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

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Network Science

Lecture outline

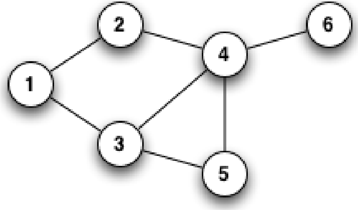
1. Random walks on graph
2. Diffusion on graph
3. Spectral graph theory
4. COVID-19 update
5. Branching process as contagion model
6. Epidemic modeling
    - SI model
    - SIS model
    - SIR model
7. Modeling epidemics on networks

Random walks on graph

- A random walk on graph G is a sequence of vertices $v_0, v_1, \ldots v_t..$, 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)

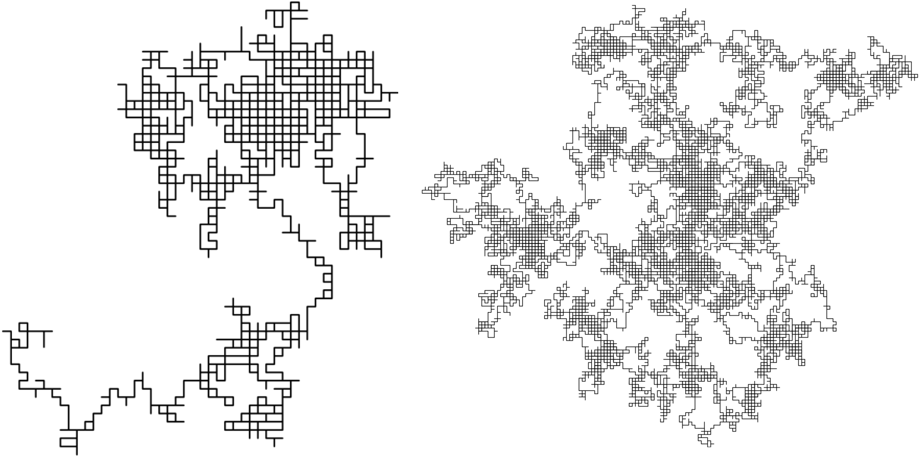


image from wikipedia.org

Random walks on graph

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

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

- 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

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

Random walks on graph

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

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

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

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

- Limiting distribution = stationary distribution

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

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

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

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

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

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

and can be found as a left eigenvector

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

$\vec{\pi}$ - 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:

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

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

  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

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

- Converges (always!) to the same stationary distribution

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

Random walks on graph

Theorem

Let λ_2 *denote second largest eigenvalue of transition matrix* $\mathrm{P} = \mathrm{D}^{-1}\mathrm{A}$, $\mathrm{p(t)}$ *probability distribution vector and* $\boldsymbol{\pi}$ *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 $\mathrm{P} = \mathrm{D}^{-1}\mathrm{A}$, $\lambda_1 = 1$, $\lambda_2 < 1$
- For $\mathrm{P}' = \frac{1}{2}(\mathrm{I} + \mathrm{D}^{-1}\mathrm{A})$, $\lambda_2' = \frac{1}{2}(1 + \lambda_2)$

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

$$\begin{aligned} \phi_i(t+1) &= \phi_i(t) + \sum_j A_{ij}(\phi_j(t) - \phi_i(t)) C \delta t \\ \frac{d\phi_i(t)}{dt} &= C \sum_j A_{ij}(\phi_j(t) - \phi_i(t)) \end{aligned}$$

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

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

Graph Laplacian

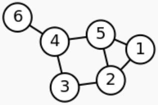
- Graph Laplacian

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

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

- Matrix form

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

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

$$\mathsf{L}\mathsf{v}_i = \lambda \mathsf{v}_i$$

- real non-negative eigenvalues $\lambda_i \geq 0$ and orthogonal eigenvectors v_i
- smallest eigenvalue always $\lambda_1 = 0$ for $\mathsf{v}_1 = \mathsf{e} = [1, 1, 1...1]^T$

