

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

I. Makarov & L.E. Zhukov

Moscow Institute of Physics and Technology

Network Science



Lecture outline

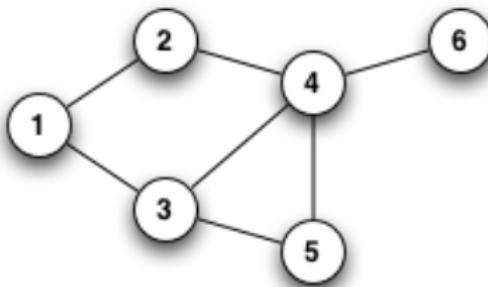
- 1 Random walks on graph
- 2 Diffusion on graph
- 3 Spectral graph theory
- 4 COVID-19 update
- 5 Branching process as contagion model
- 6 Epidemic modeling
 - SI model
 - SIS model
 - SIR model

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)

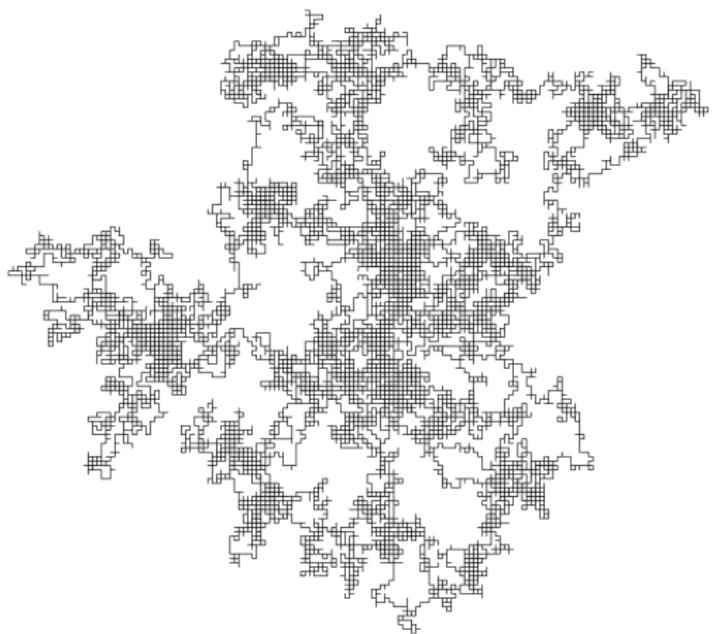
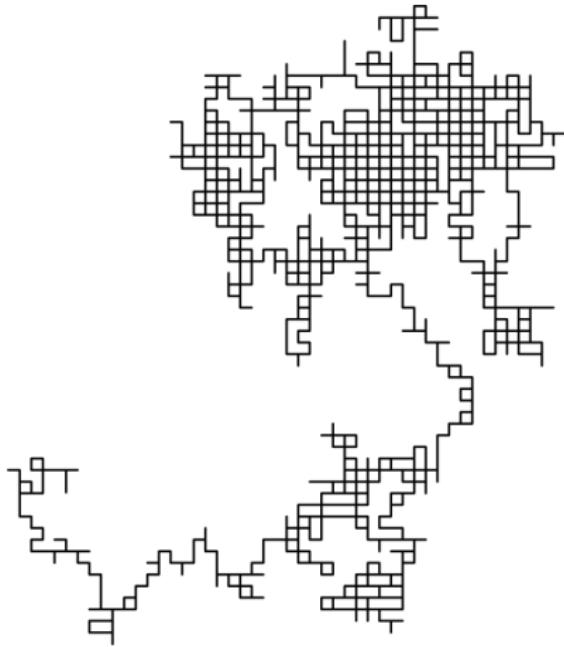


image from wikipedia.org

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 λ_2 denote second largest eigenvalue of transition matrix $P = D^{-1}A$, $p(t)$ probability distribution vector and π 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)

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

Δ - 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 $i > 1$, $\lambda_1 = 0$:

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

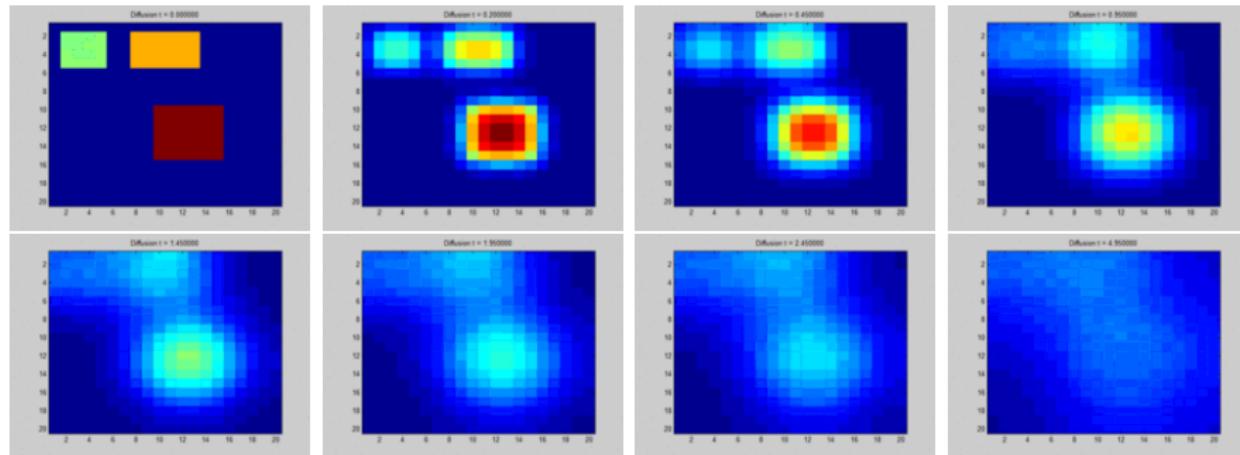
- Normalized solution $v_1 = \frac{1}{\sqrt{N}} e$

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

- 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

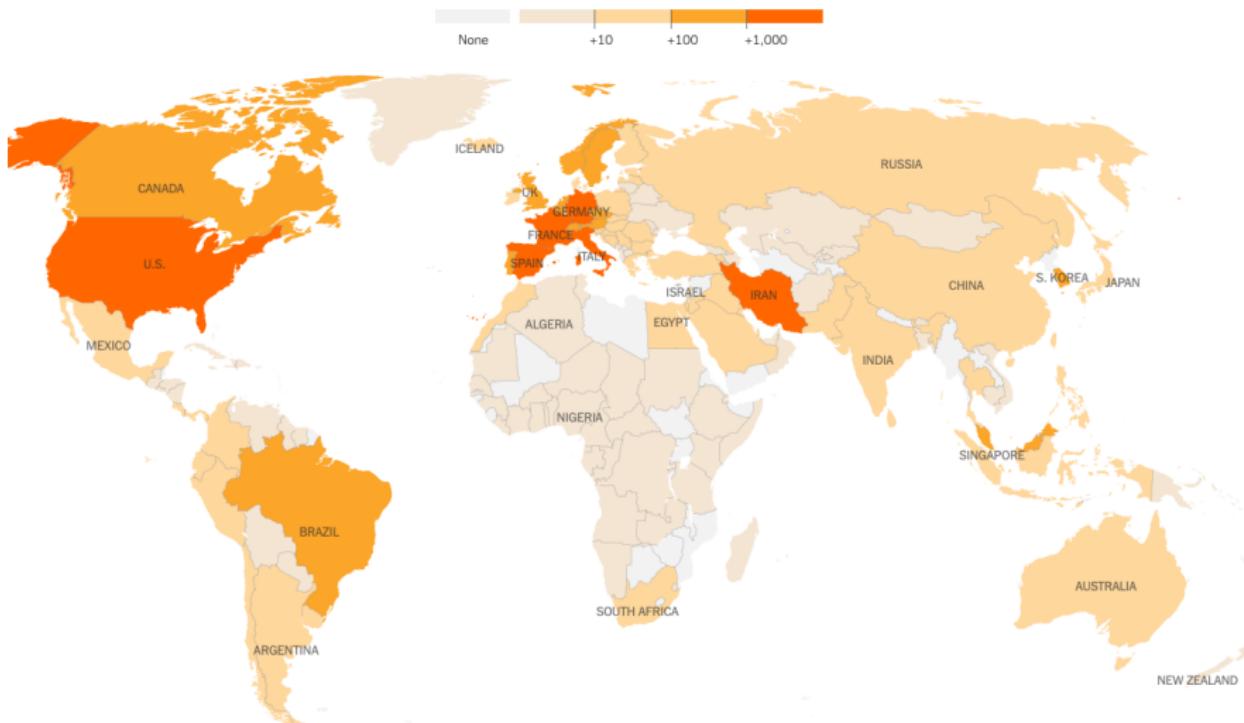
$$\lambda_2(\mathcal{L})/2 \leq \min_S \phi(S) \leq \sqrt{2\lambda_2(\mathcal{L})}$$

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

Lecture outline

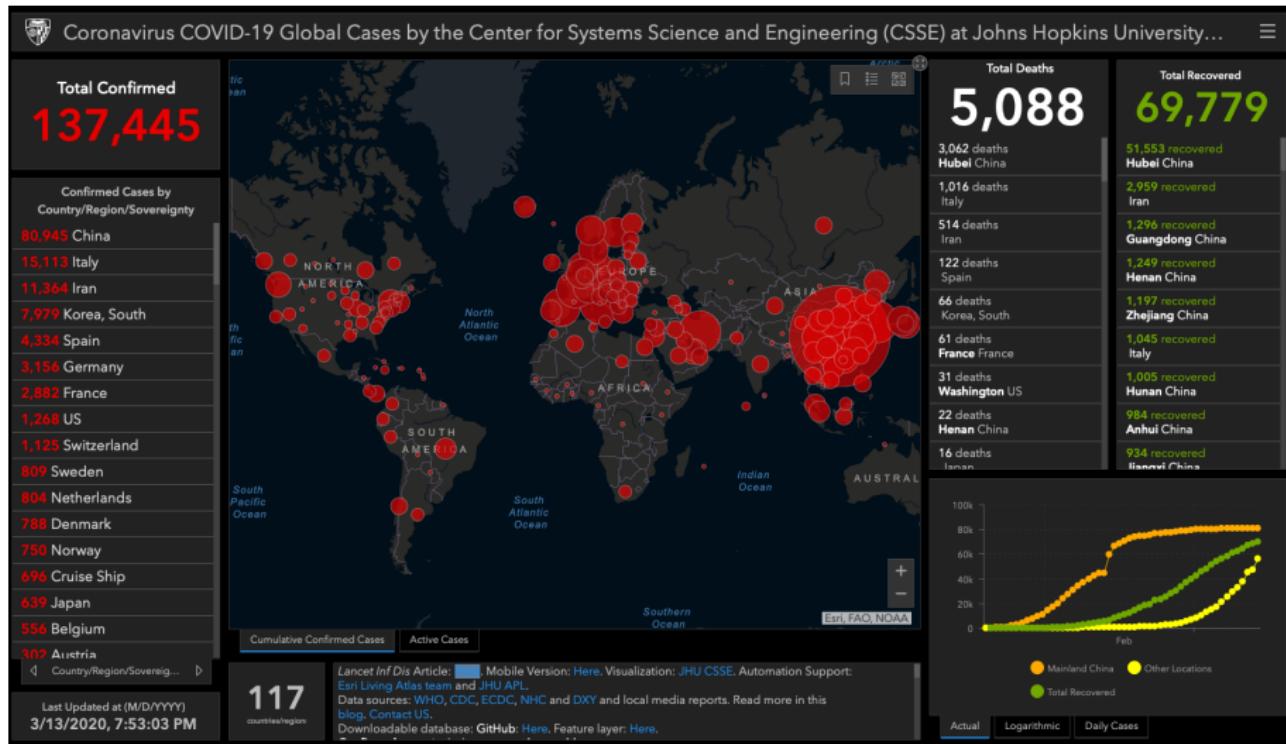
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Coronavirus COVID-19



