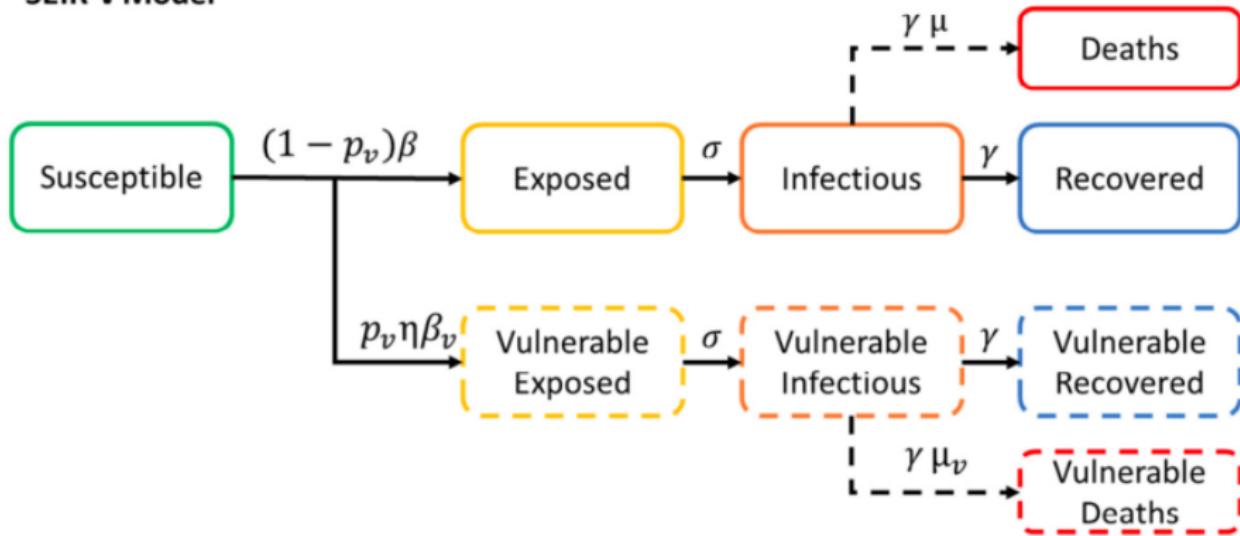
# Advanced Compartmental Models



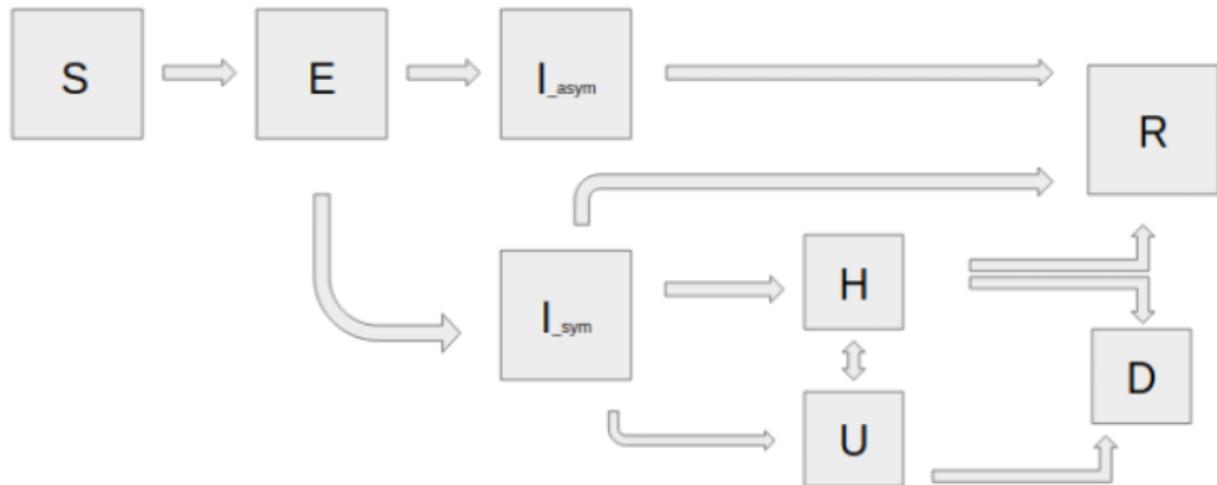
D. Anderez et al., 2020

# SEIR-vulnerable

## SEIR-v Model



D. Anderez et al., 2020



8-compartmental model: S - susceptible, E - exposed, I -infectious, H - hospitalized, U - ICU units, R - recovered

# 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
- $\beta$  - individual transmission/infection rate (probably to get infected on a contact in time  $\delta t$ ) f transmitting contacts per unit time;  $\beta_c = \beta\langle k \rangle$
- $\gamma$  - recovery rate (probability to recover in a unit time  $\delta t$ ). In compartmental model  $\beta_c$  - transmission/infection rate, number o
- 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  $t$

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

- $\beta$  - 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,  $t \rightarrow 0$ ,  $x_i(t) \ll 1$

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

$$\frac{dx(t)}{dt} = \beta Ax(t)$$

- Solution in the basis

$$Av_k = \lambda_k v_k$$

$$x(t) = \sum_k a_k(t) v_k$$

# SI model

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

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

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

- Solution

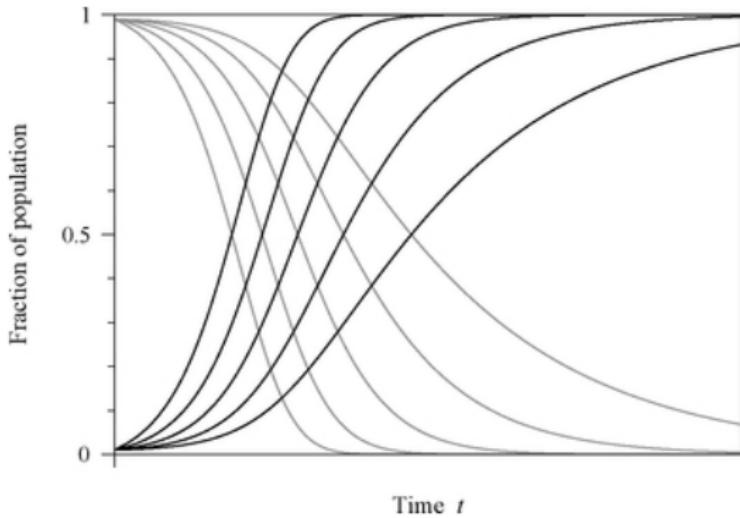
$$x(t) = \sum_k a_k(0) e^{\lambda_k \beta t} v_k$$

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

$$x(t) = v_1 e^{\lambda_1 \beta t}$$

- ① growth rate of infections depends on  $\lambda_1$
- ② probability of infection of nodes depends on  $v_1$ , i.e eigenvector centrality

# SI model



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

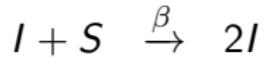
The highest values of  $k$  give the fastest growth

image from M. Newman, 2010

# SI simulation

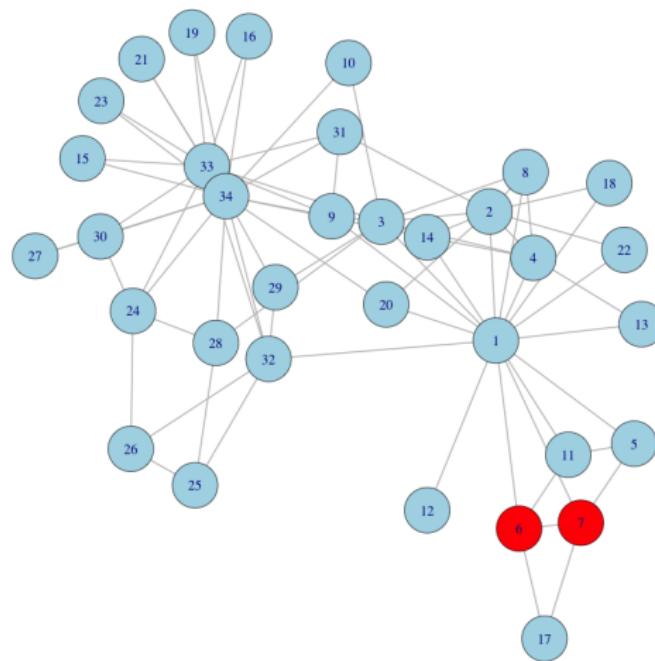
- ① Every node at any time step is in one state  $\{S, I\}$
- ② Initialize  $c$  nodes in state  $I$
- ③ On each time step each  $I$  node has a probability  $\beta$  to infect its nearest neighbors (NN),  $S \rightarrow I$

Model dynamics:



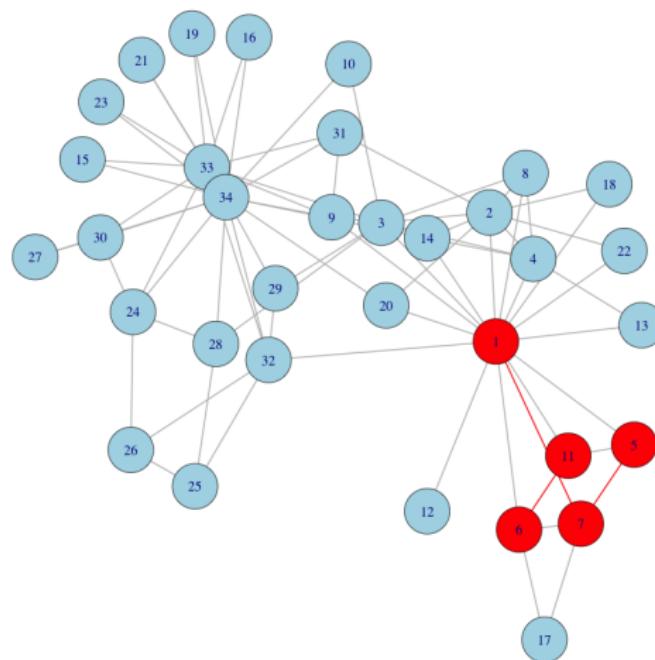
# SI model simulation

$$\beta = 0.5$$



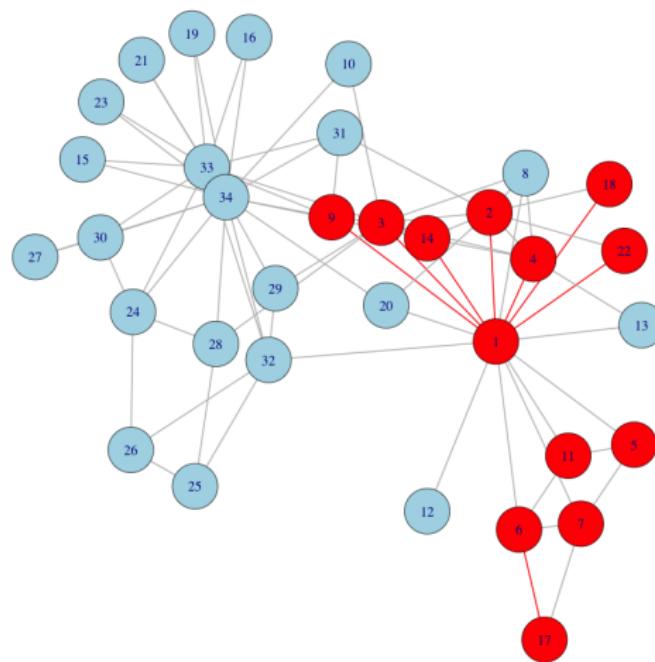
# SI model simulation

$$\beta = 0.5$$



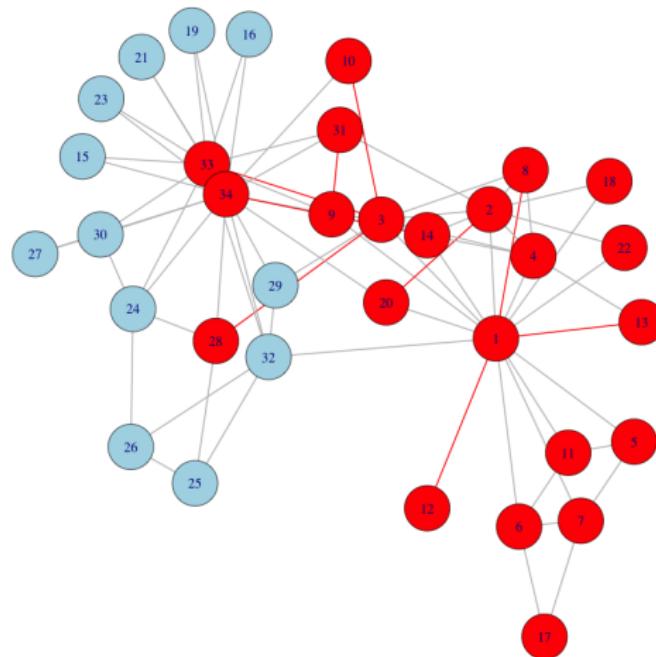
# SI model simulation

$$\beta = 0.5$$



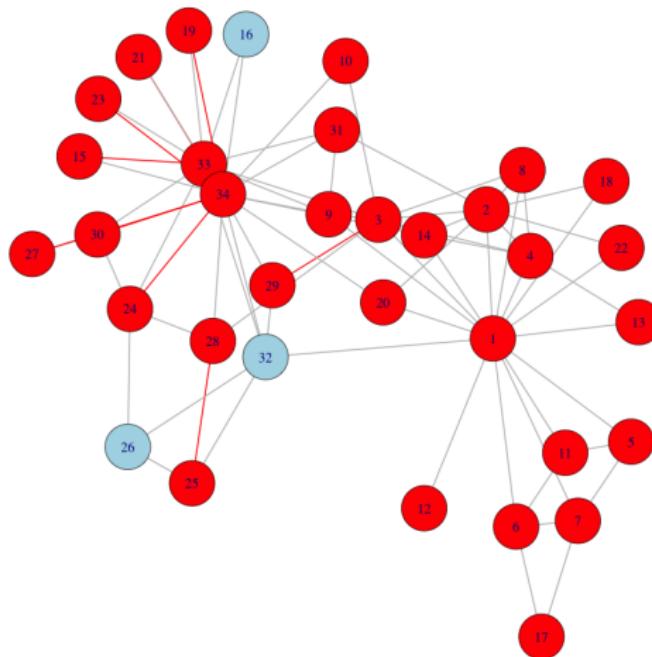
# SI model simulation

$$\beta = 0.5$$



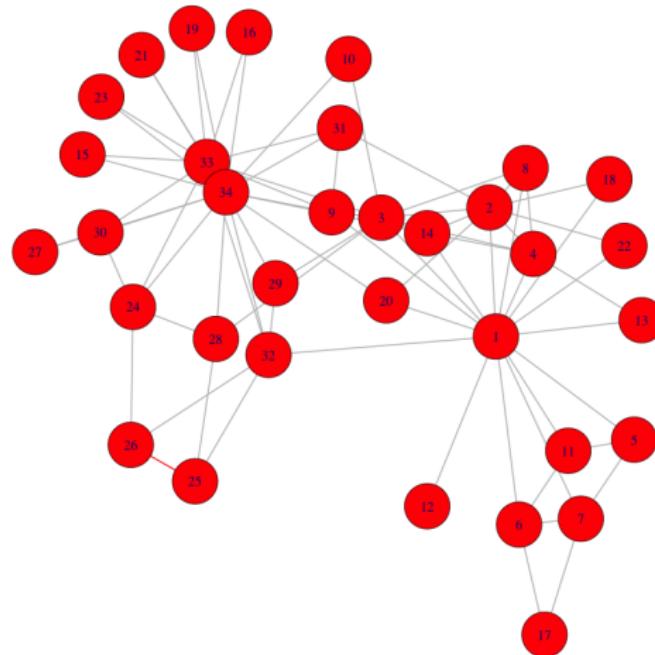
# SI model simulation

$$\beta = 0.5$$

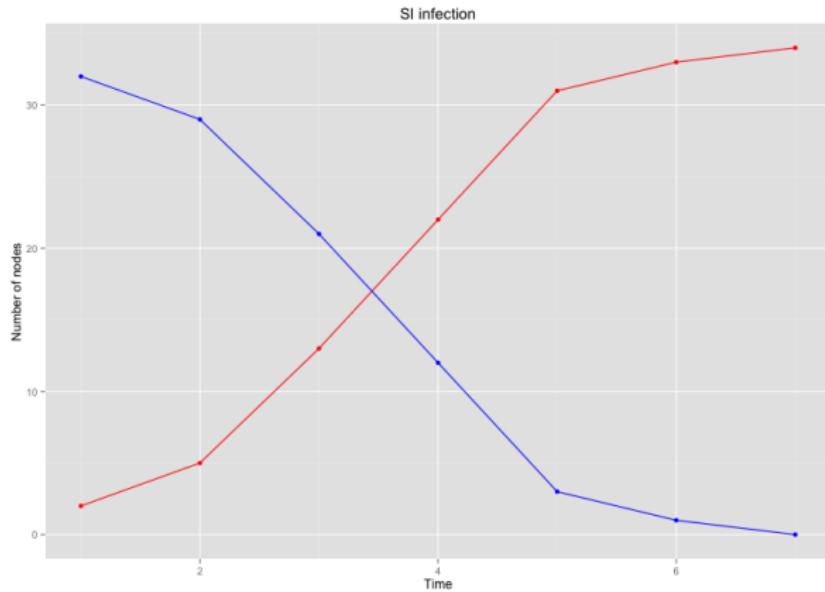


# SI model simulation

$$\beta = 0.5$$



# SI model



# SIS model

- SIS Model

$$S \longrightarrow I \longrightarrow S$$

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

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

- $\beta$  - infection rate,  $\gamma$  - 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,  $x_i(t) \ll 1$

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

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

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

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

# SIS model

- Eigenvector basis

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

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

# SIS model

Define epidemic threshold  $R$ :

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

In compartmental SIS model  $\frac{\beta_c}{\gamma}$ :

$$R = 1$$

In network SIS model  $\frac{\beta}{\gamma}$ :

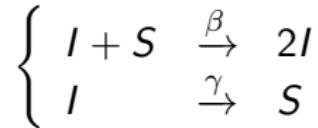
$$R = \frac{1}{\lambda_1}, \quad \lambda_1 - \text{largest eigenvalue of the adjacency matrix}$$