$$\mathsf{L}\mathsf{e} = (\mathsf{D} - \mathsf{A})\mathsf{e} = 0$$

- 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

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

- Eigenvector basis

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

- ODE

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

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

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

- Solution

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

Diffusion on Graph

- Solution

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

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

$$\lim_{t\to\infty} \phi(t) = a_1(0)\mathrm{v}_1$$

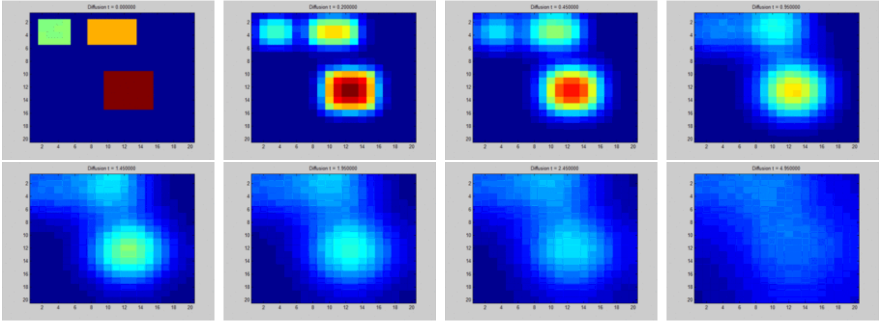
- Normalized solution $\mathrm{v}_1 = \frac{1}{\sqrt{N}}\mathrm{e}$

$$a_1(0) = \phi(0)^T\mathrm{v}_1 = \frac{1}{\sqrt{N}}\sum_j \phi_j(0)$$

- Steady state

$$\lim_{t\to\infty} \phi(t) = (\frac{1}{N}\sum_j \phi_j(0))\mathrm{e} = const$$

Diffusion on Graph



Smoothing operator

- L - symmetric positive semidefinite

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

- Smoothing operator

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

- Laplace equation $\nabla\phi = 0, \quad (L\phi)_i = 0$, 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

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

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

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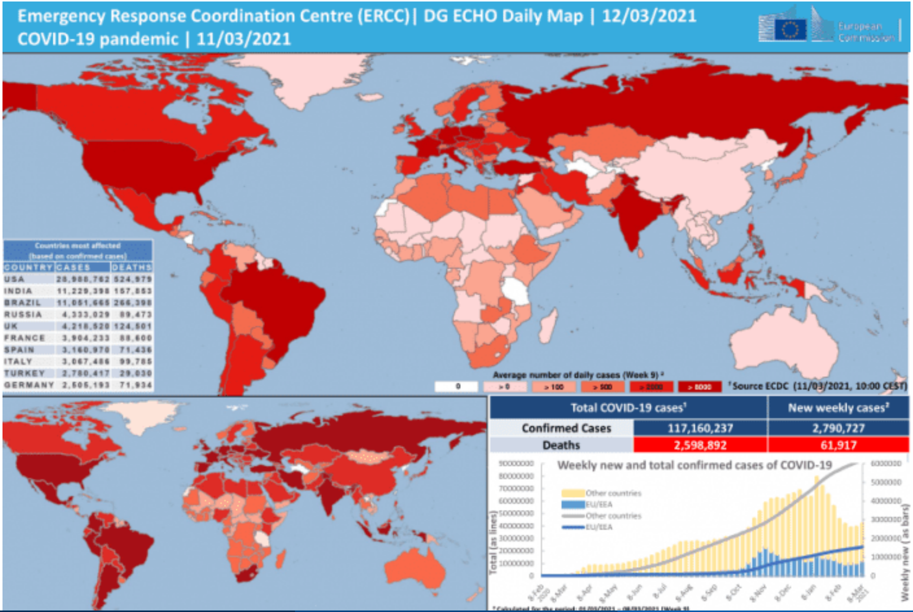
Coronavirus COVID-19



Emergency Response Coordination Centre (ERCC)| DG ECHO Daily Map | 12/03/2021

COVID-19 pandemic | 11/03/2021

Countries most affected
(based on confirmed cases)

COUNTRY	CASES	DEATHS
USA	28,988,762	524,979
INDIA	11,229,398	157,853
BRAZIL	11,051,665	266,398
RUSSIA	4,333,029	89,473
UK	4,218,520	124,501
FRANCE	3,904,233	88,600
SPAIN	3,160,970	71,436
ITALY	3,067,486	99,785
TURKEY	2,780,417	29,030
GERMANY	2,505,193	71,934

Average number of daily cases (Week 9) [2]