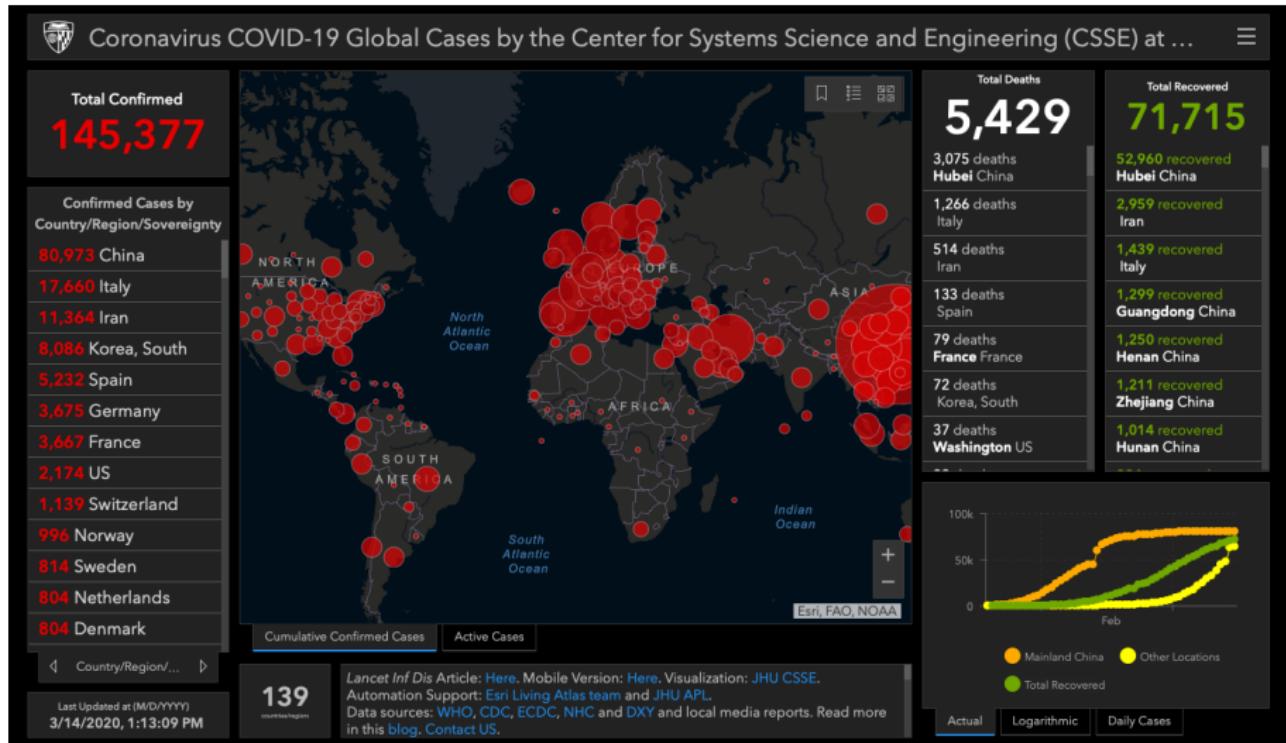
from The NYT

Coronavirus COVID-19



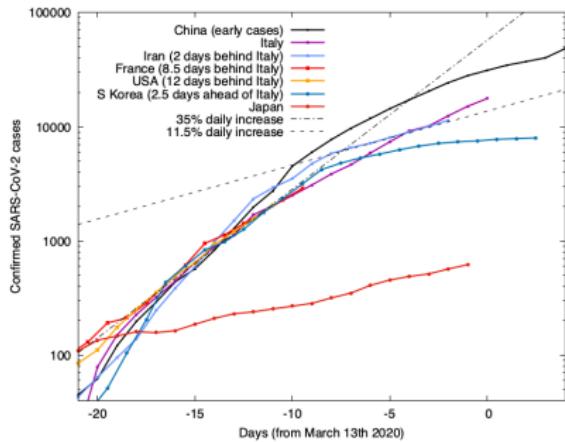
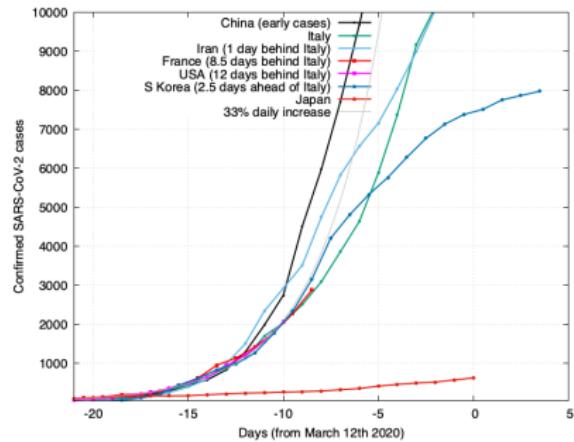
Dashboard from Johns Hopkins University, <https://coronavirus.jhu.edu/map.html>

Coronavirus COVID-19



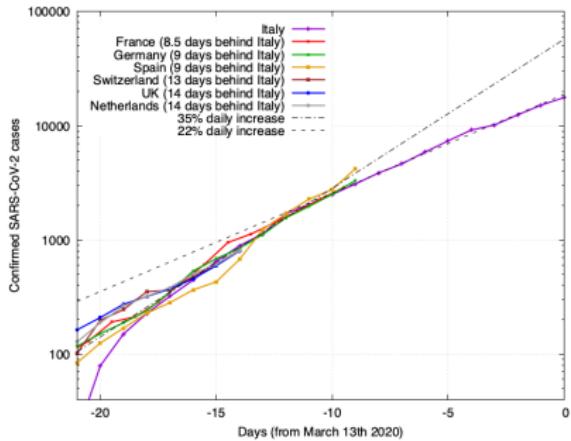
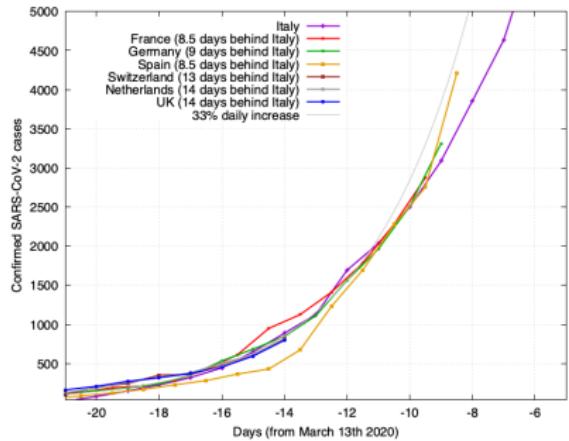
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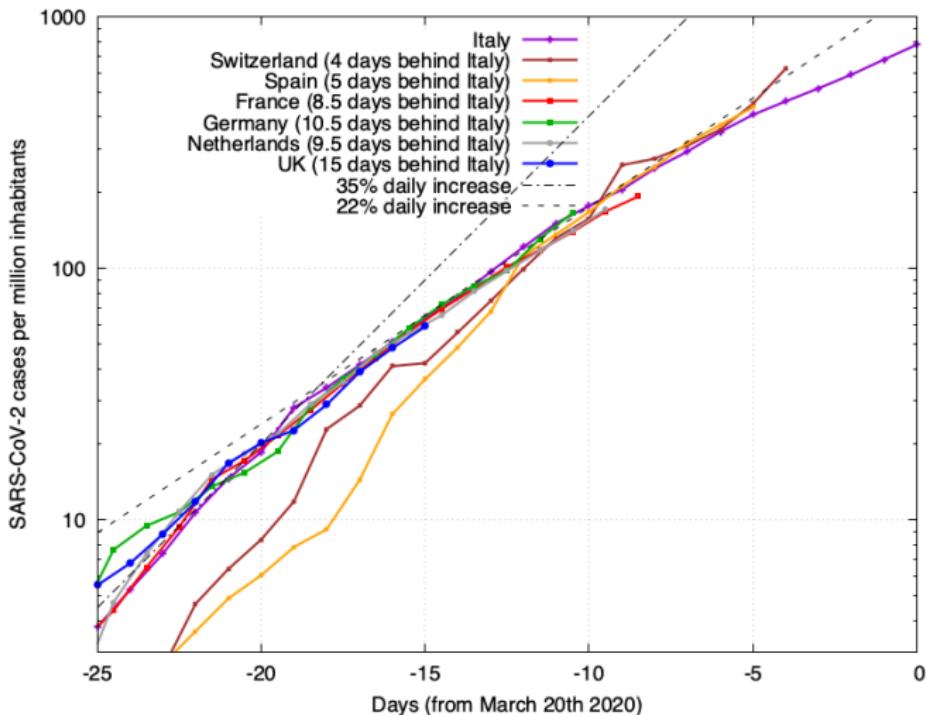
from Mark Handley, UCL

Coronavirus COVID-19



from Mark Handley, UCL

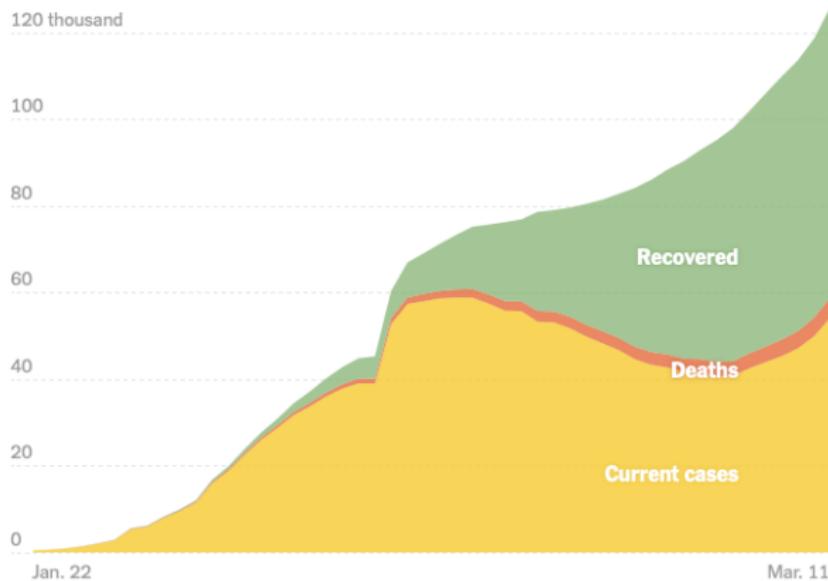
Coronavirus COVID-19



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

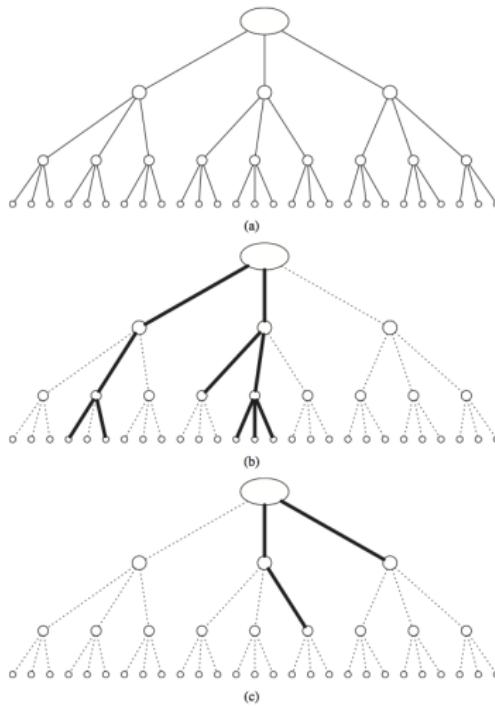
Simple model of contagion (decease transmission)

- 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

$$S \longrightarrow I$$

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

- β - 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

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

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

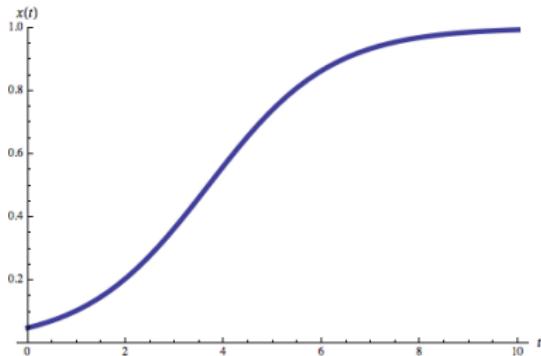
- Differential equation, $i(t = 0) = i_0$

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

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,

$$S \longrightarrow I \longrightarrow S$$

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

- β - infection rate (on contact), γ - recovery rate; $T_r = 1/\gamma$ - average time to recovery
- Infection equations:

$$\frac{ds}{dt} = -\beta si + \gamma i$$

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

$$s + i = 1$$

- 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

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

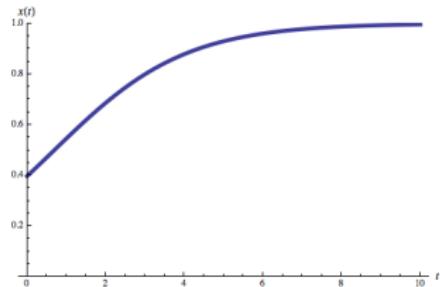
- Limit $t \rightarrow \infty$

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

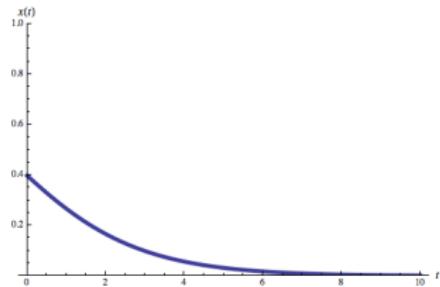
$$\beta < \gamma \quad , \quad i(t) = i_0 e^{(\beta-\gamma)t} \rightarrow 0$$

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

$$S \longrightarrow I \longrightarrow R$$

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

- 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

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

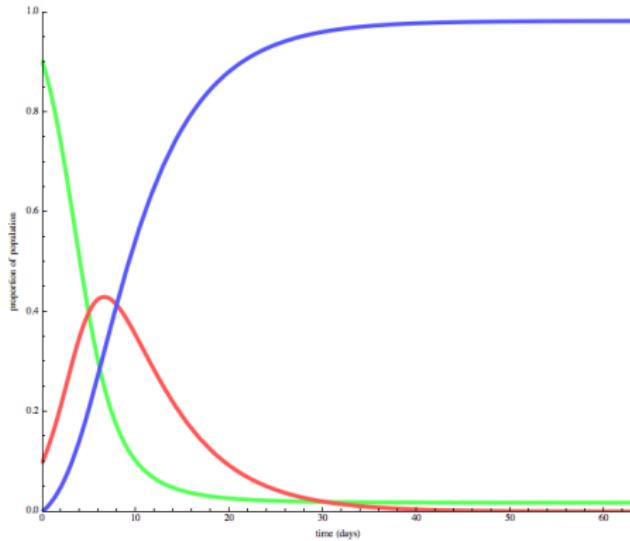
$$s = s_0 e^{-\frac{\beta}{\gamma} r}$$

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

- Solution

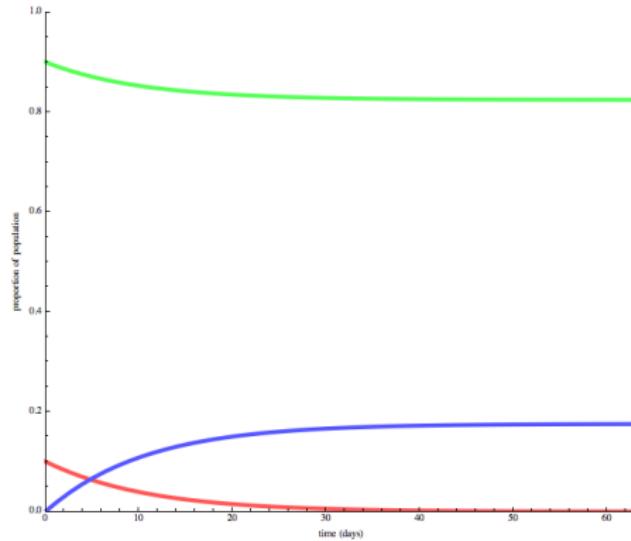
$$t = \frac{1}{\gamma} \int_0^r \frac{dr}{1 - r - s_0 e^{-\frac{\beta}{\gamma} r}}$$