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

# SIS simulation

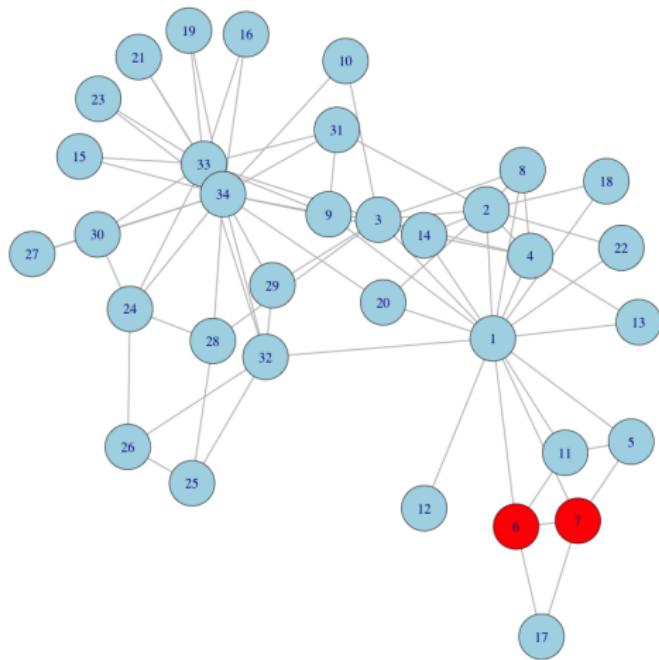
- ① Every node at any time step is in one state  $\{S, I\}$
- ② Initialize  $c$  nodes in state  $I$
- ③ Each node stays infected  $\tau_\gamma = \int_0^\infty \tau e^{-\tau\gamma} d\tau = 1/\gamma$  time steps
- ④ On each time step each  $I$  node has a probability  $\beta$  to infect its nearest neighbours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

Model dynamics:



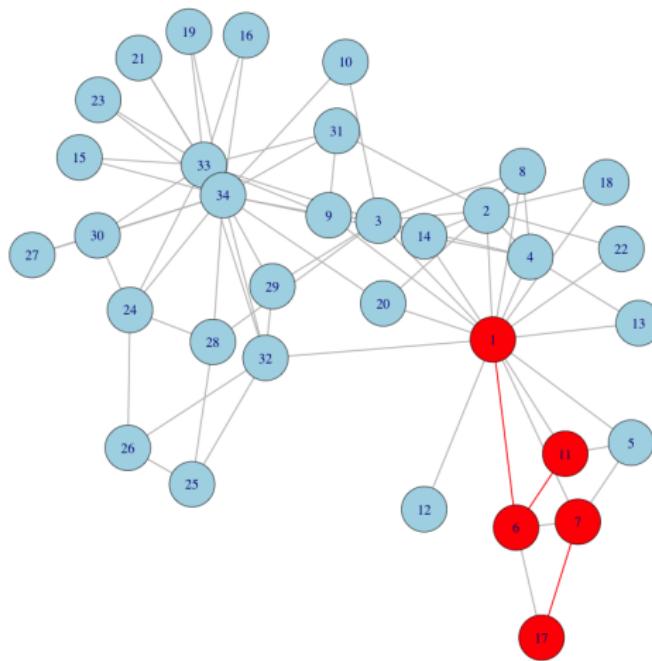
# SIS model simulation

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



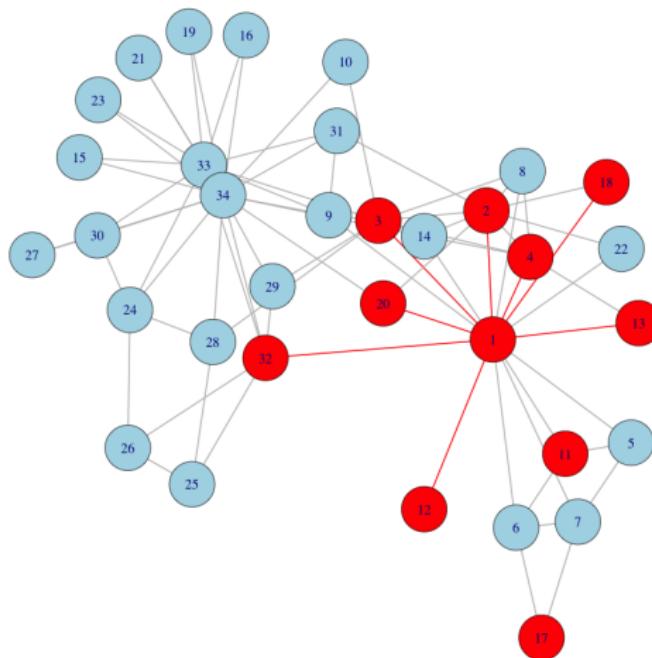
# SIS model simulation

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



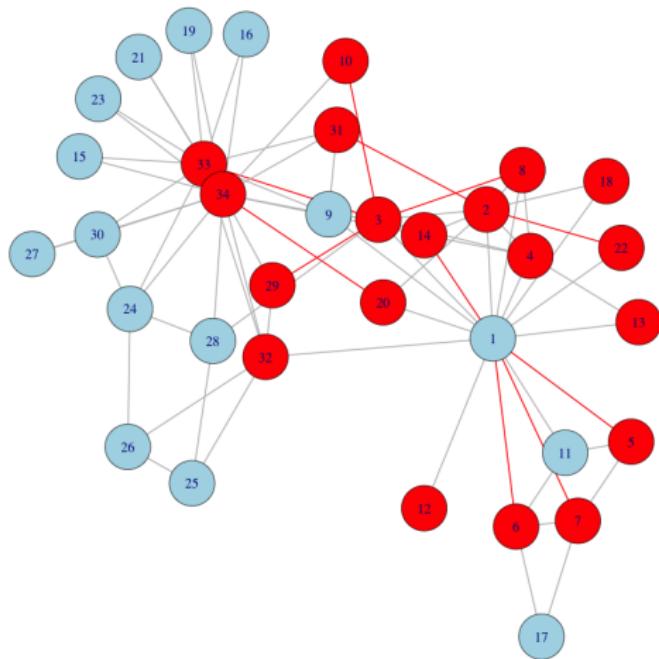
# SIS model simulation

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



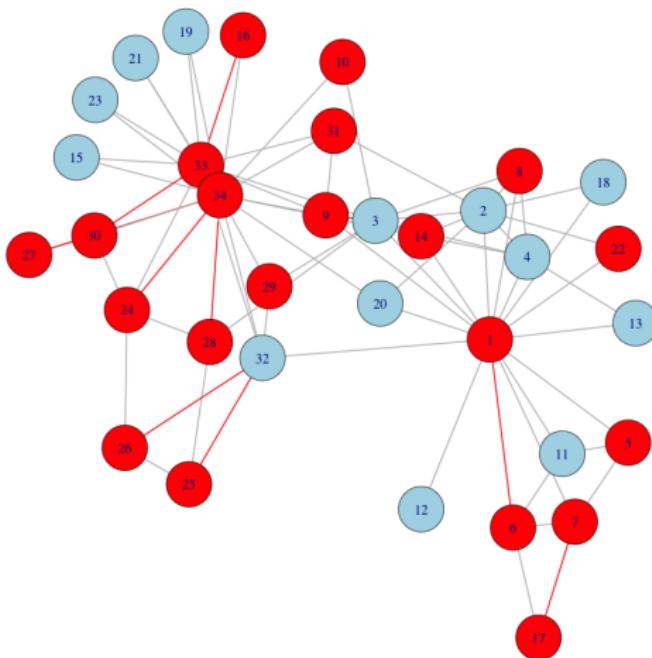
# SIS model simulation

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



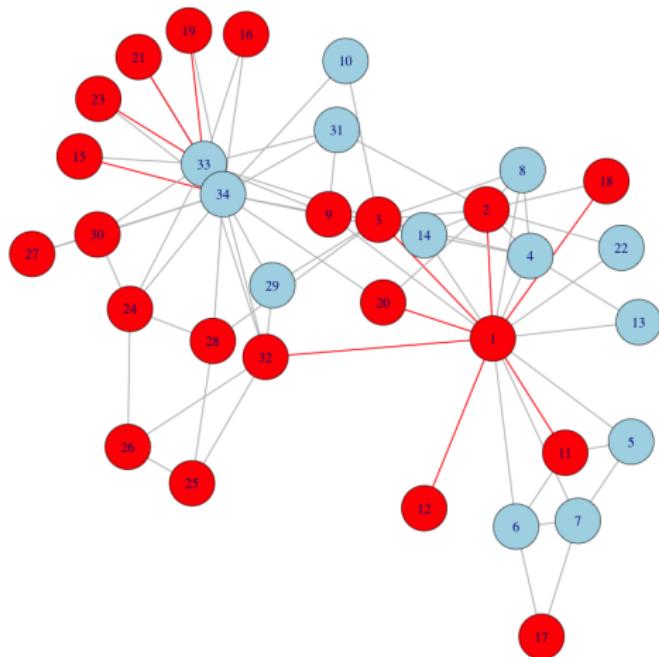
# SIS model simulation

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



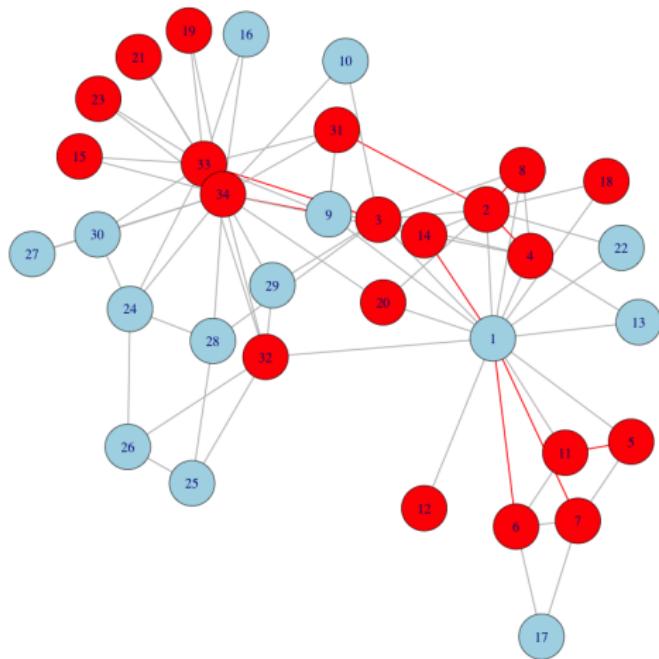
# SIS model simulation

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

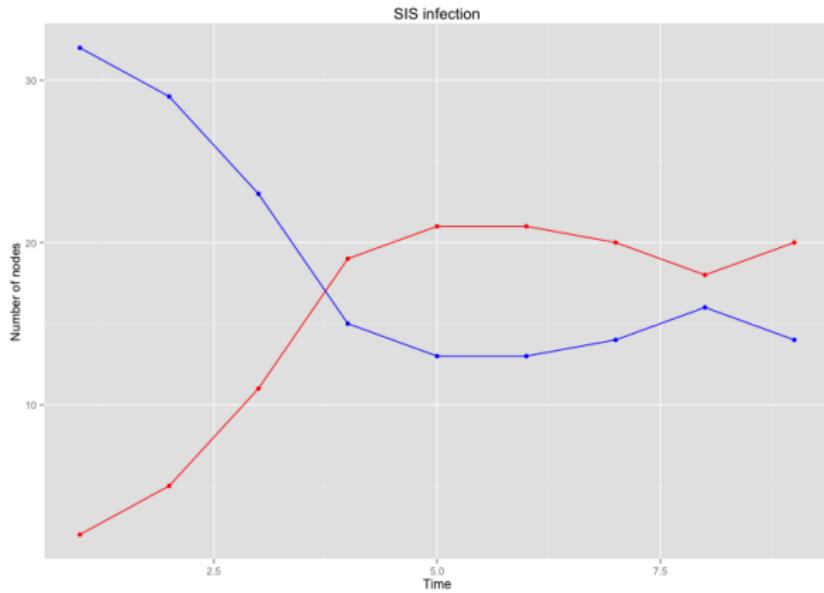


# SIS model simulation

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

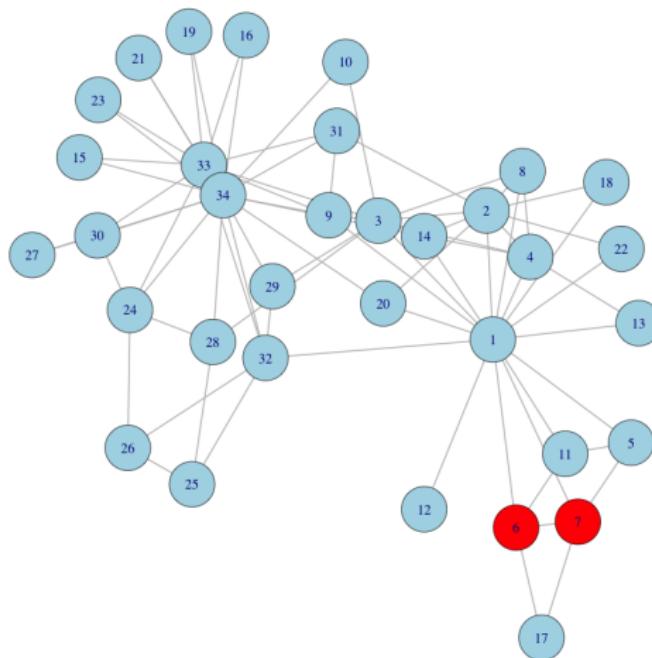


# SIS model



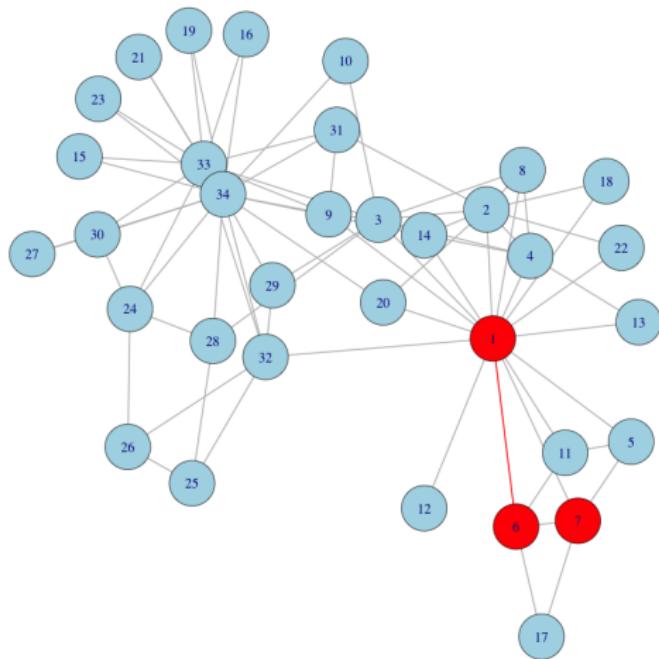
# SIS model simulation

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



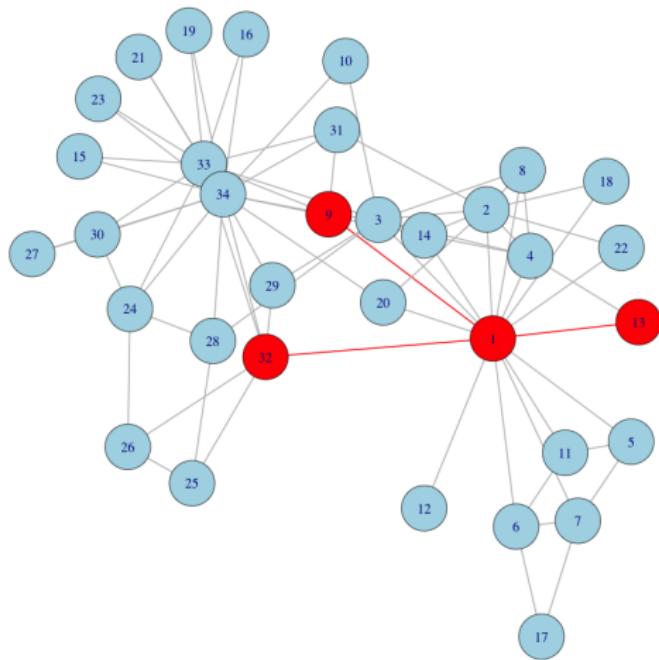
# SIS model simulation

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



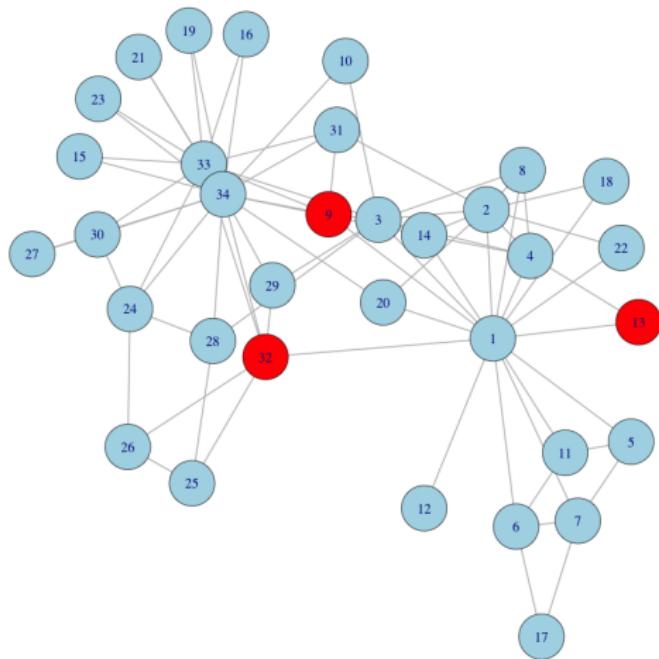
# SIS model simulation

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



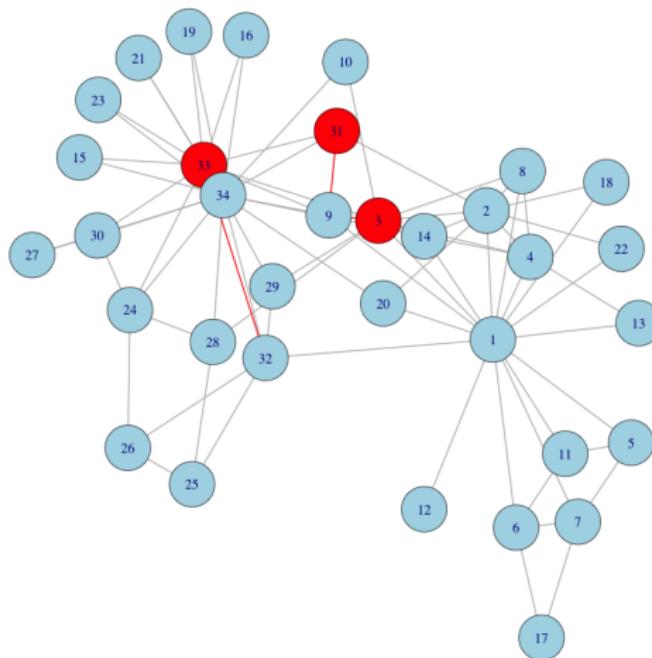
# SIS model simulation

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



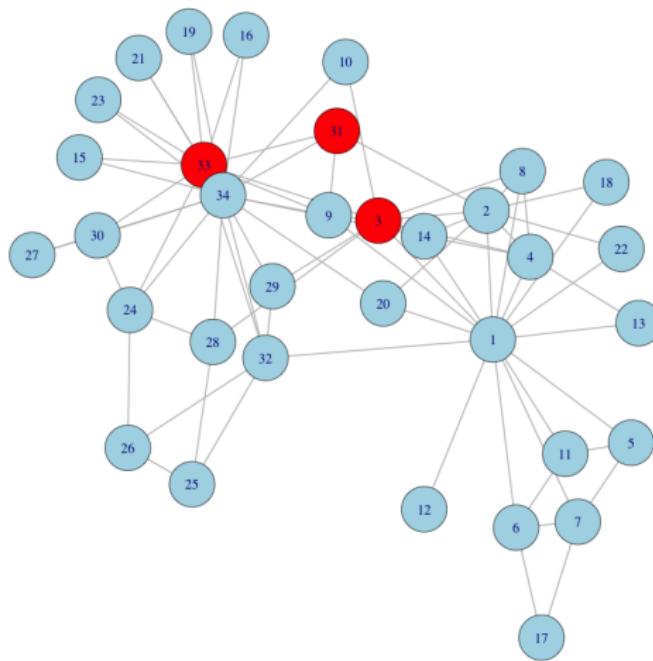
# SIS model simulation

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