0	> 0	> 100	> 500	> 2000	> 8000

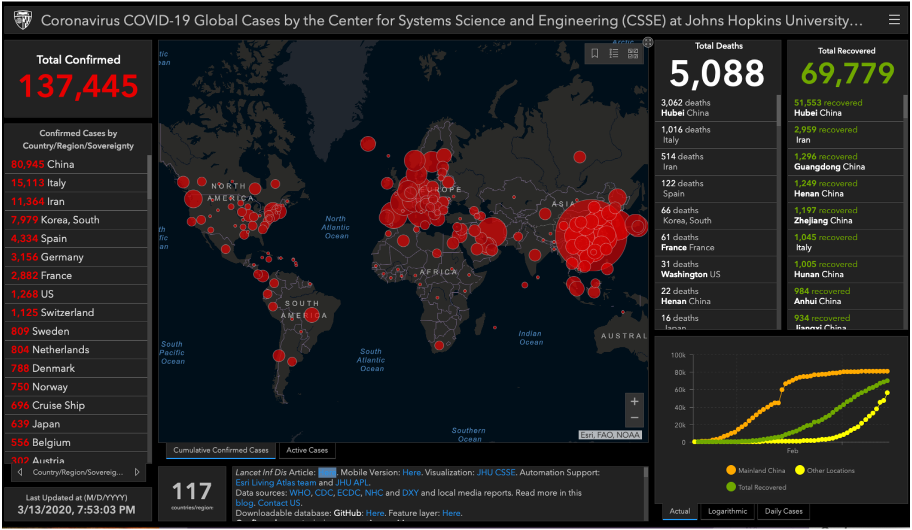
[1] Source ECDC (11/03/2021, 10:00 CEST)

	Total COVID-19 cases[1]	New weekly cases[2]
Confirmed Cases	117,160,237	2,790,727
Deaths	2,598,892	61,917

Weekly new and total confirmed cases of COVID-19

[2] Calculated for the period: 01/03/2021 – 08/03/2021 (Week 9)

Coronavirus COVID-19



Coronavirus COVID-19 Global Cases by the Center for Systems Science and Engineering (CSSE) at Johns Hopkins University...

Total Confirmed
137,445

Confirmed Cases by Country/Region/Sovereignty	
80,945	China
15,113	Italy
11,364	Iran
7,979	Korea, South
4,334	Spain
3,156	Germany
2,882	France
1,268	US
1,125	Switzerland
809	Sweden
804	Netherlands
788	Denmark
750	Norway
696	Cruise Ship
639	Japan
556	Belgium
302	Austria

Last Updated at (M/D/YYYY)
3/13/2020, 7:53:03 PM

117
countries/regions

Total Deaths
5,088

Total Deaths	
3,062 deaths	**Hubei** China
1,016 deaths	Italy
514 deaths	Iran
122 deaths	Spain
66 deaths	Korea, South
61 deaths	**France** France
31 deaths	**Washington** US
22 deaths	**Henan** China
16 deaths	Japan

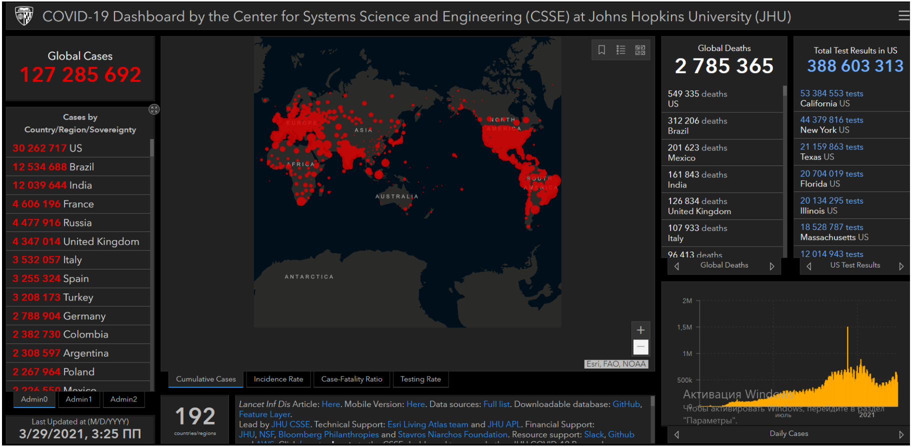
Total Recovered
69,779

Total Recovered	
51,553 recovered	**Hubei** China
2,959 recovered	Iran
1,296 recovered	**Guangdong** China
1,249 recovered	**Henan** China
1,197 recovered	**Zhejiang** China
1,045 recovered	Italy
1,005 recovered	**Hunan** China
984 recovered	**Anhui** China
934 recovered	**Jiangxi** China

Lancet Inf Dis Article: Here. Mobile Version: Here. Visualization: JHU CSSE. Automation Support: Esri Living Atlas team and JHU APL.
Data sources: WHO, CDC, ECDC, NHC and DXY and local media reports. Read more in this blog. Contact US.
Downloadable database: GitHub: Here. Feature layer: Here.