SIR model



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

SIR model



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

SIR model

- Equation

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

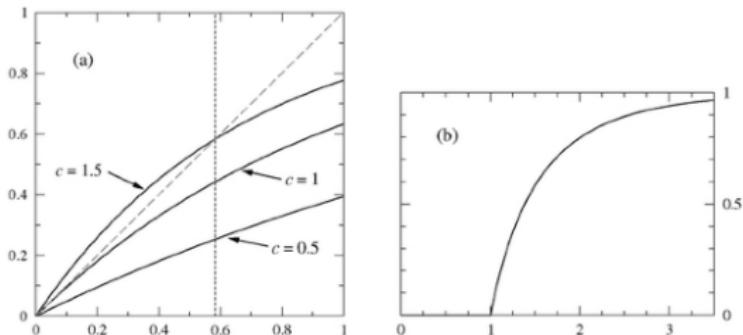
- Limits: $t \rightarrow \infty$, $\frac{dr}{dt} = 0$, $r_\infty = \text{const}$,

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

- 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_∞ - the total size of the outbreak
- Epidemic threshold

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

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

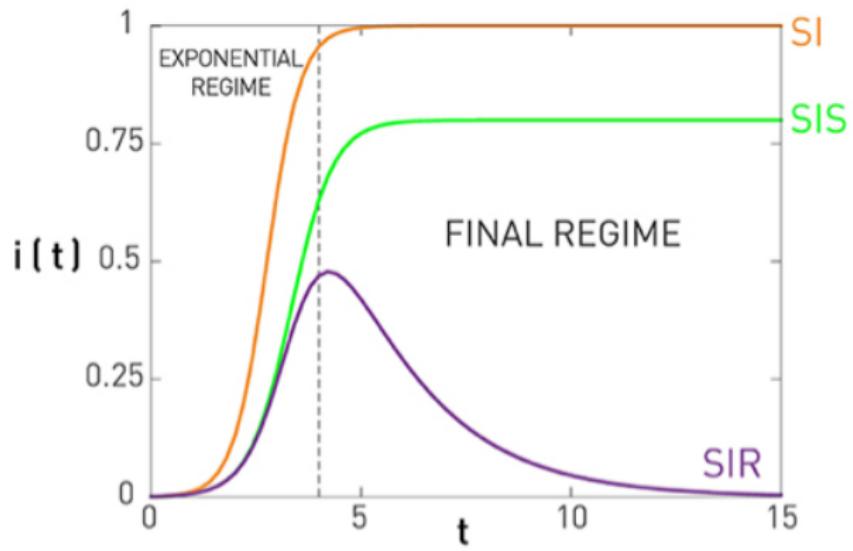
- β - infection rate, γ - recovery rate \rightarrow
- Basic reproduction number

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

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

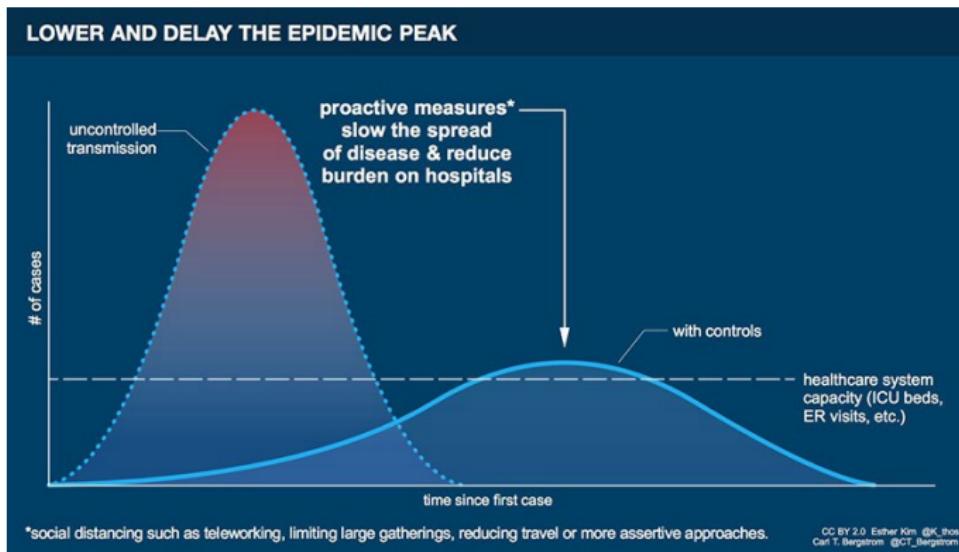
$$R_0 = E[\beta\tau] = \beta \int_0^\infty \gamma\tau e^{-\gamma\tau} d\tau = \frac{\beta}{\gamma}$$

Compartmental models summary

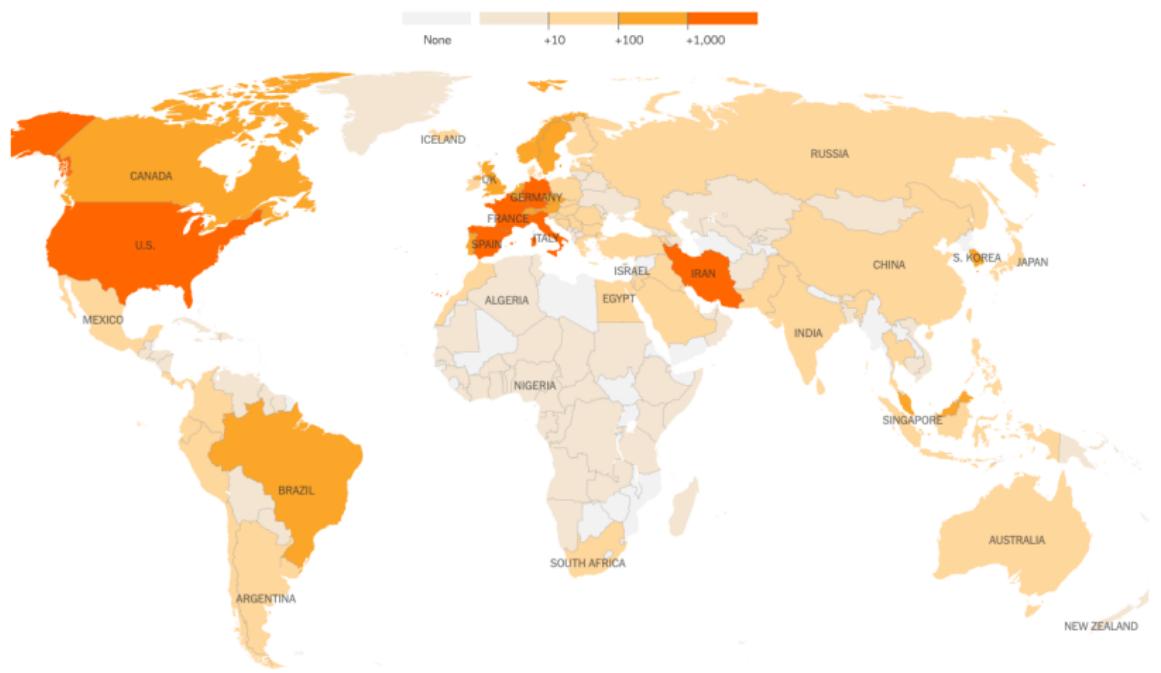


from Barabasi, 2016

Flatten the curve!