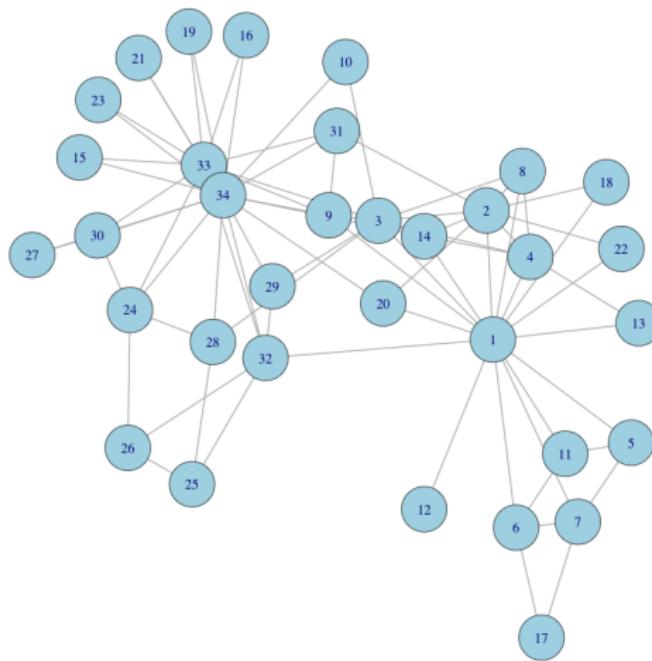
# SIS model simulation

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

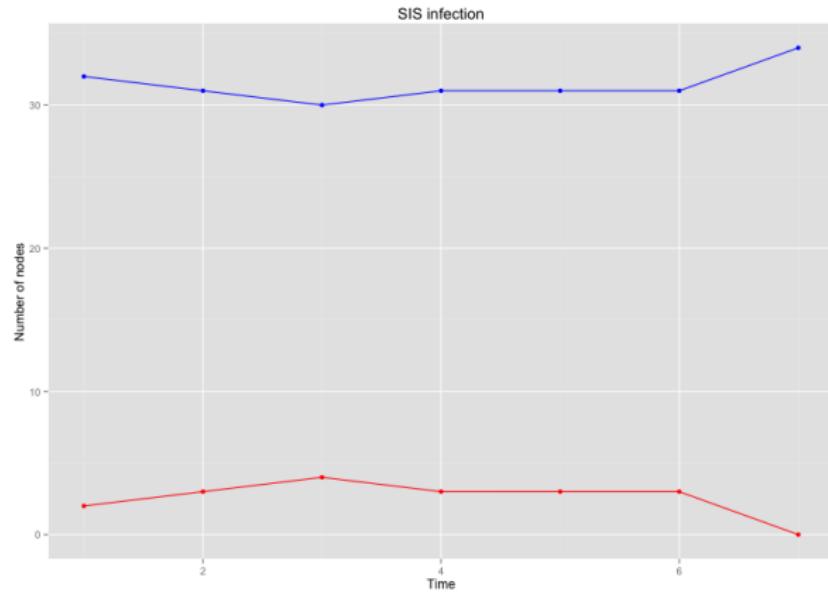


# SIS model simulation

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



# SIS model



# SIR model

- SIR Model

$$S \longrightarrow I \longrightarrow R$$

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

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

- $\beta$  - infection rate,  $\gamma$  - recovery rate
- Infection equation:

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

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

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

# 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,  $t \rightarrow 0$ ,  $r_i \sim 0$ , SIS = SIR

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

- Solution

$$x(t) \sim v_1 e^{(\beta\lambda_1 - \gamma)t}$$

# SIR model

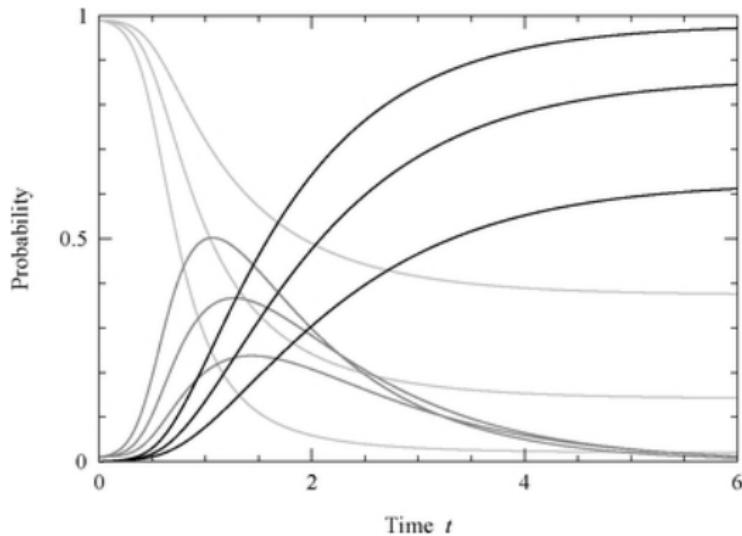
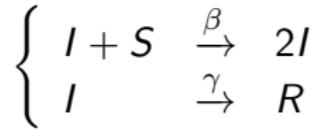


image from M. Newman, 2010

# SIR simulation

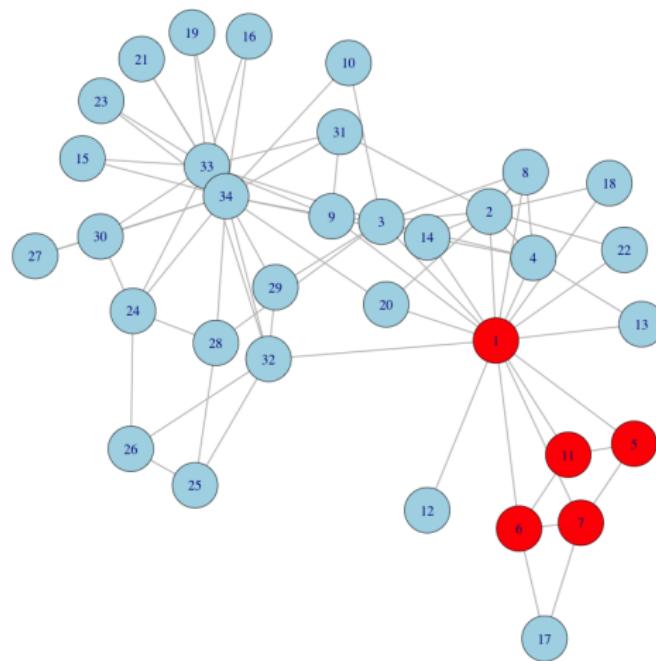
- ① Every node at any time step is in one state  $\{S, I, R\}$
- ② Initialize  $c$  nodes in state  $I$
- ③ Each node stays infected  $\tau_\gamma = 1/\gamma$  time steps
- ④ On each time step each  $I$  node has a probability  $\beta$  to infect its nearest neighbours (NN),  $S \rightarrow I$
- ⑤ After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

Model dynamics:



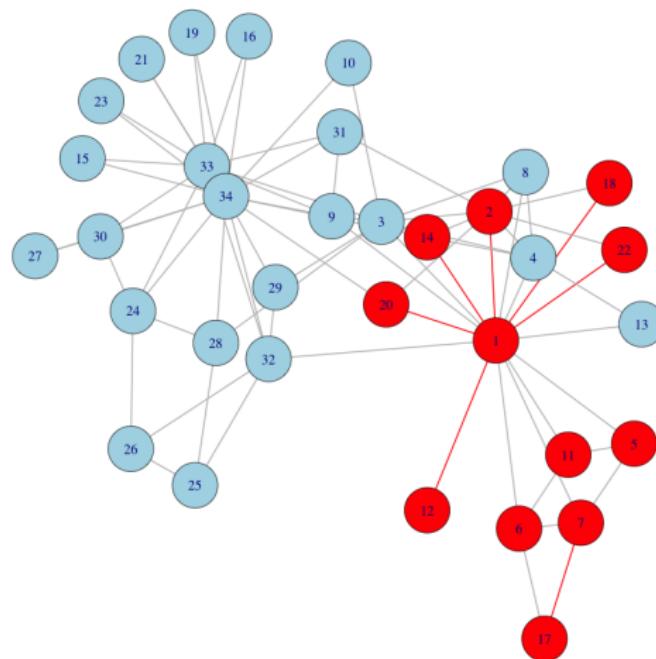
# SIR model

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



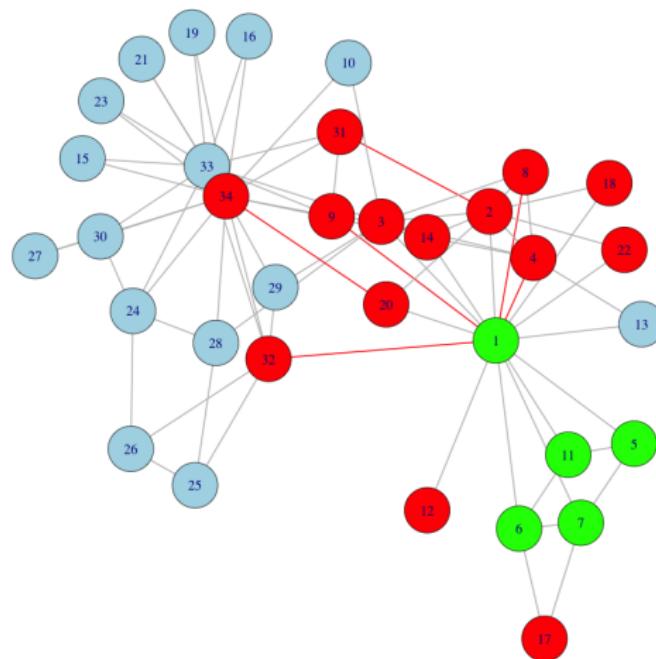
# SIR model

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



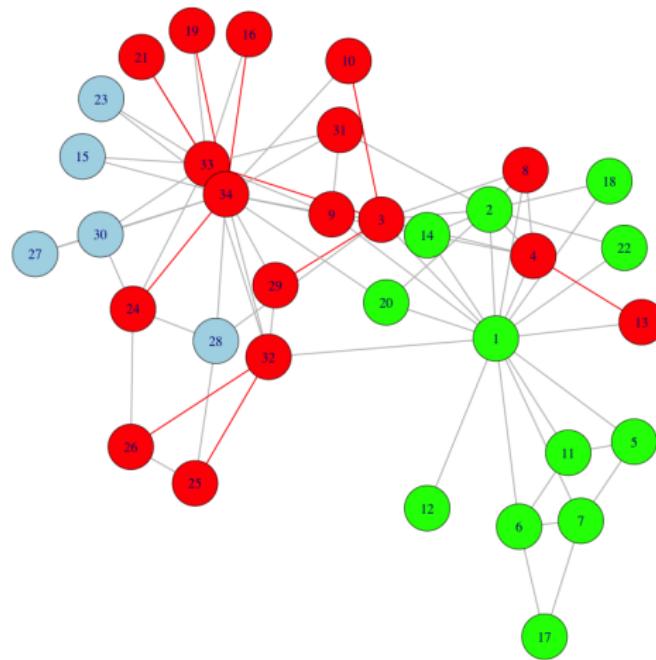
# SIR model

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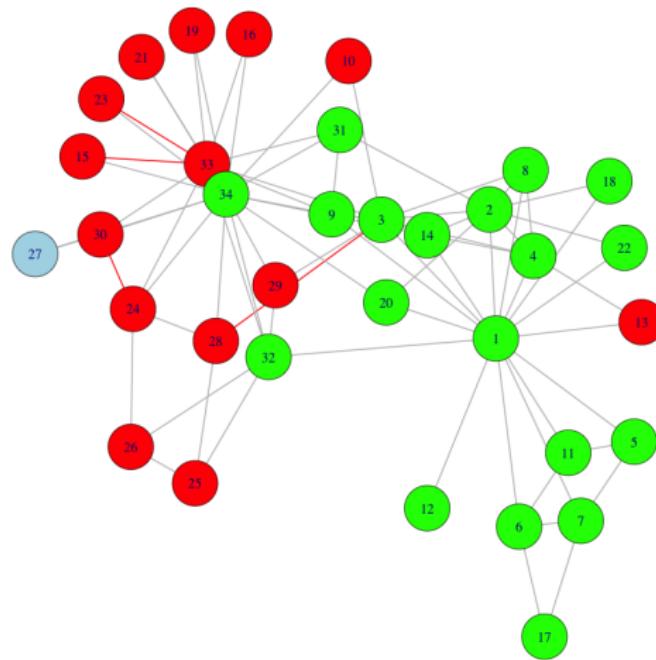
# SIR model

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



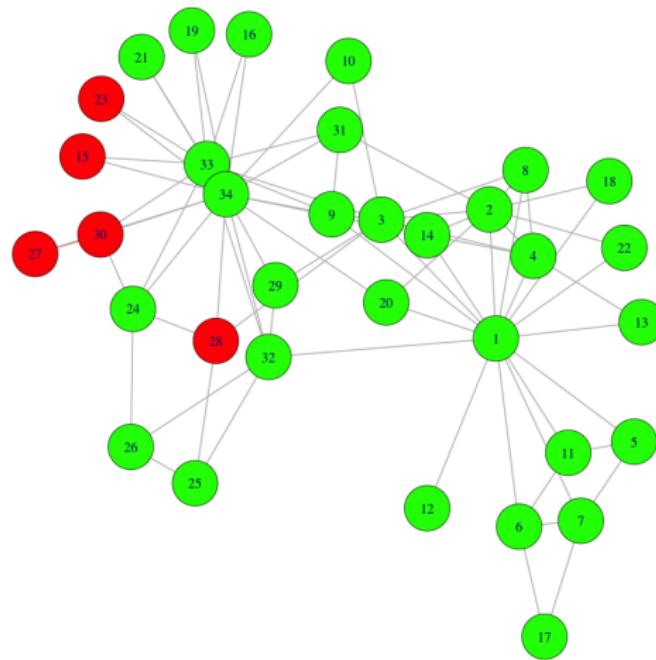
# SIR model

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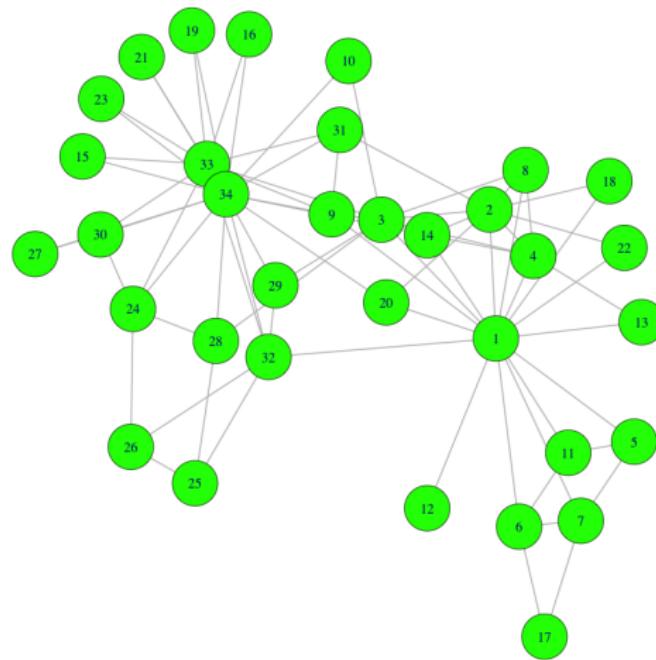
# SIR model