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

Coronavirus COVID-19



COVID-19 Dashboard by the Center for Systems Science and Engineering (CSSE) at Johns Hopkins University (JHU)

Global Cases
127 285 692

Cases by Country/Region/Sovereignty

30 262 717	US
12 534 688	Brazil
12 039 644	India
4 606 196	France
4 477 916	Russia
4 347 014	United Kingdom
3 532 057	Italy
3 255 324	Spain
3 208 173	Turkey
2 788 904	Germany
2 382 730	Colombia
2 308 597	Argentina
2 267 964	Poland
2 226 550	Mexico

Last Updated at (M/D/YYYY)
3/29/2021, 3:25 ПП

192
countries/regions

Lancet Inf Dis Article: Here. Mobile Version: Here. Data sources: Full list. Downloadable database: GitHub, Feature Layer.
Lead by JHU CSSE. Technical Support: Esri Living Atlas team and JHU APL. Financial Support: JHU, NSF, Bloomberg Philanthropies and Stavros Niarchos Foundation. Resource support: Slack, Github

Global Deaths
2 785 365

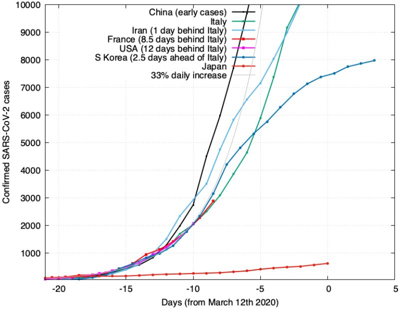
549 335 deaths	US
312 206 deaths	Brazil
201 623 deaths	Mexico
161 843 deaths	India
126 834 deaths	United Kingdom
107 933 deaths	Italy
96 413 deaths	

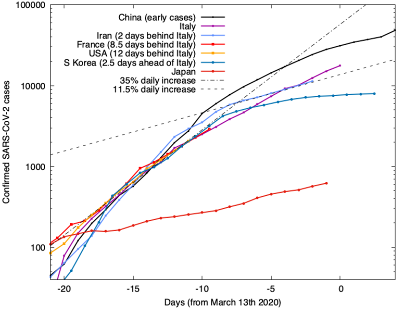
Total Test Results in US
388 603 313

53 384 553 tests	California US
44 379 816 tests	New York US
21 159 863 tests	Texas US
20 704 019 tests	Florida US
20 134 295 tests	Illinois US
18 528 787 tests	Massachusetts US
12 014 943 tests	