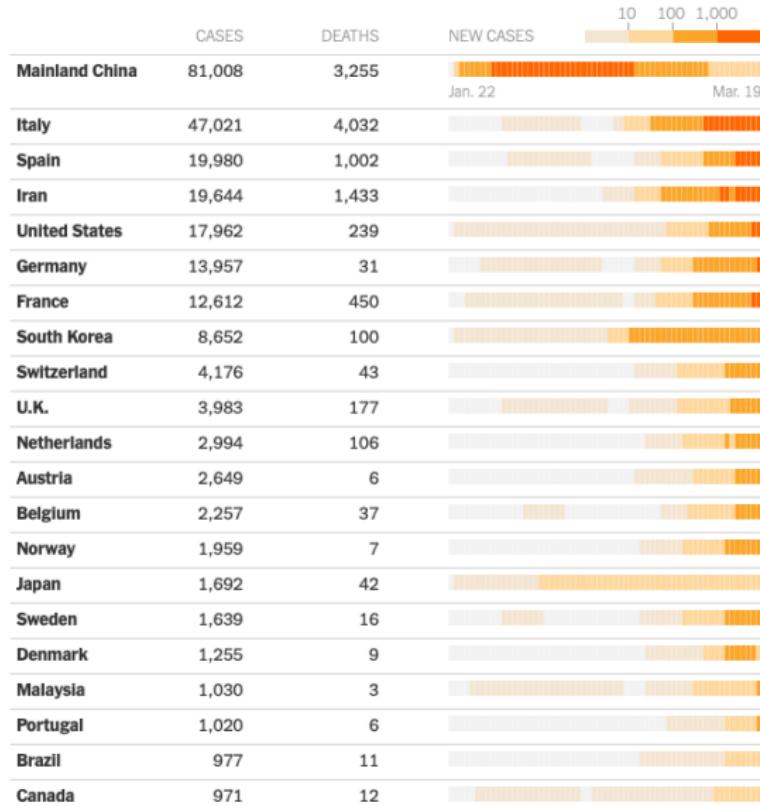


Global contagion: Coronavirus COVID-19

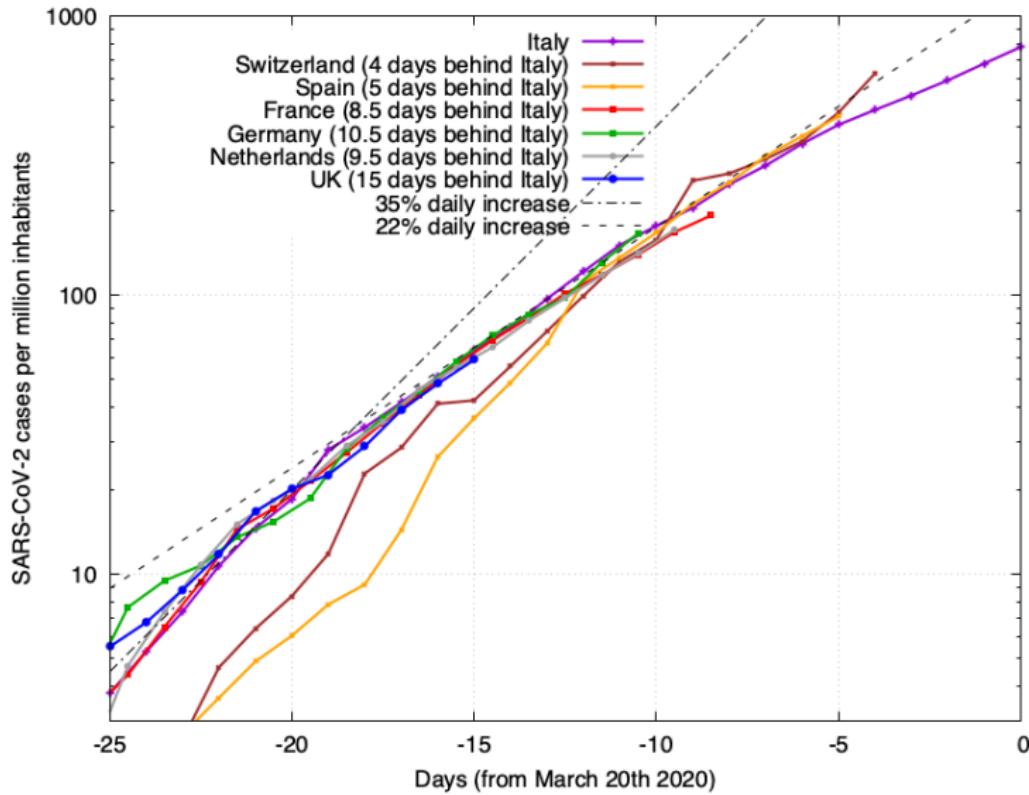


from NYT

Global contagion: Coronavirus COVID-19

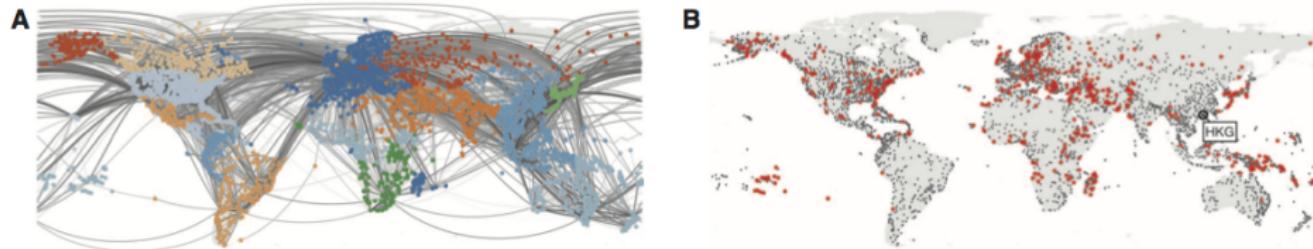


Coronavirus COVID-19



Modeling SARS outbreak

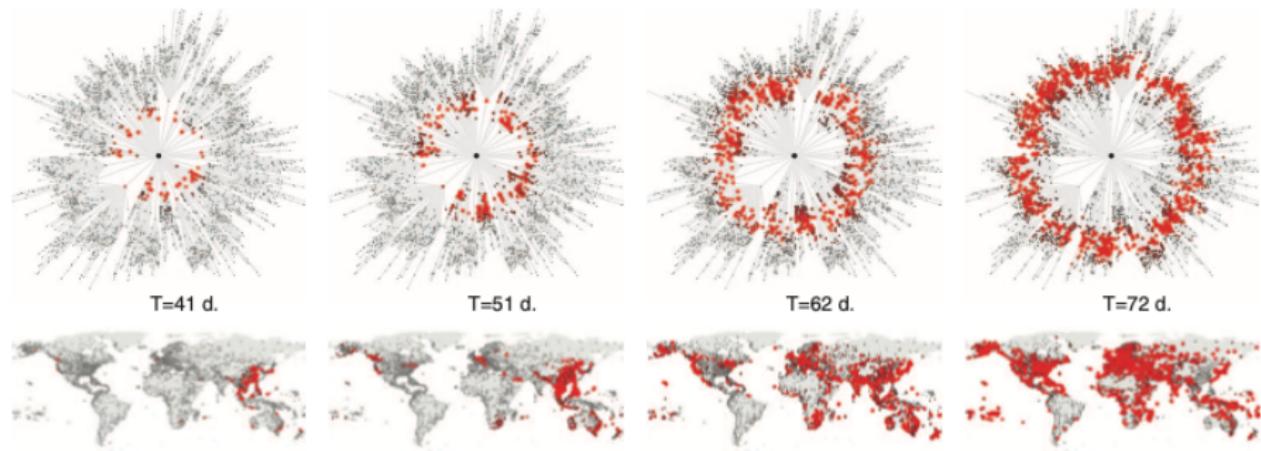
SARS 2003: > 8,000 cases, 37 countries



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

D. Brockmann, D. Helbing, 2013

Modeling SARS outbreak



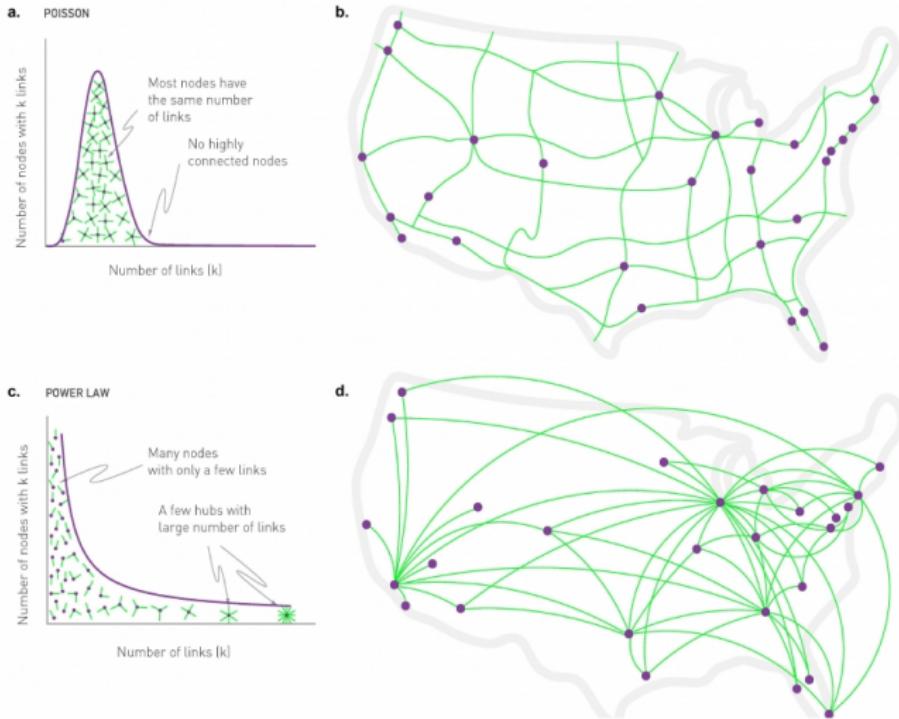
Shortest path tree from Hong Kong

D. Brockmann, D. Helbing, 2013

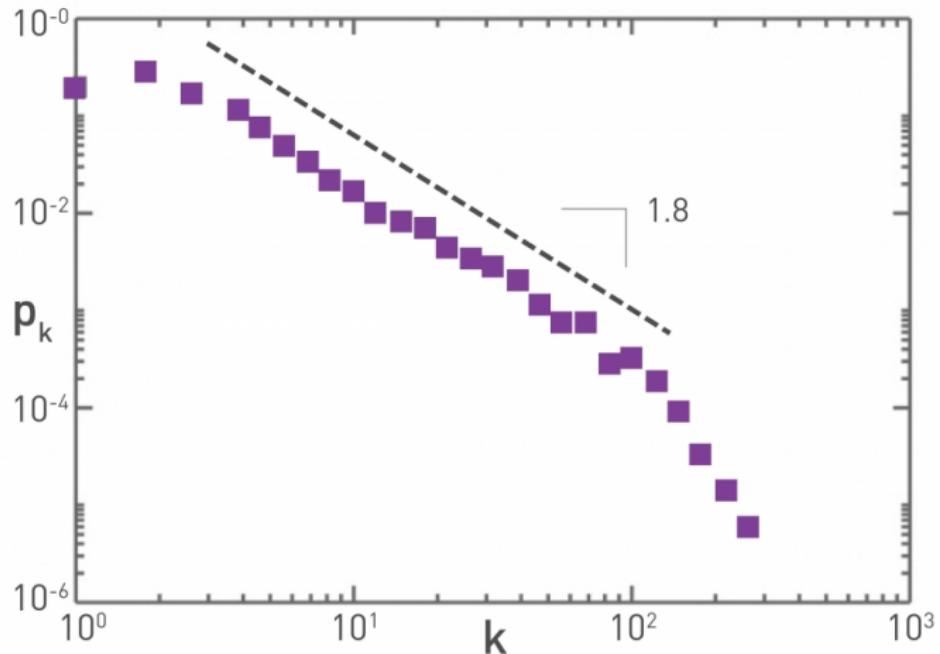
Flight routes of the world



Flight routes form a scale free network

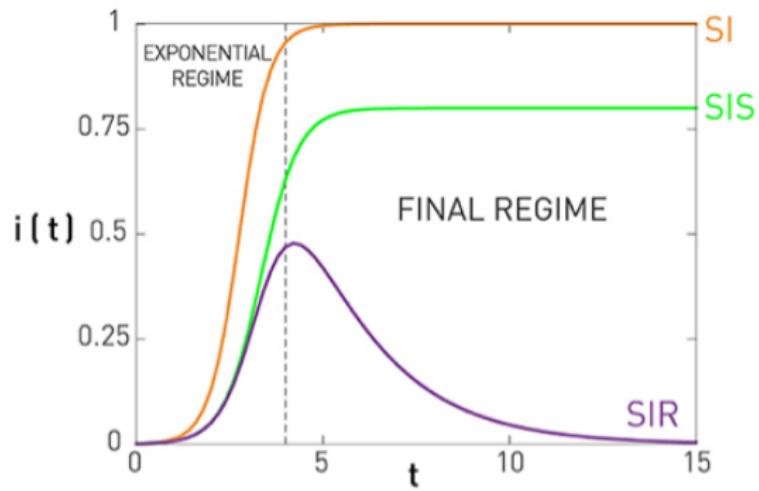


Flight routes form a scale free network



Alessandro Vespignani et all, 2006

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

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 - individual transmission/infection rate (probably to get infected on a contact in time δt) f transmitting contacts per unit time; $\beta_c = \beta \langle k \rangle$
- γ - recovery rate (probability to recover in a unit time δt). In compartmental model β_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

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

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

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

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

- 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

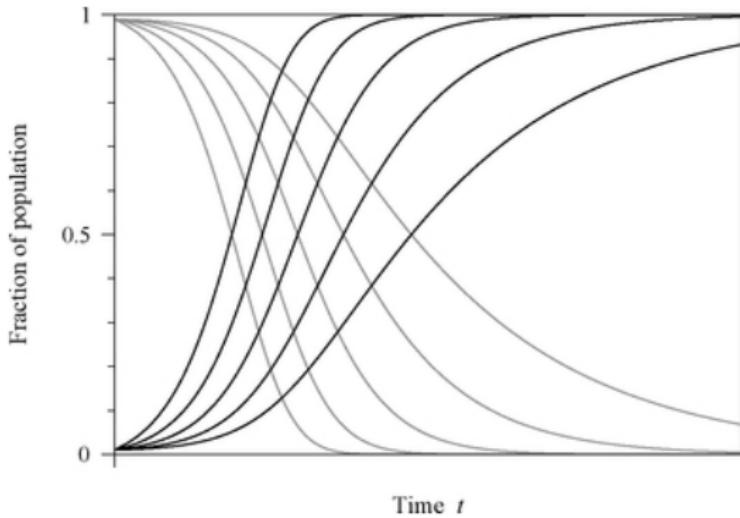
$$x(t) = \sum_k a_k(0) e^{\lambda_k \beta t} v_k$$

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

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

- ① growth rate of infections depends on λ_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

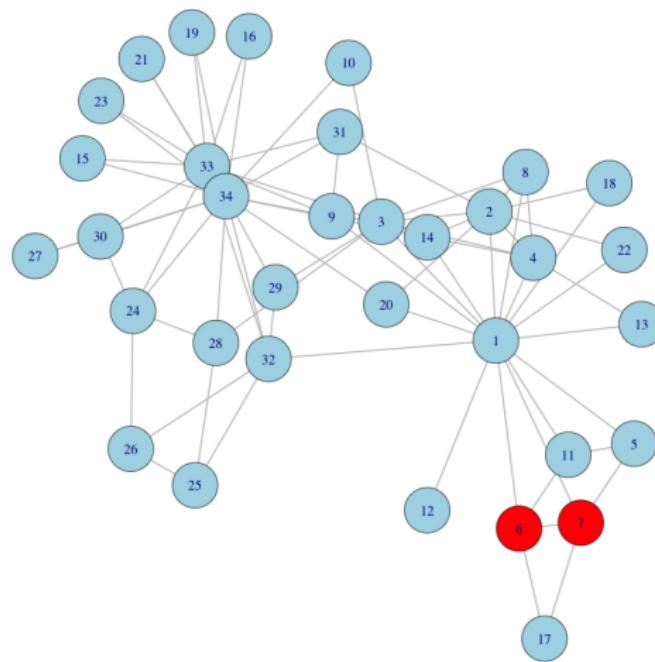
- ① Every node at any time step is in one state $\{S, I\}$
- ② Initialize c nodes in state I
- ③ On each time step each I node has a probability β to infect its nearest neighbors (NN), $S \rightarrow I$

Model dynamics:



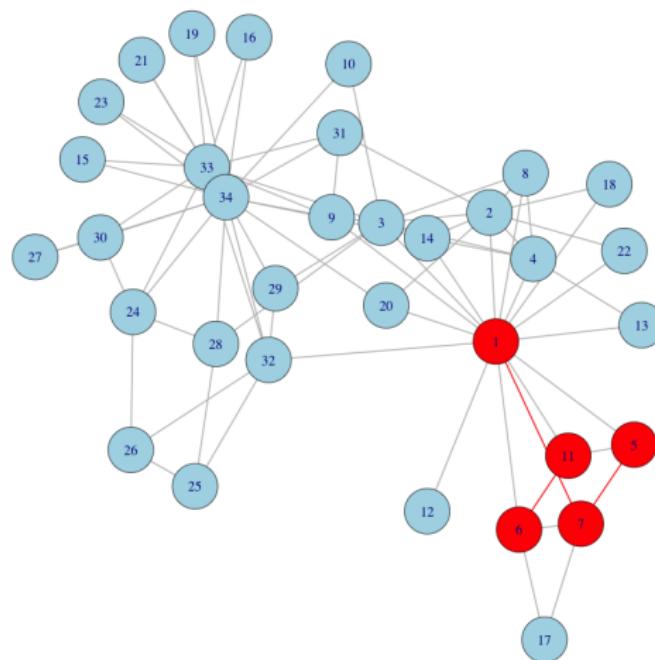
SI model simulation

$$\beta = 0.5$$



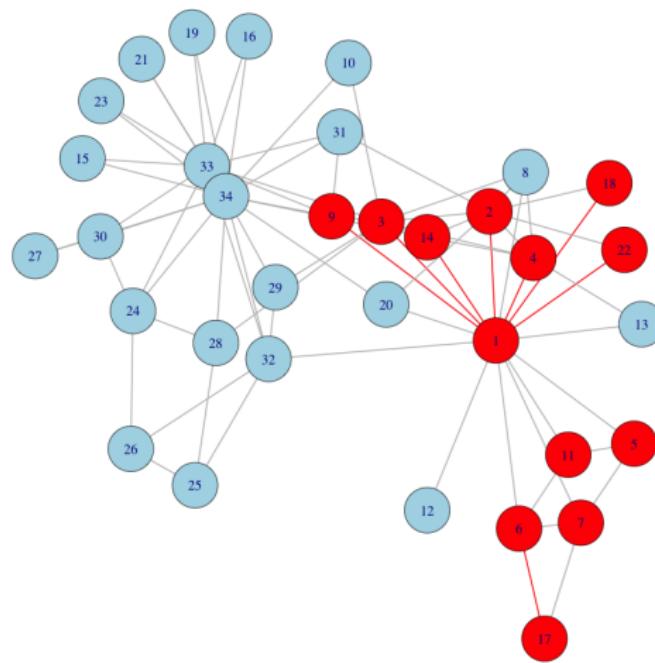
SI model simulation

$$\beta = 0.5$$



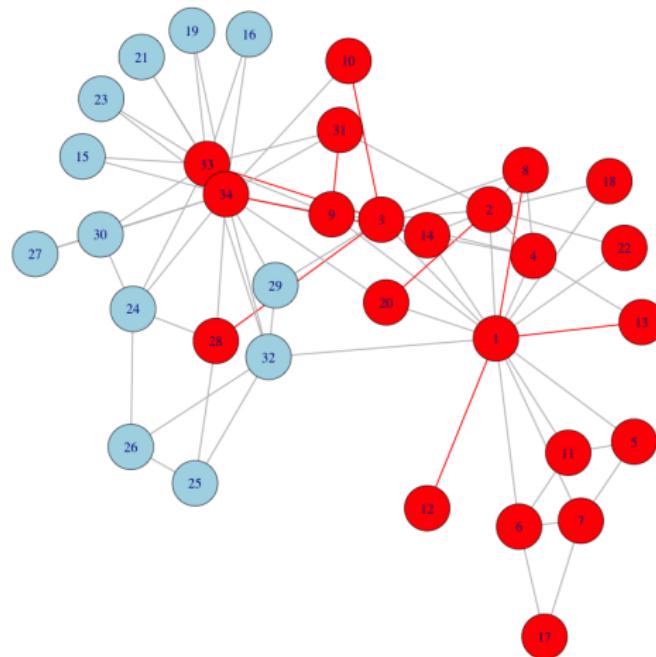
SI model simulation

$$\beta = 0.5$$



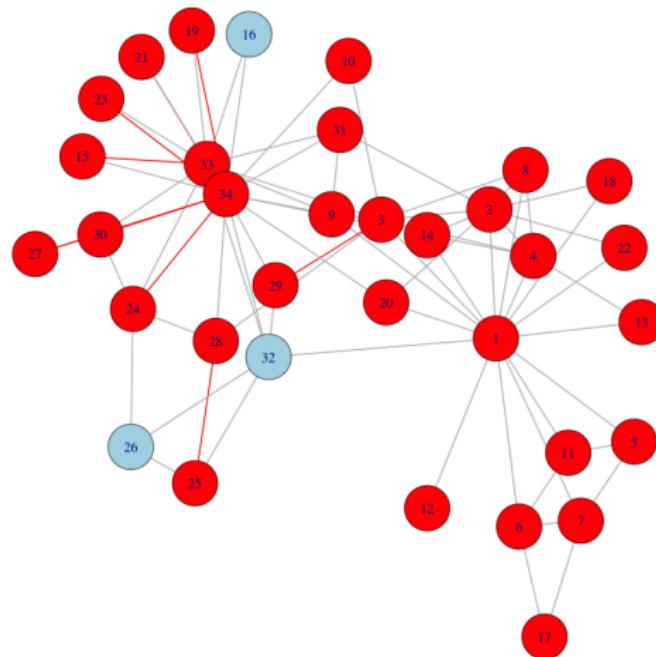
SI model simulation

$$\beta = 0.5$$



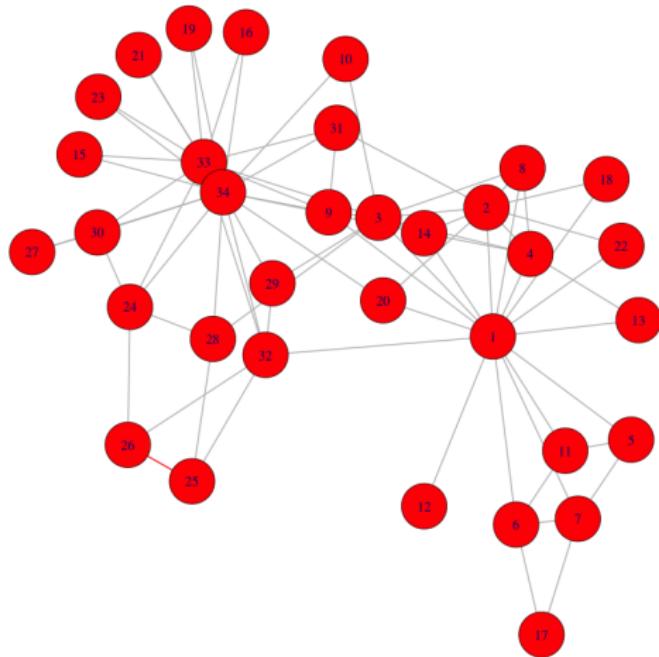
SI model simulation

$$\beta = 0.5$$

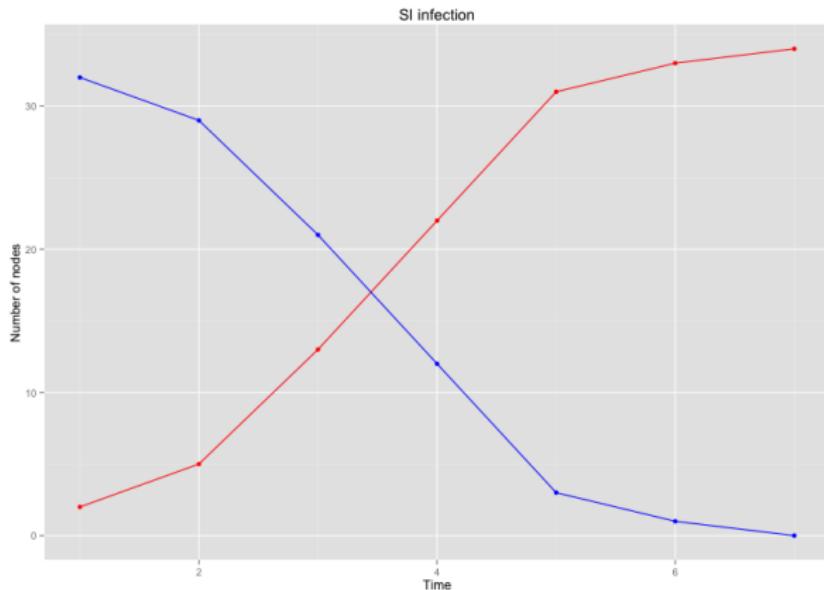


SI model simulation

$$\beta = 0.5$$



SI model



SIS model

- SIS Model

$$S \longrightarrow I \longrightarrow S$$

- 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, $x_i(t) \ll 1$

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

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

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

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

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 $\frac{\beta}{\gamma}$:

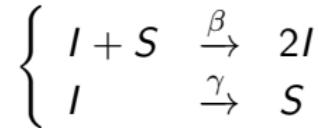
$$R = \frac{1}{\lambda_1}, \quad \lambda_1 - \text{largest eigenvalue of the adjacency matrix}$$

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

SIS simulation

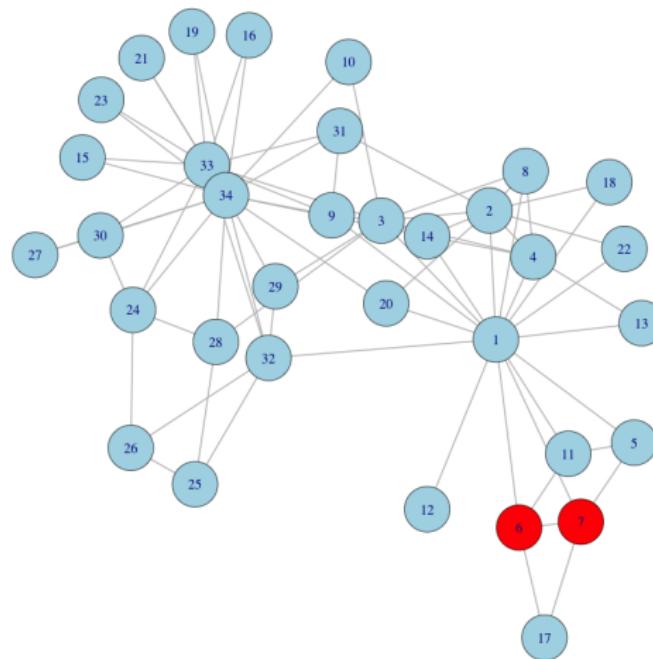
- ① Every node at any time step is in one state $\{S, I\}$
- ② Initialize c nodes in state I
- ③ Each node stays infected $\tau_\gamma = \int_0^\infty \tau e^{-\tau\gamma} d\tau = 1/\gamma$ time steps
- ④ On each time step each I node has a probability β to infect its nearest neighbours (NN), $S \rightarrow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

Model dynamics:



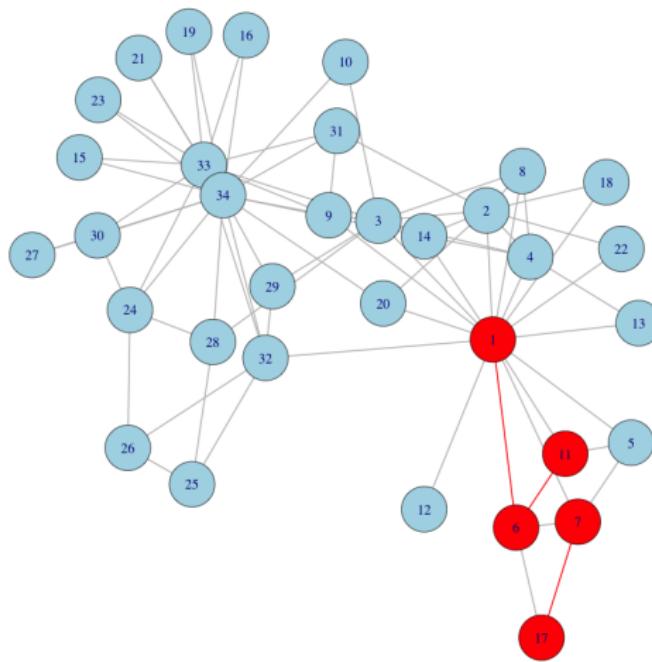
SIS model simulation

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



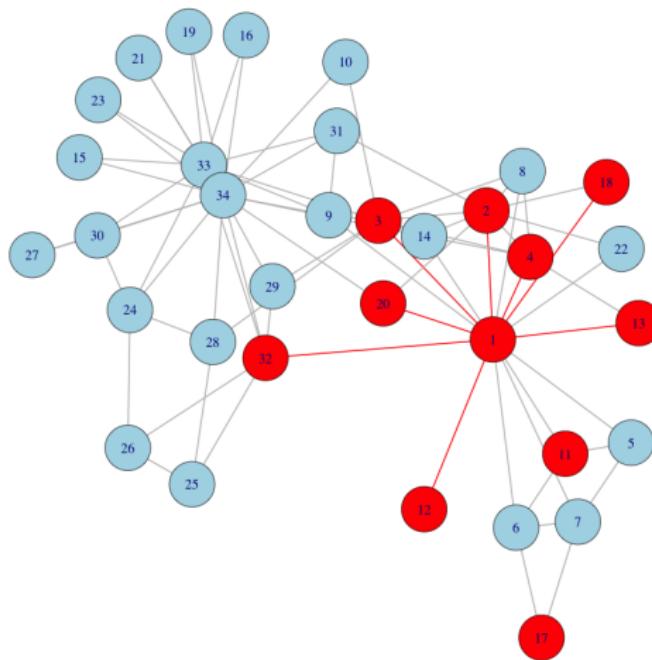
SIS model simulation

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



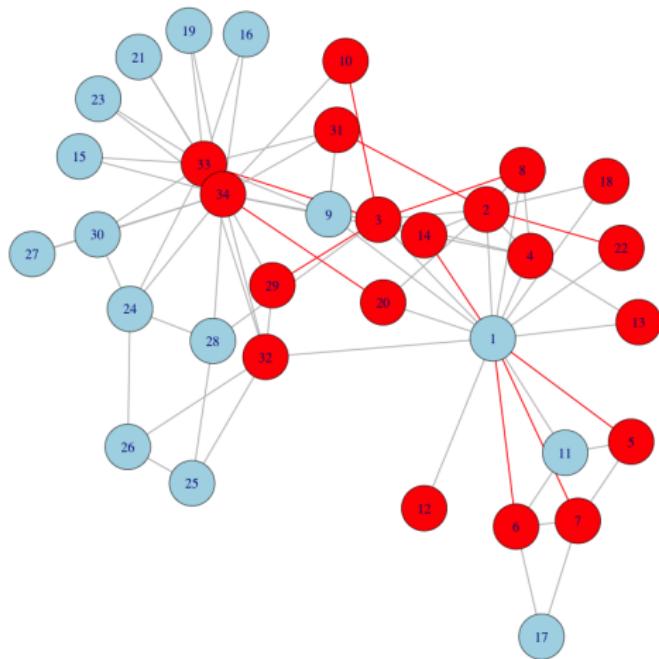
SIS model simulation

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



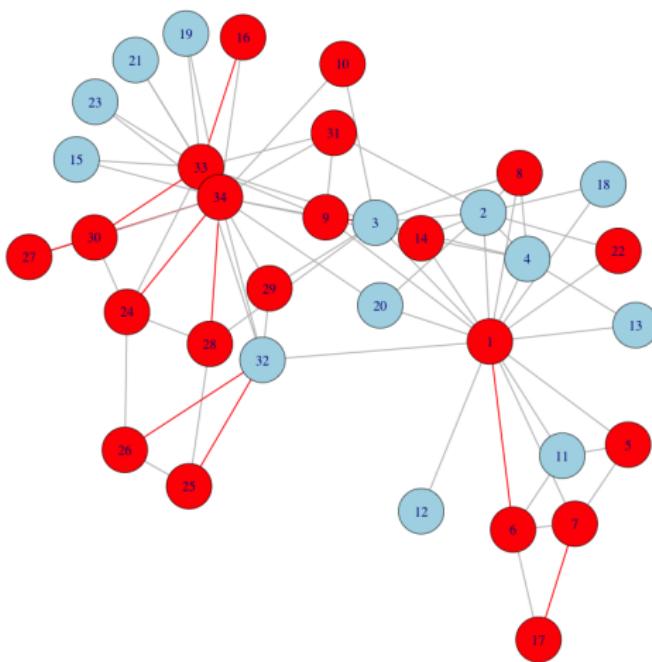
SIS model simulation

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



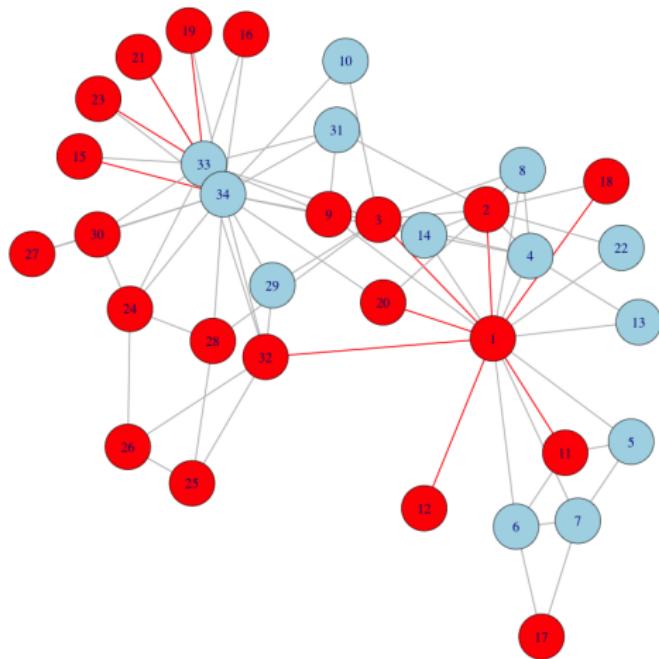
SIS model simulation

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



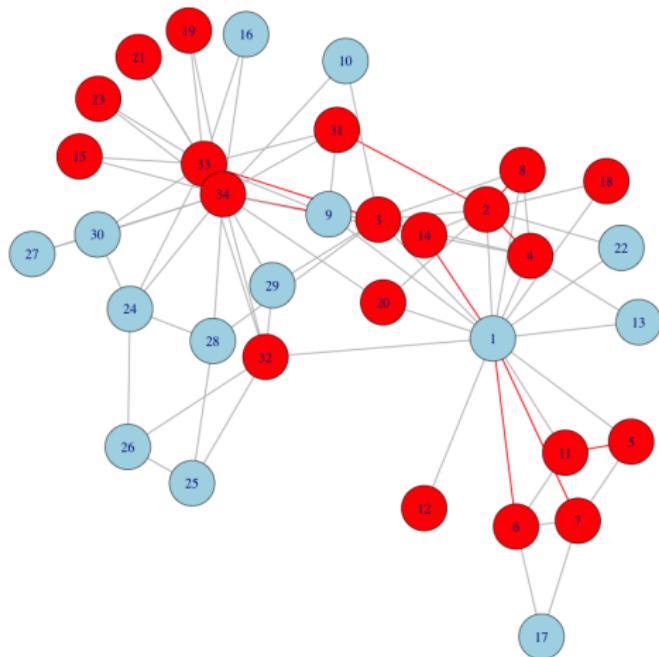
SIS model simulation

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

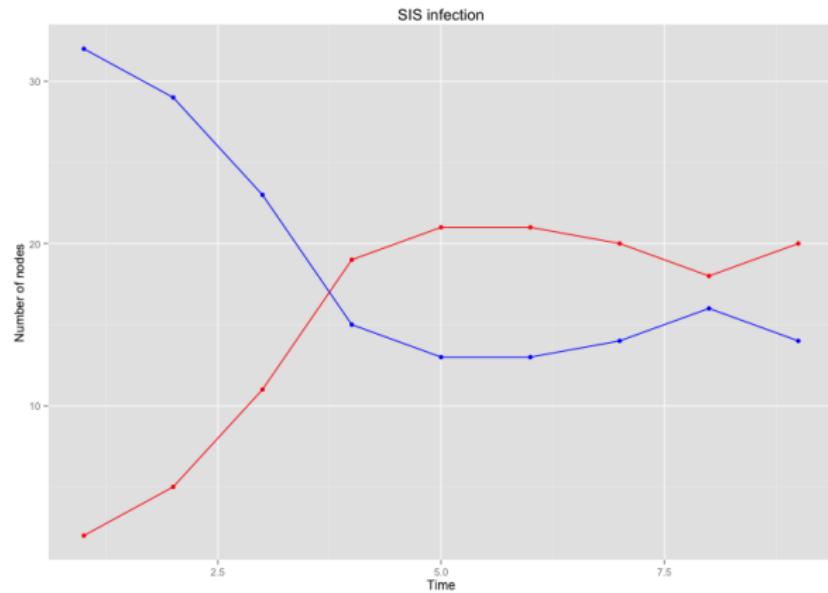


SIS model simulation

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

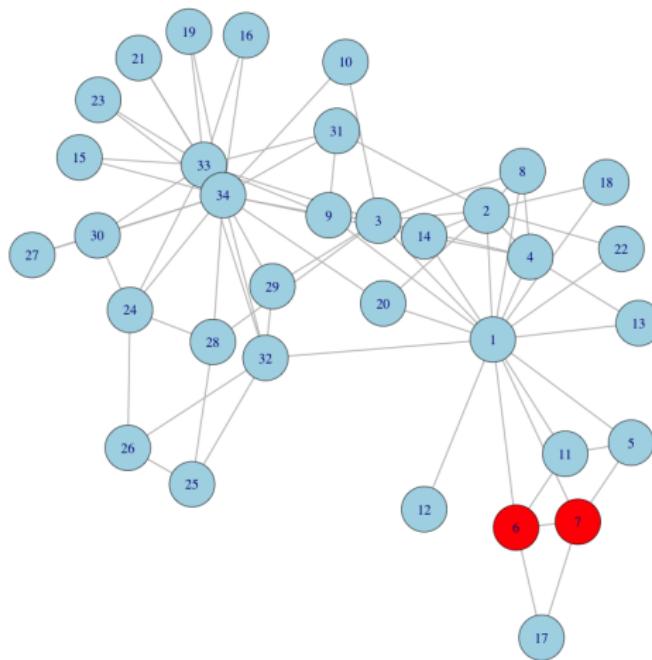


SIS model



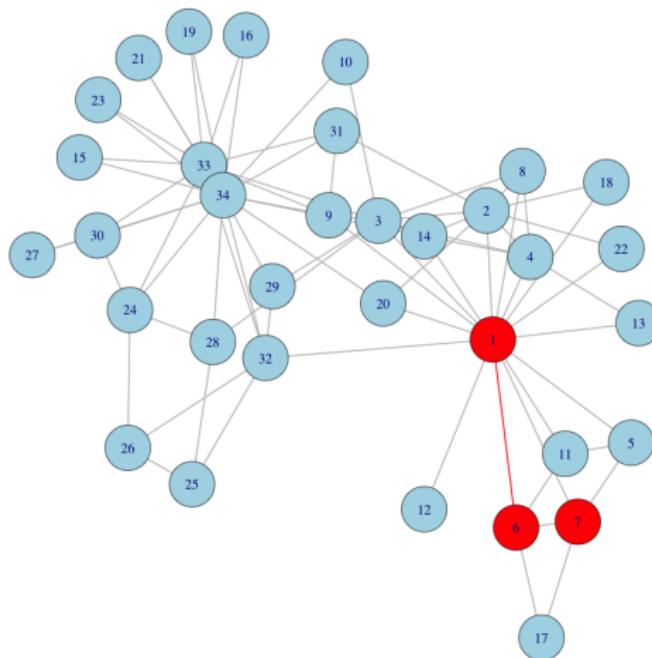
SIS model simulation

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



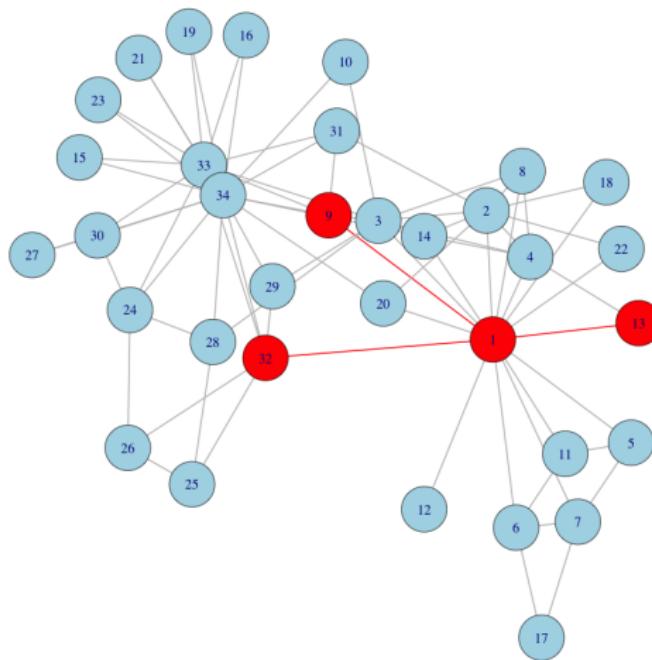
SIS model simulation

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



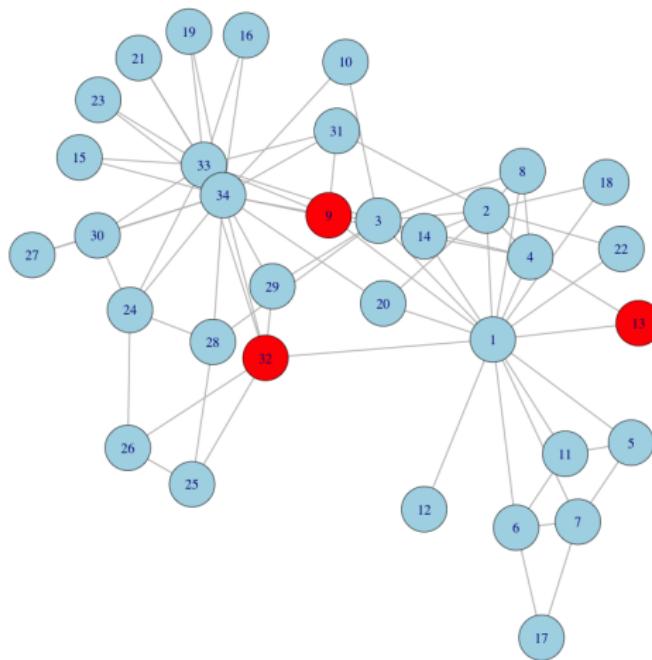
SIS model simulation

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



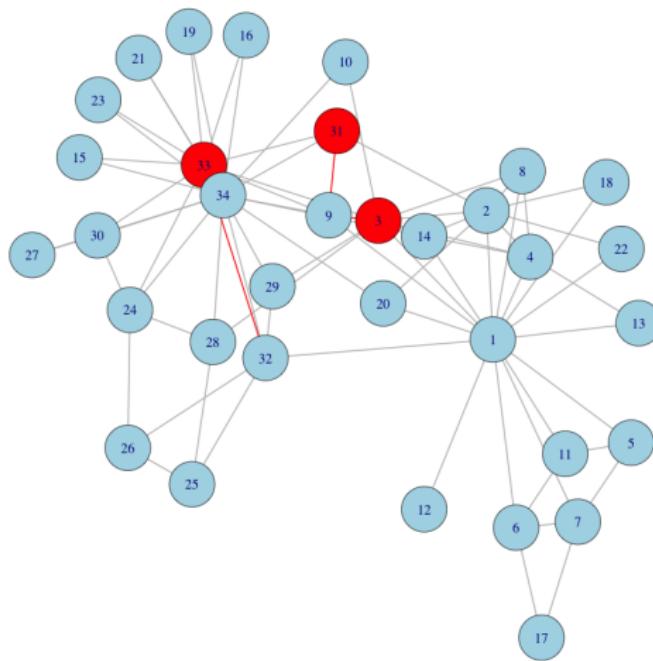
SIS model simulation

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