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

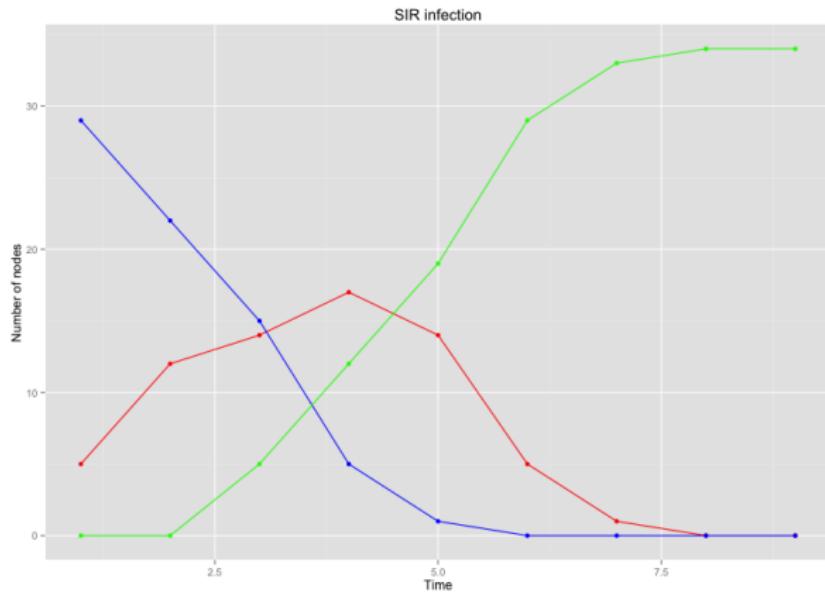


# SIR model

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

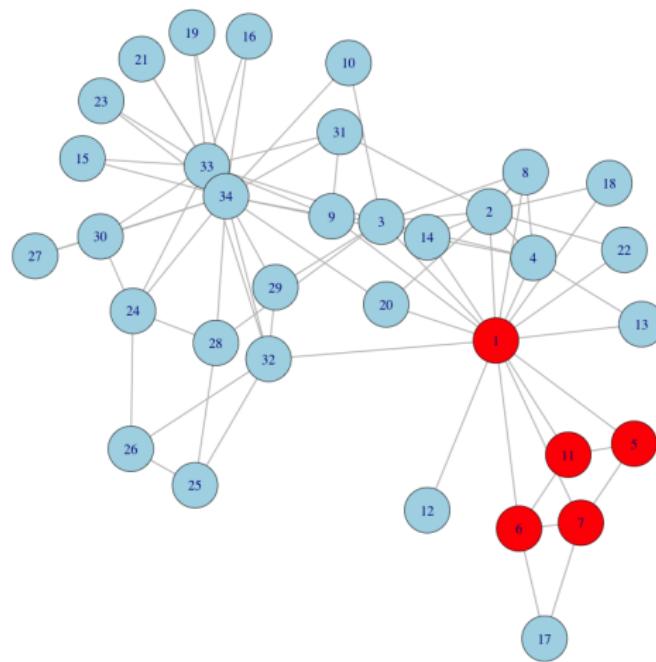


# SIR model



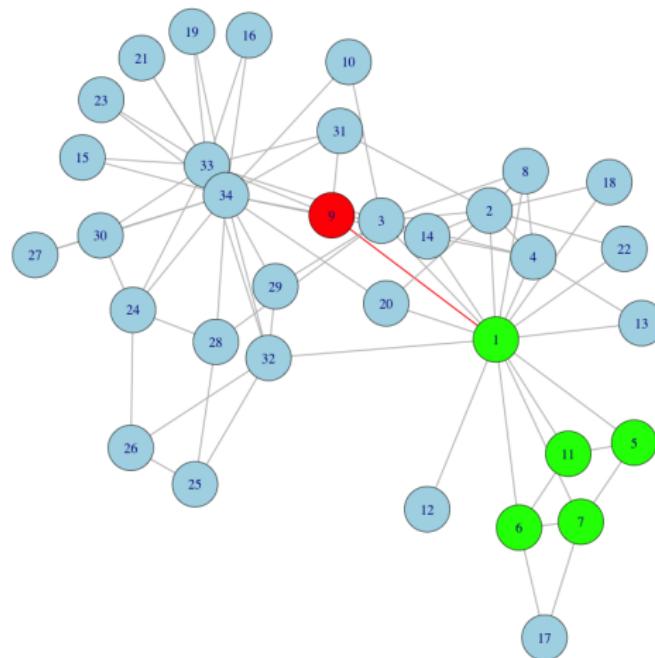
# SIR model

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



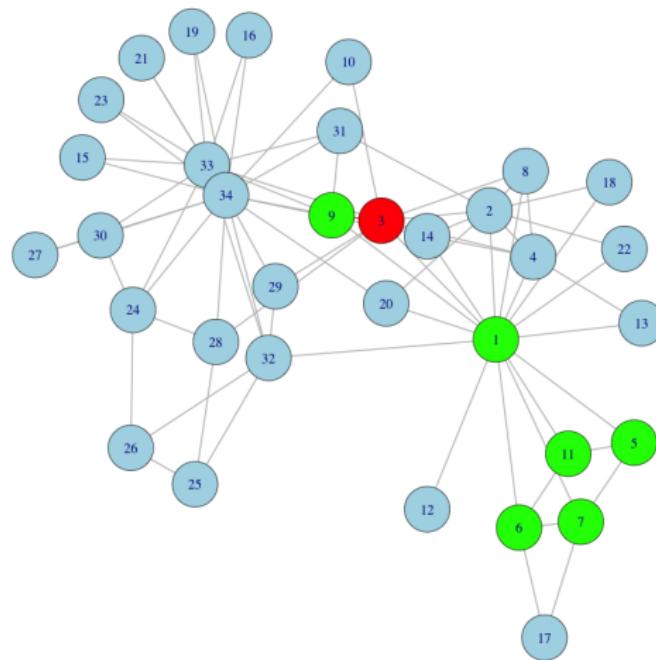
# SIR model

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



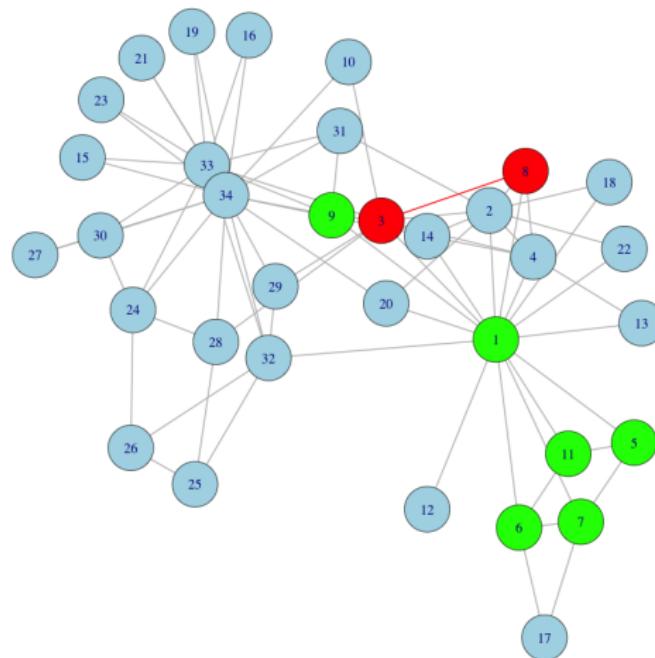
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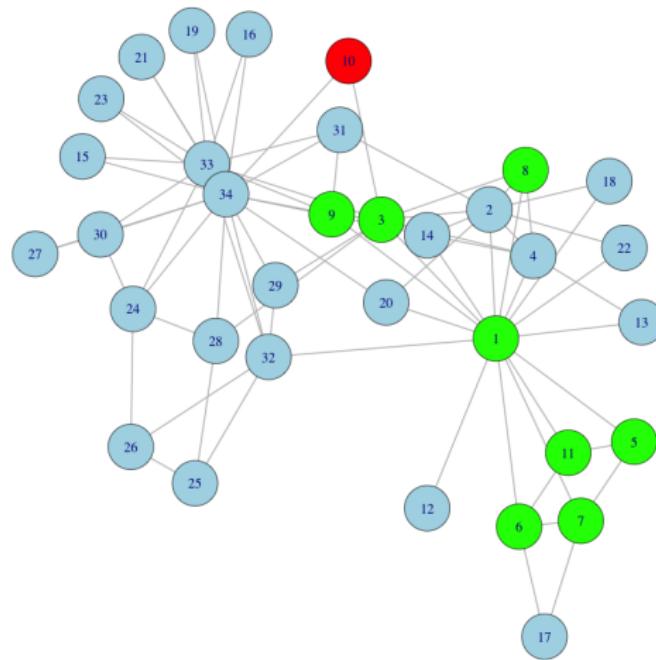
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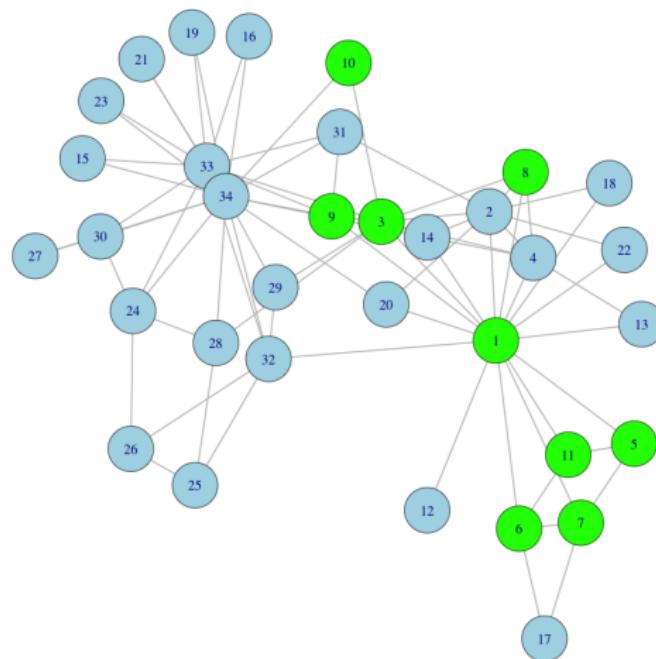
# SIR model