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

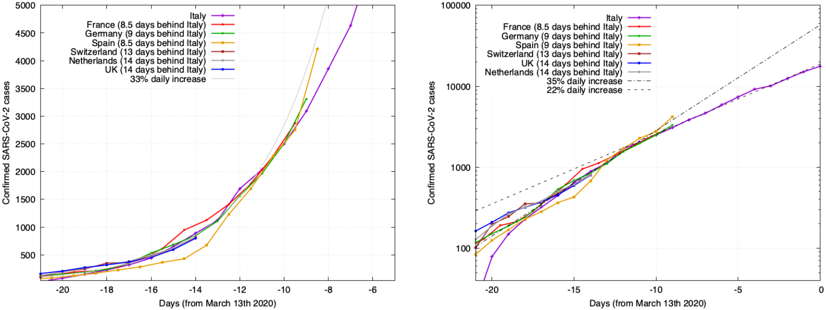
Coronavirus COVID-19





from Mark Handley, UCL

Coronavirus COVID-19



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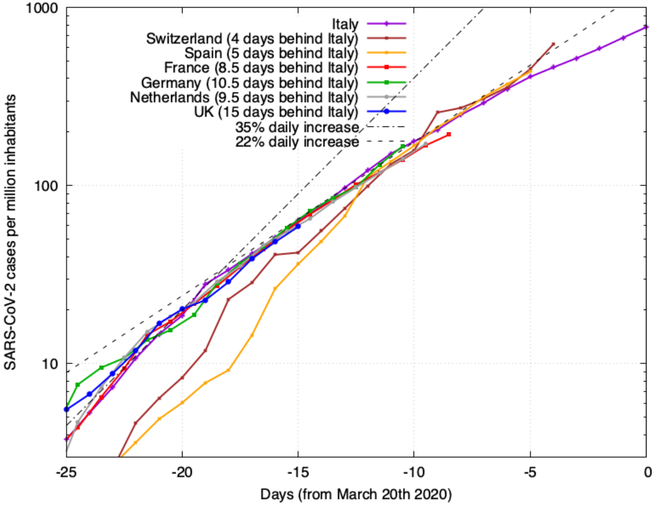
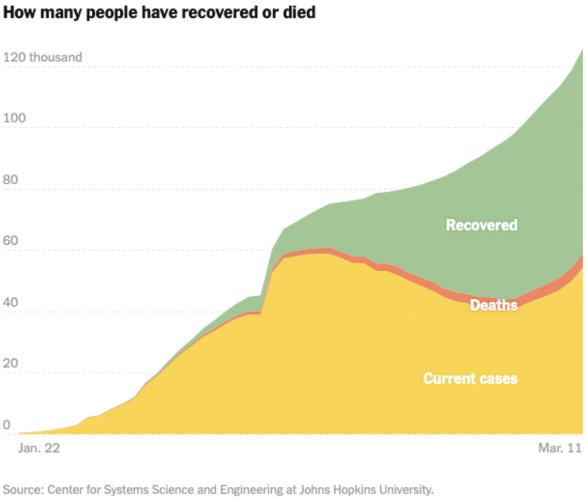
Coronavirus COVID-19



from Mark Handley, UCL

Coronavirus COVID-19



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

from the NYT

Simple model of contagion

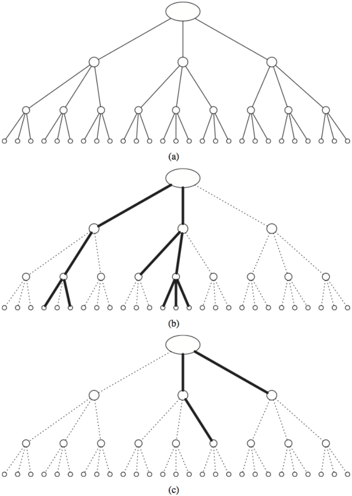
Simple model of contagion (decease transmission)

- 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

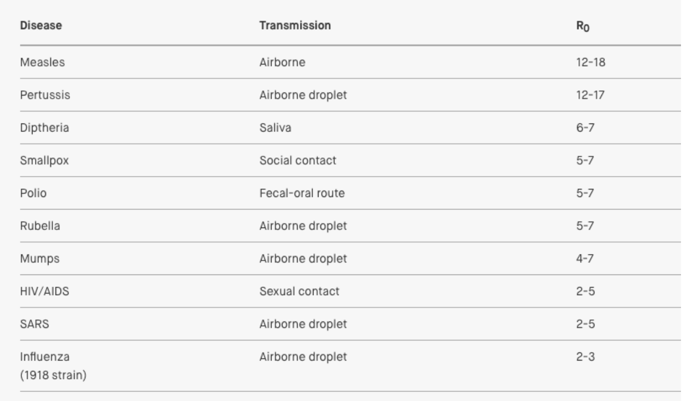
image from David Easley, Jon Kleinberg, 2010

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 $n \to t$, geometric growth $\to$ 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
Diptheria	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 epidimiology

- 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

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

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

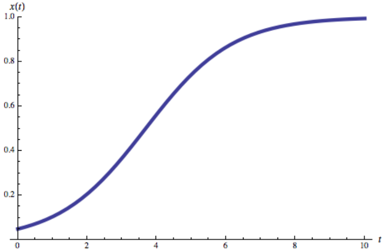
- Differential equation, $i(t = 0) = i_0$

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

Logistic growth function

- Solution:

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



- Limit $t \to \infty$

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

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

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:

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

$$s + i = 1$$

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

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

SIS model

- Solution

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

where

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

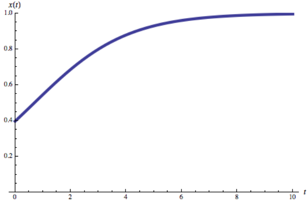
- Limit $t \to \infty$

$$\beta > \gamma \quad , \qquad i(t) \to (1 - \frac{\gamma}{\beta})$$

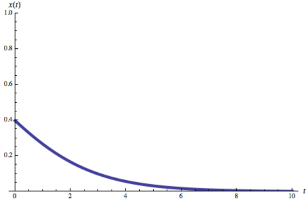
$$\beta < \gamma \quad , \qquad i(t) = i_0 e^{(\beta-\gamma)t} \to 0$$

Logistic function

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



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



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

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

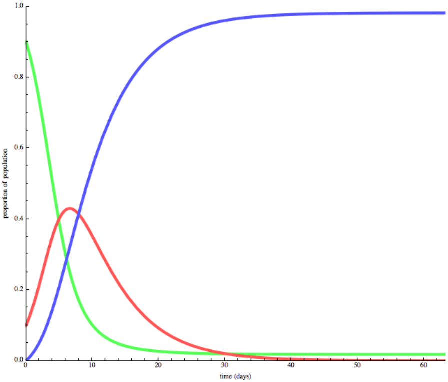
$$s = s_0 e^{-\frac{\beta}{\gamma} r}$$

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

- Solution

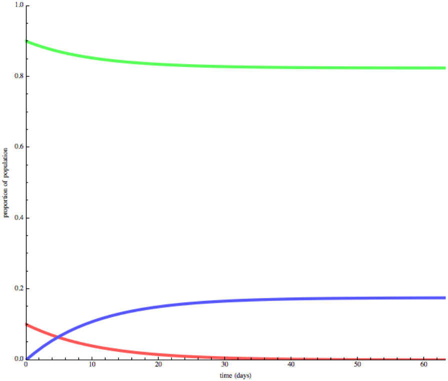
$$t = \frac{1}{\gamma}\int_0^r \frac{dr}{1 - r - s_0 e^{-\frac{\beta}{\gamma} r}}$$

SIR model



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

SIR model



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

SIR model

- Equation

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

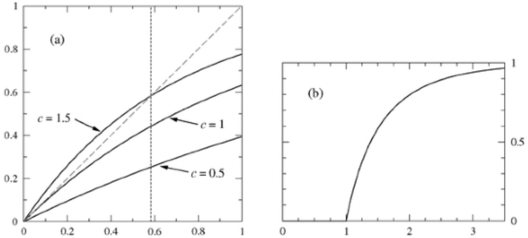
- Limits: $t \to \infty, \quad \frac{dr}{dt} = 0,\ r_\infty = const,$

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

- 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

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

$$\begin{array}{ll} \text{Epidemics:} & R_0 > 1, \quad \beta > \gamma \quad , \quad r_\infty = const > 0 \\ \text{No epidemics:} & R_0 < 1, \quad \beta < \gamma \quad , \quad r_\infty \to 0 \end{array}$$

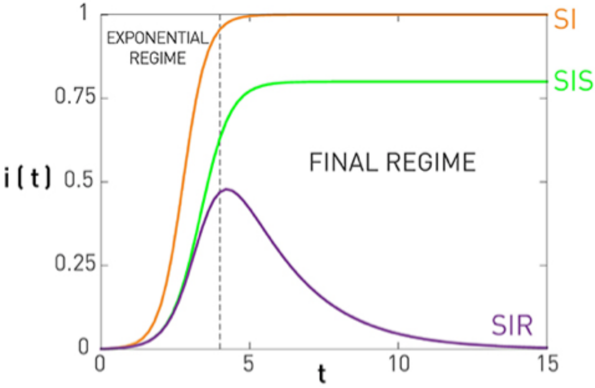
- β - infection rate, γ - recovery rate →
- Basic reproduction number