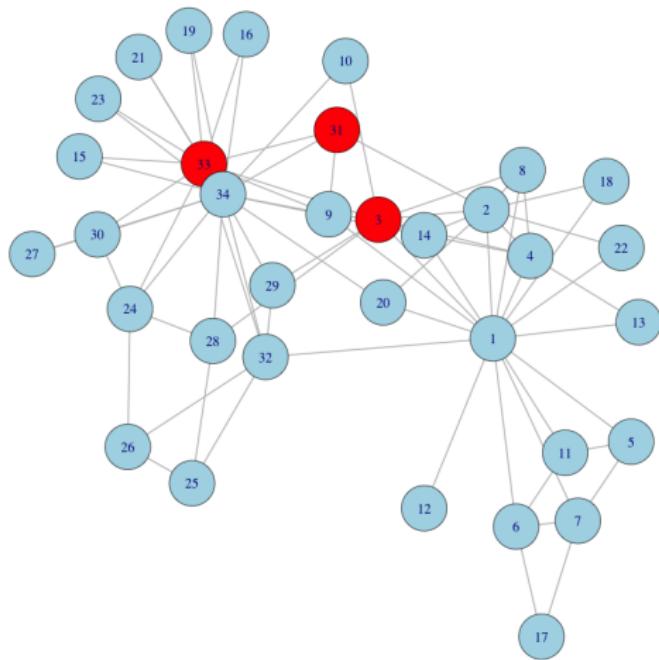
SIS model simulation

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



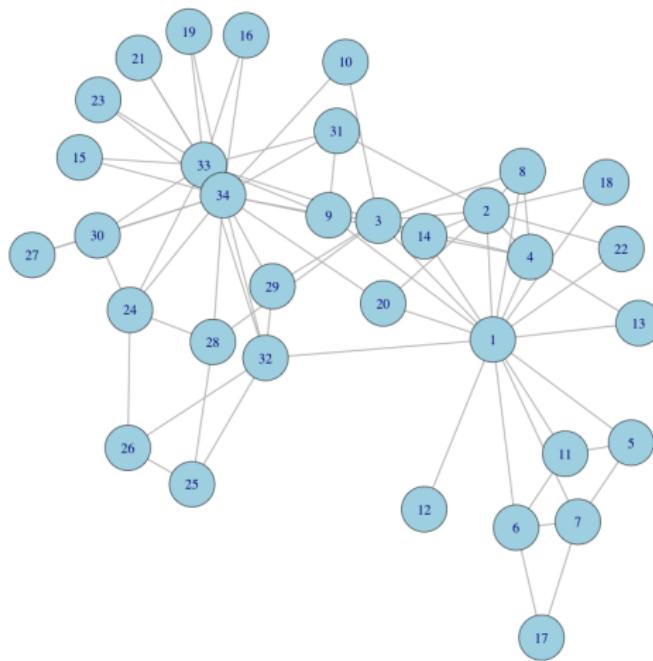
SIS model simulation

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

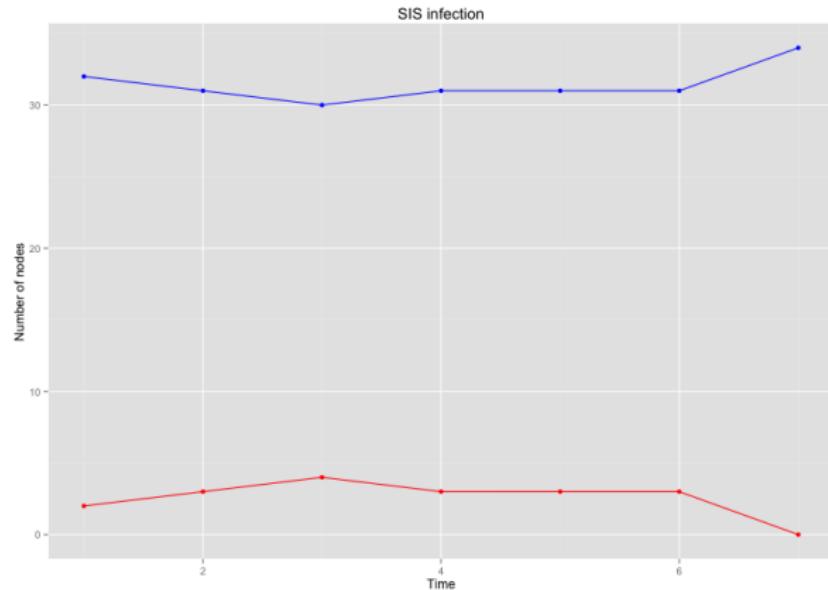


SIS model simulation

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



SIS model



SIR model

- SIR Model

$$S \longrightarrow I \longrightarrow R$$

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

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

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

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

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

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

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

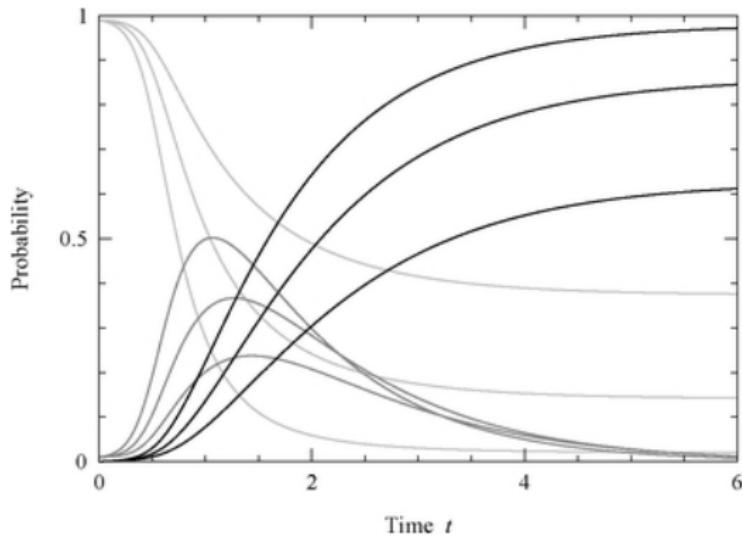
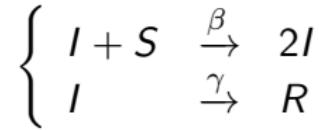


image from M. Newman, 2010

SIR simulation

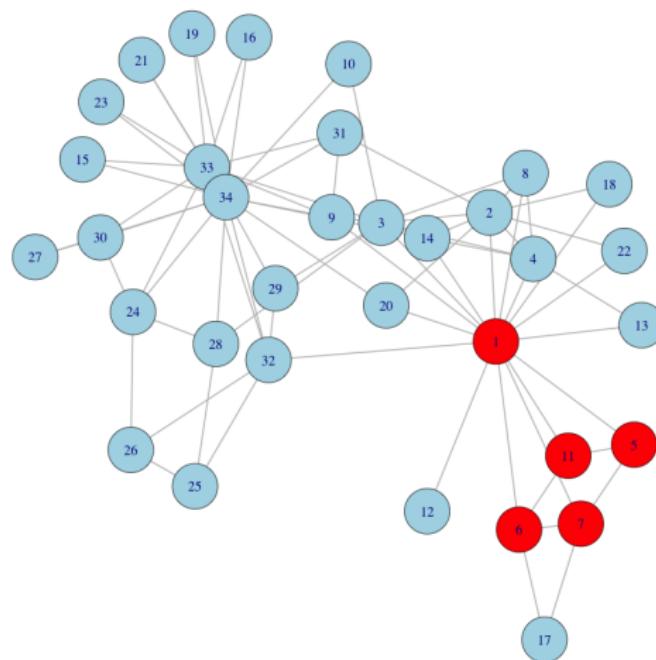
- ① Every node at any time step is in one state $\{S, I, R\}$
- ② Initialize c nodes in state I
- ③ Each node stays infected $\tau_\gamma = 1/\gamma$ time steps
- ④ On each time step each I node has a probability β to infect its nearest neighbours (NN), $S \rightarrow I$
- ⑤ After τ_γ time steps node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

Model dynamics:



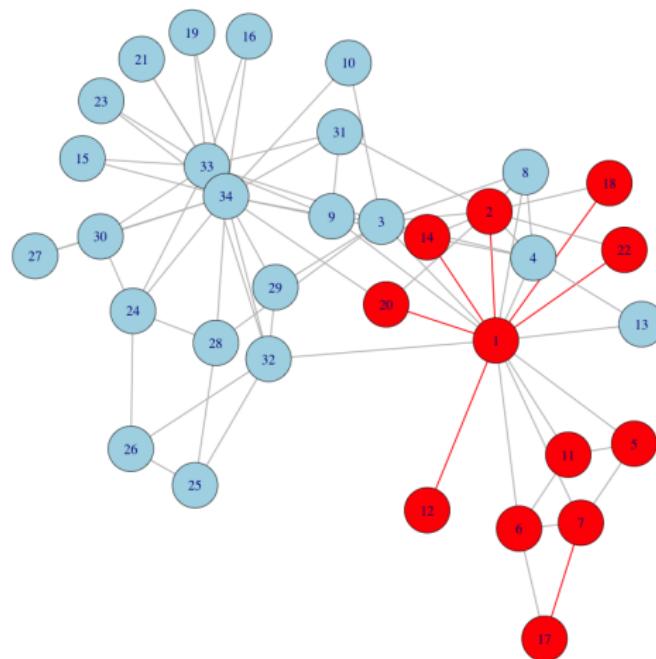
SIR model

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



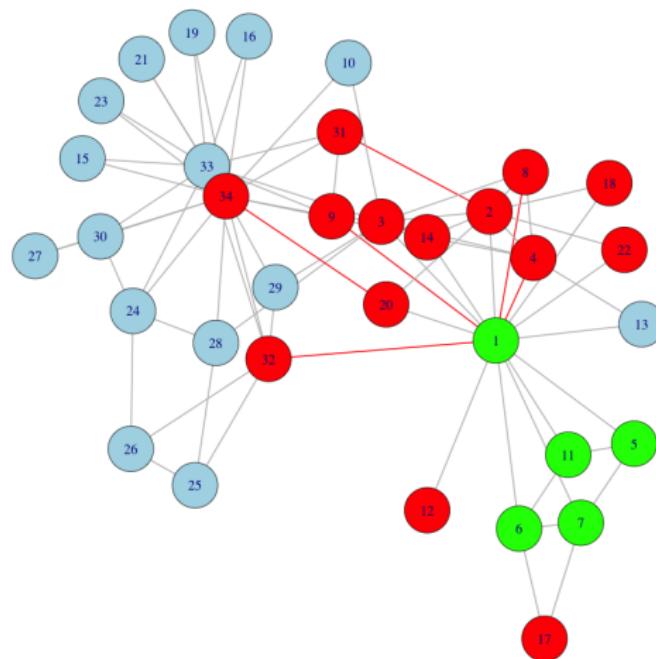
SIR model

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



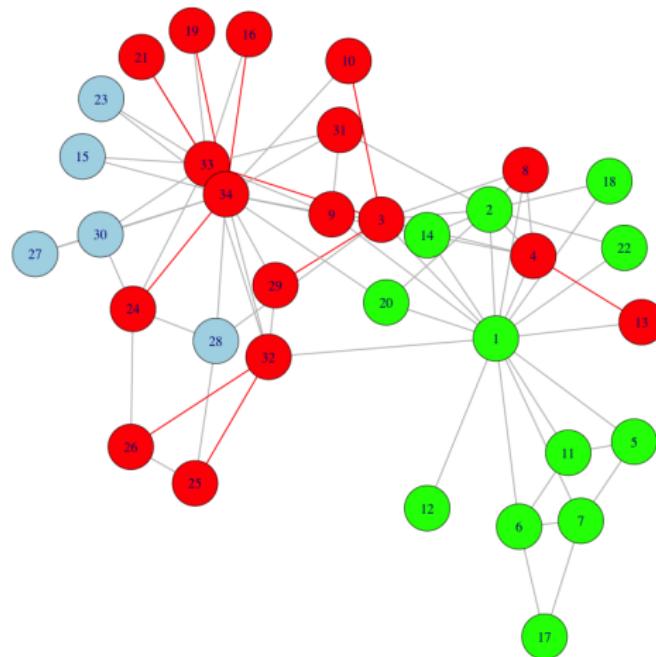
SIR model

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



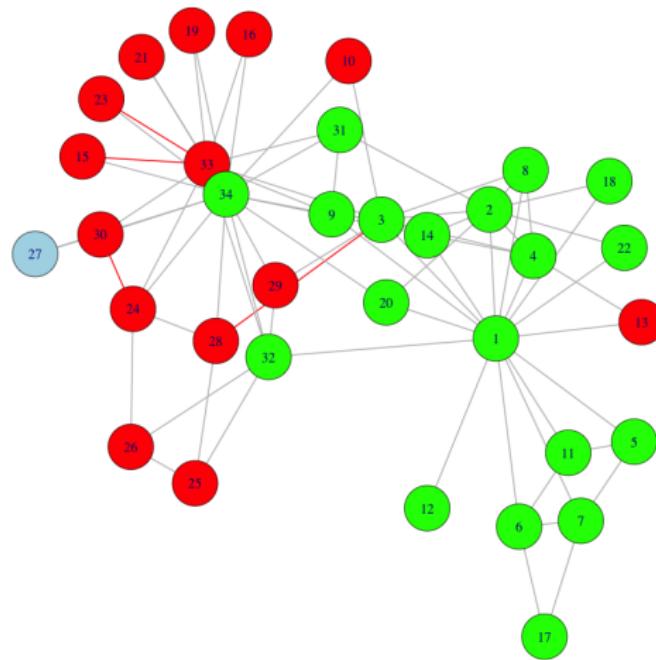
SIR model

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



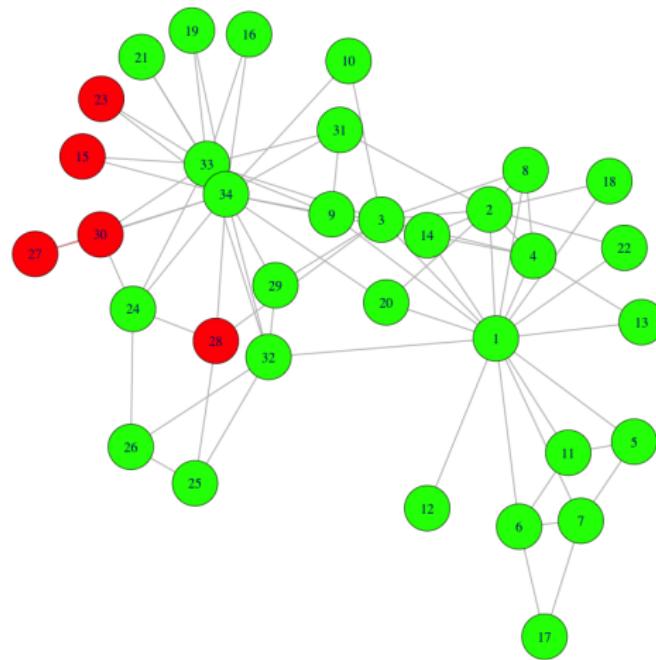
SIR model

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



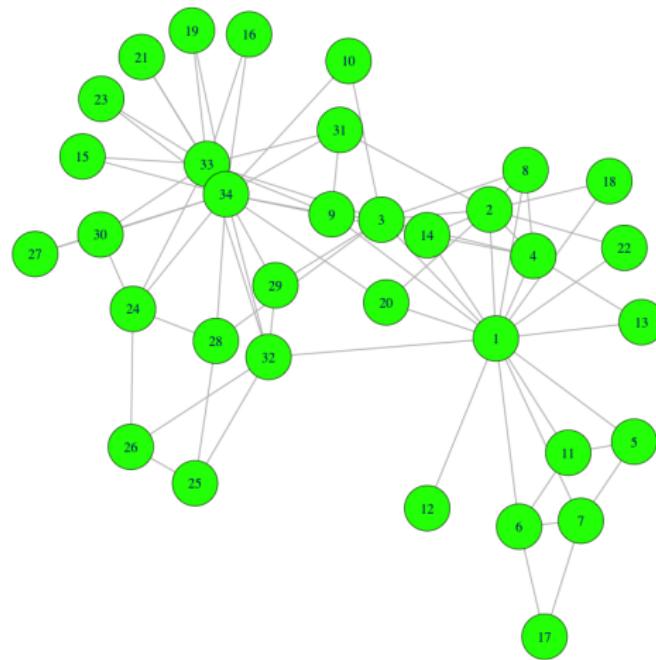
SIR model

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

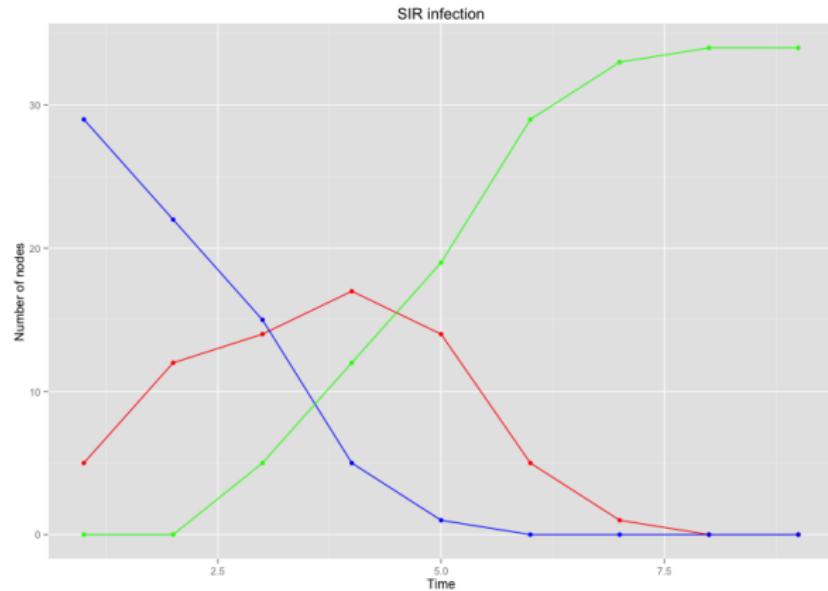


SIR model

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

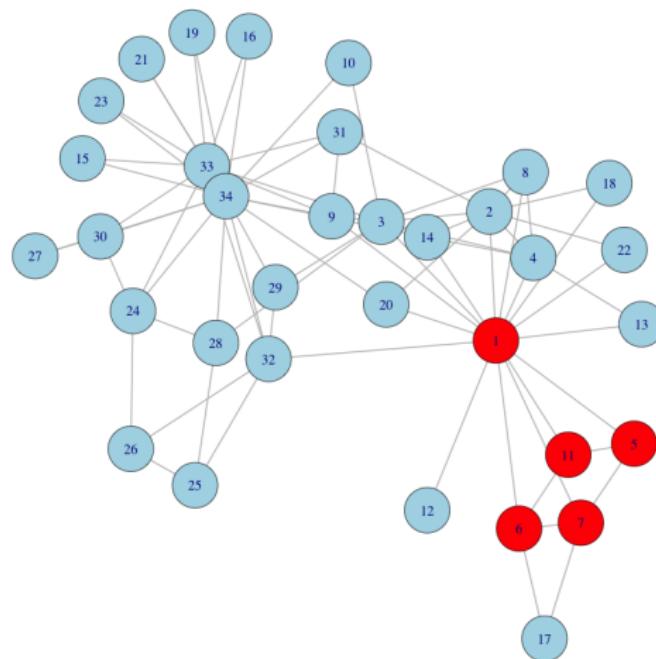


SIR model



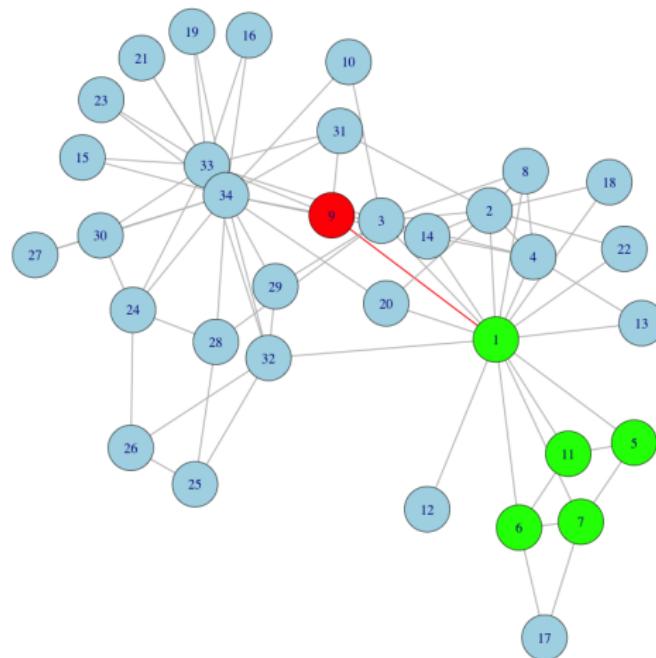
SIR model

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



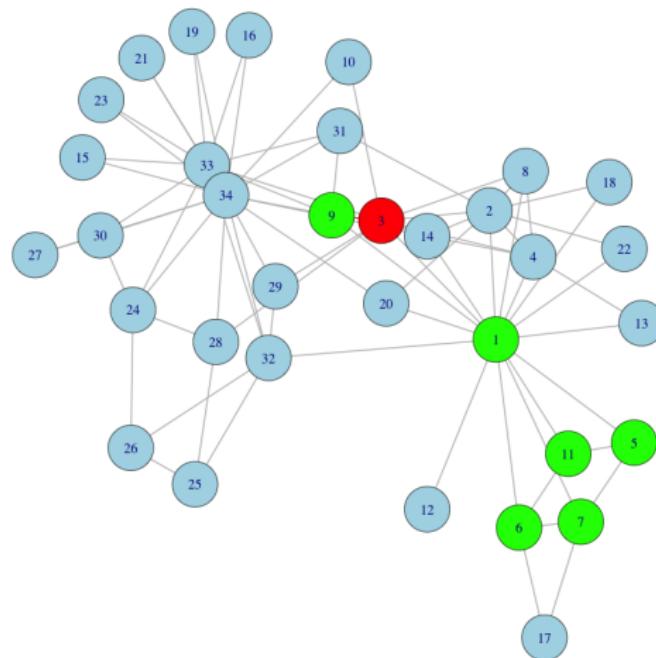
SIR model

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



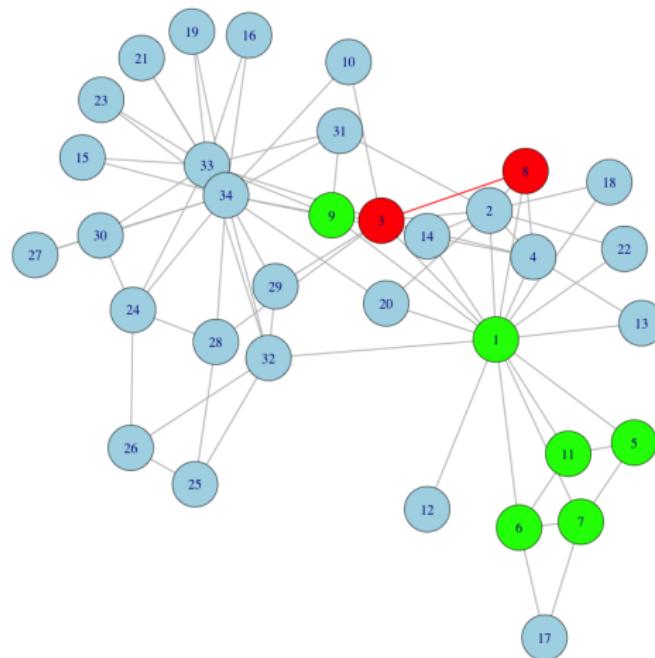
SIR model

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



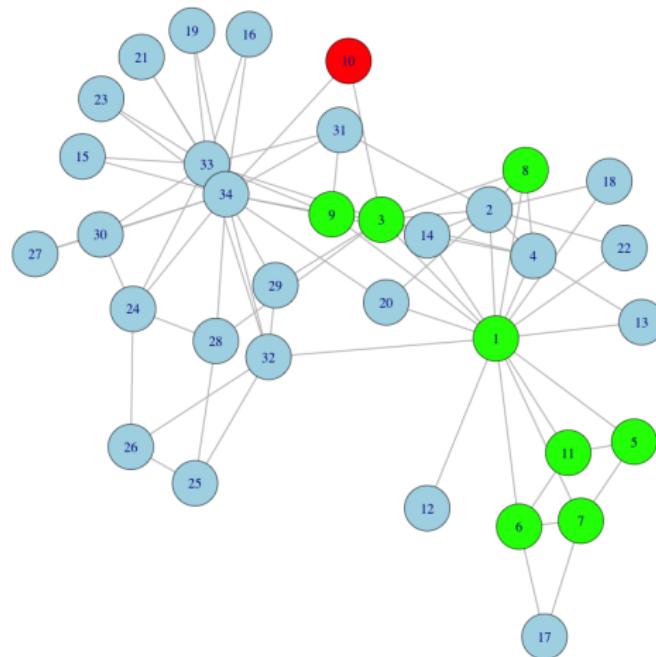
SIR model

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



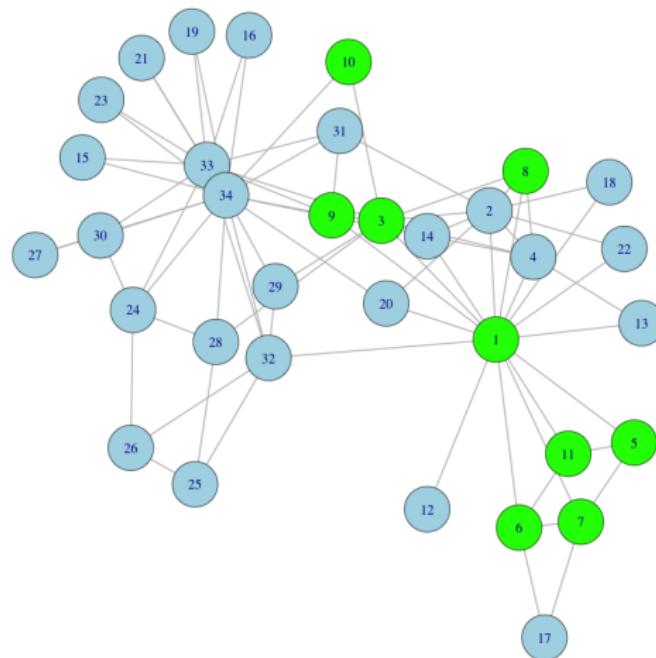
SIR model

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

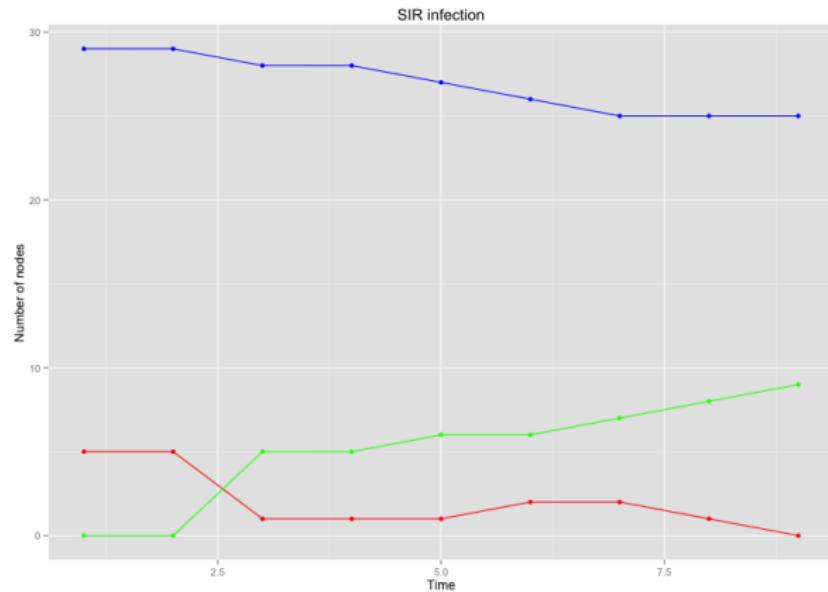


SIR model

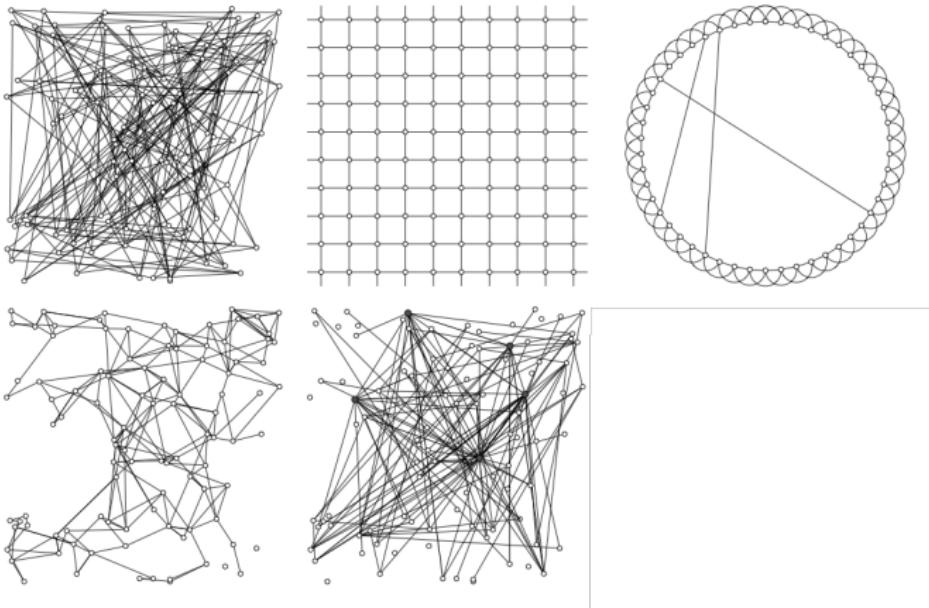
$$\beta = 0.2, \tau = 2$$



SIR model



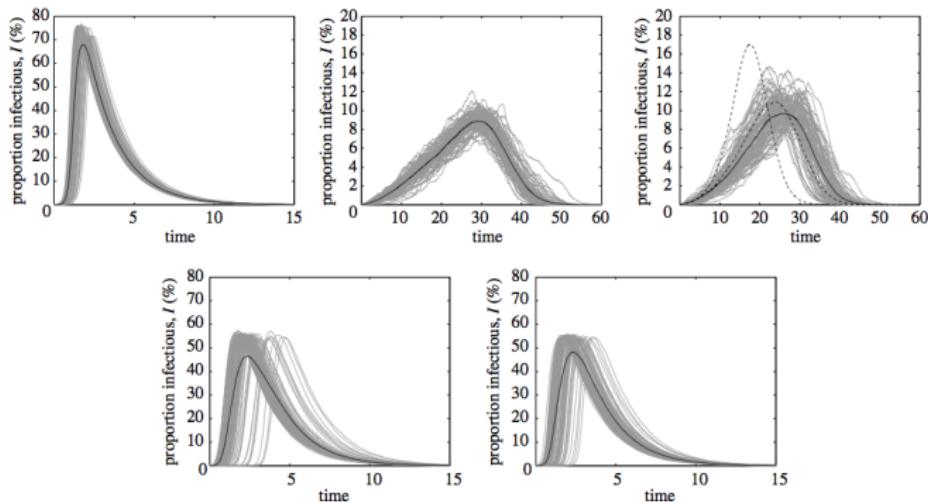
5 Networks, SIR



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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