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

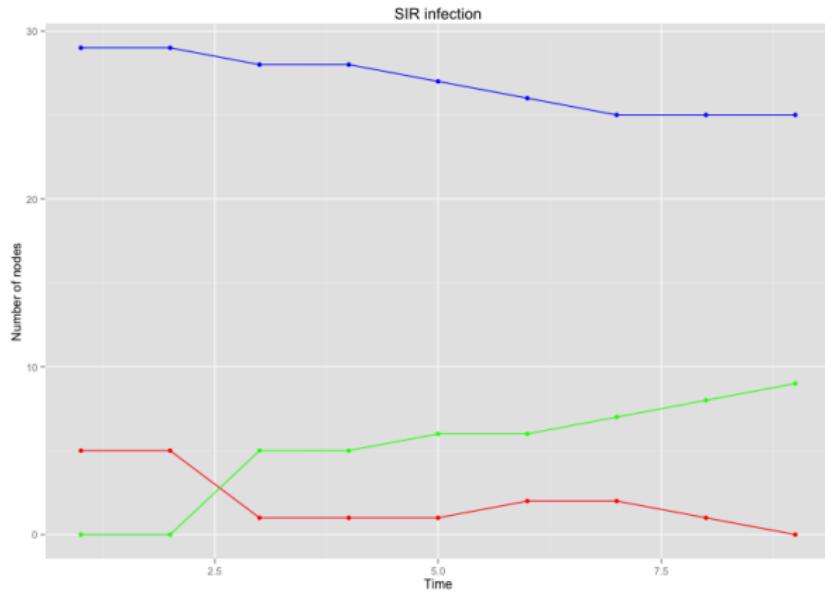


# SIR model

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

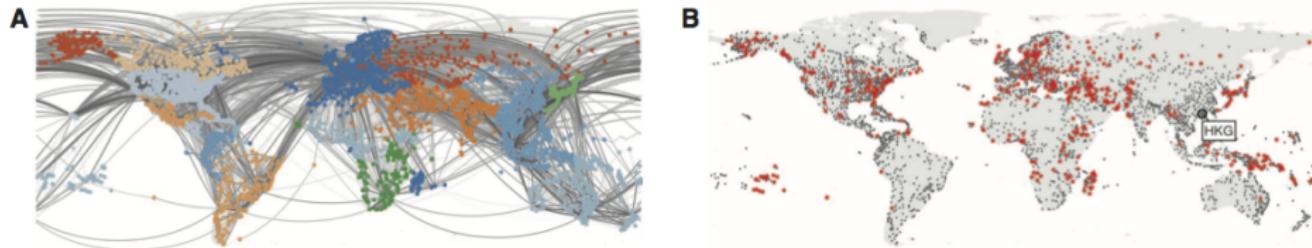


# SIR model



# Modeling SARS outbreak

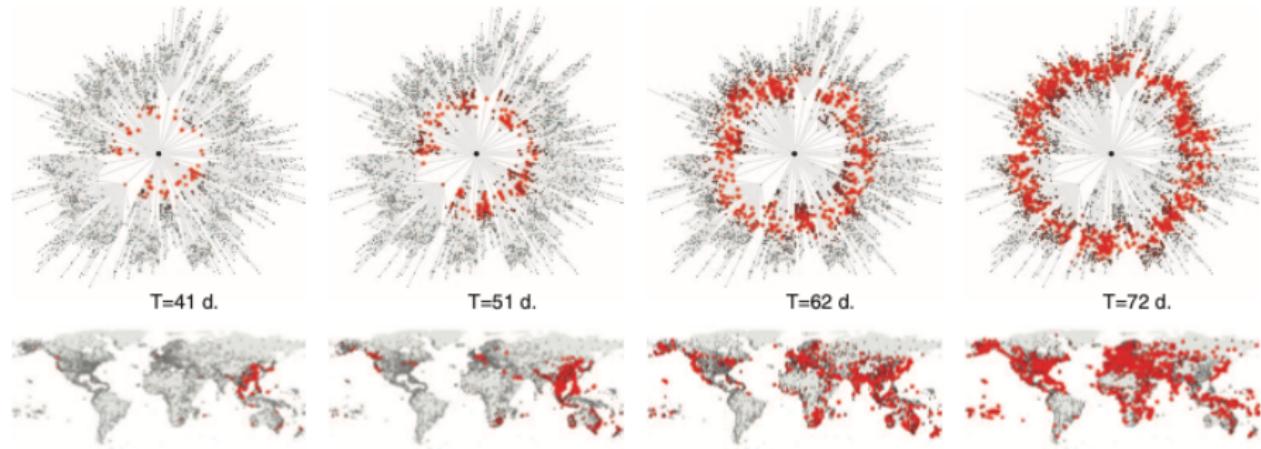
SARS 2003: > 8,000 cases, 37 countries



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

D. Brockmann, D. Helbing, 2013

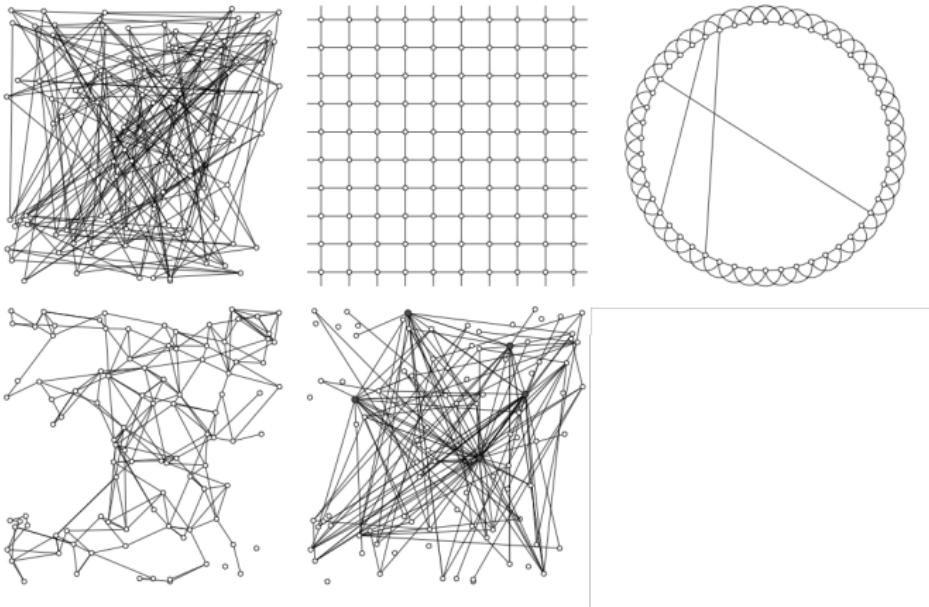
# Modeling SARS outbreak



Shortest path tree from Hong Kong

D. Brockmann, D. Helbing, 2013

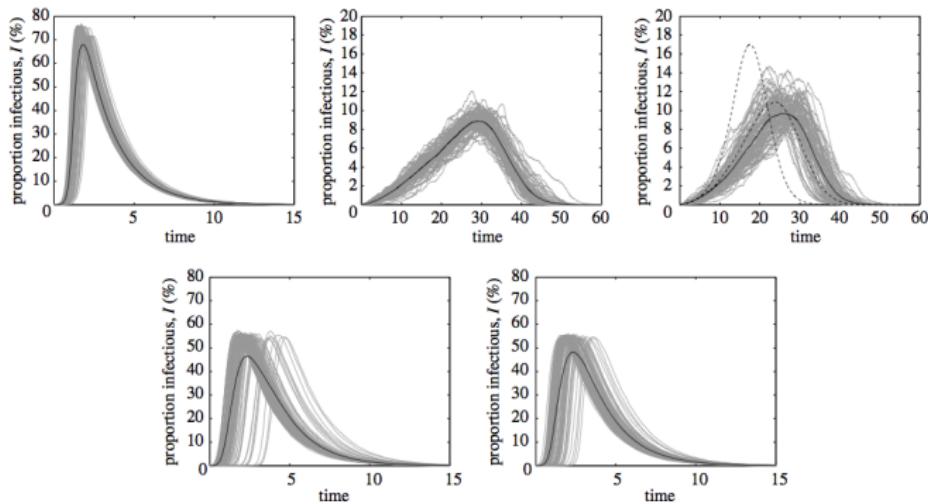
## 5 Networks, SIR



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

image from Keeling et al, 2005

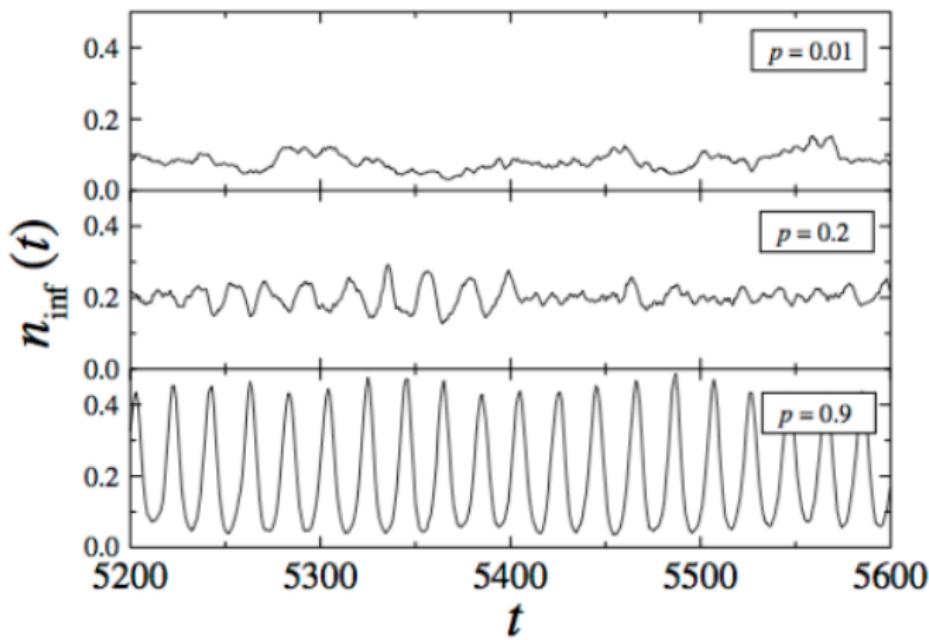
# 5 Networks, SIR



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

Keeling et al, 2005

# 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  $\sigma_k^2 = \langle k^2 \rangle - \langle k \rangle^2$

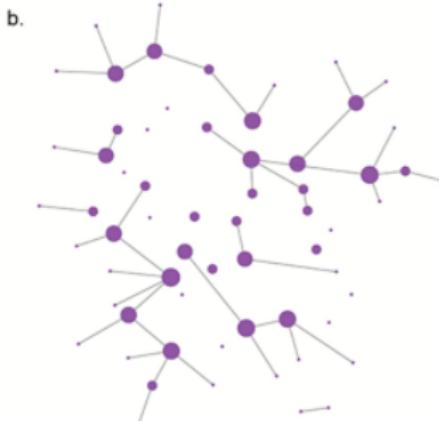
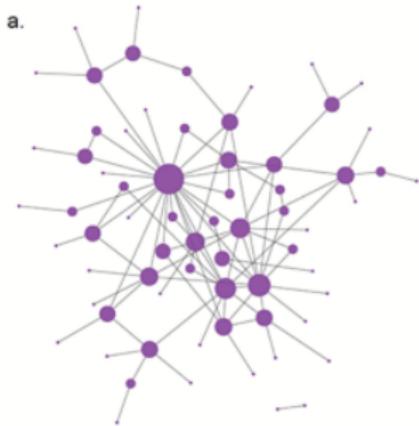
$$R = \frac{\langle k \rangle}{\langle k^2 \rangle}$$

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

Kuperman et al, 2001

# Vaccination strategies

- random vaccination (bad even in simulation)
- hub vaccination,  $k > k_{min}$
- following random edge with probability proportional to target node degree
- random friend vaccination (“friendship paradox” )



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