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

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

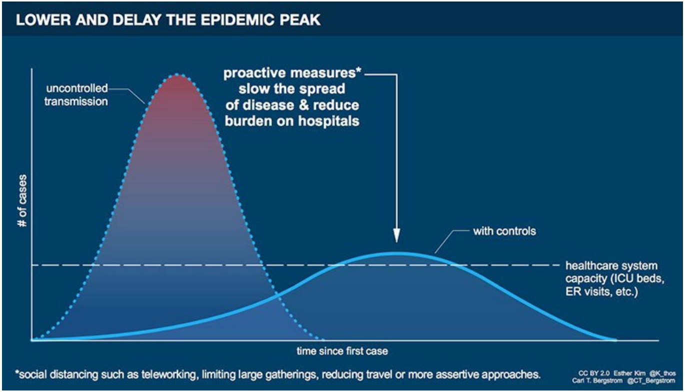
$$R_0 = E[\beta\tau] = \beta \int_0^\infty \gamma\tau e^{-\gamma\tau} d\tau = \frac{\beta}{\gamma}$$

Compartmental models summary



from Barabasi, 2016

Flatten the curve!

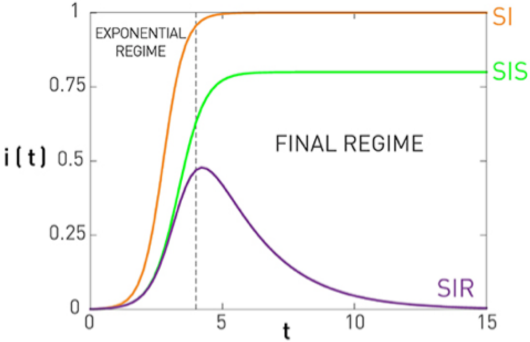


LOWER AND DELAY THE EPIDEMIC PEAK

*social distancing such as teleworking, limiting large gatherings, reducing travel or more assertive approaches.

CC BY 2.0 Esther Kim @K_thos Carl T. Bergstrom @CT_Bergstrom

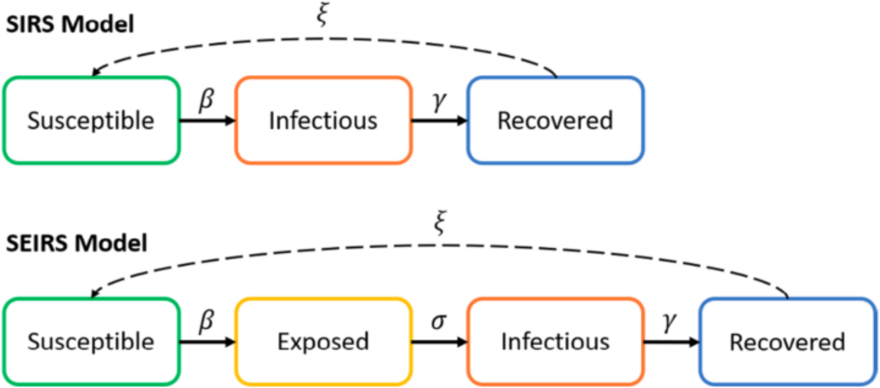
Compartmental models summary



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	$R_0 = 1$

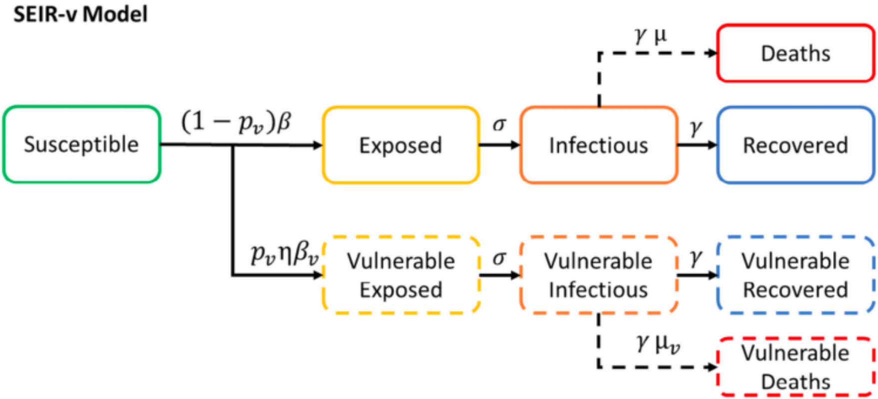
from Barabasi, 2016

Advanced Compartmental Models



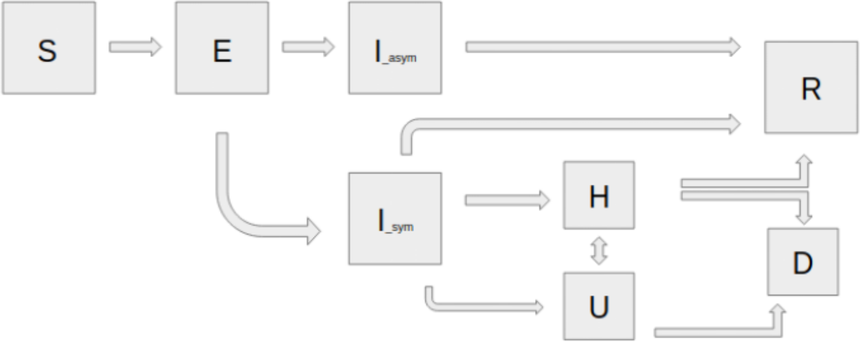
D. Anderez et al., 2020

SEIR-vulnerable



D. Anderez et al., 2020

SEIIHURD



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

Juliane F. Oliveira et.al, 2020

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, $t \to 0, \;\; x_i(t) \ll 1$

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

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

- Solution in the basis

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

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

SI model

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

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

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

- Solution

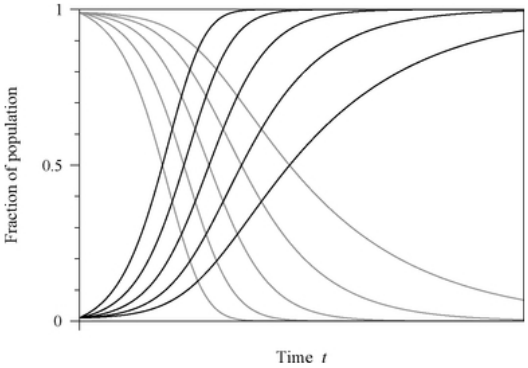
$$\mathrm{x}(t) = \sum_k a_k(0)e^{\lambda_k \beta t}\mathrm{v}_k$$

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

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

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

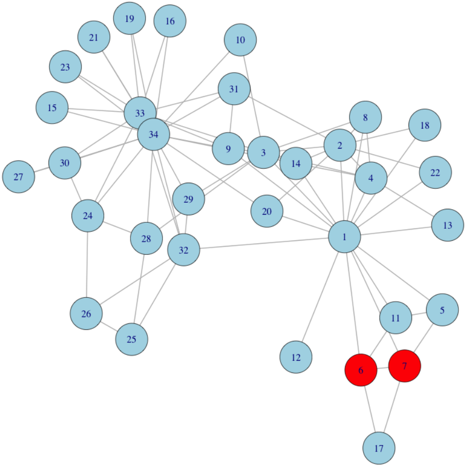
1. Every node at any time step is in one state $\{S, I\}$
2. Initialize c nodes in state I
3. On each time step each I node has a probability β to infect its nearest neighbors (NN), $S \to I$

Model dynamics:

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

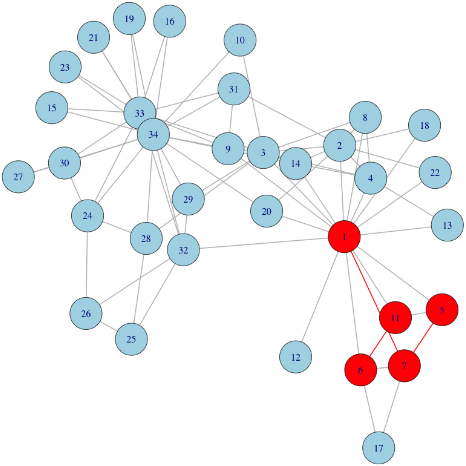
SI model simulation

$\beta = 0.5$



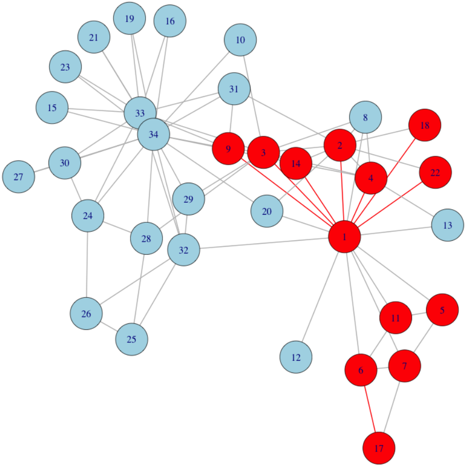
SI model simulation

$\beta = 0.5$



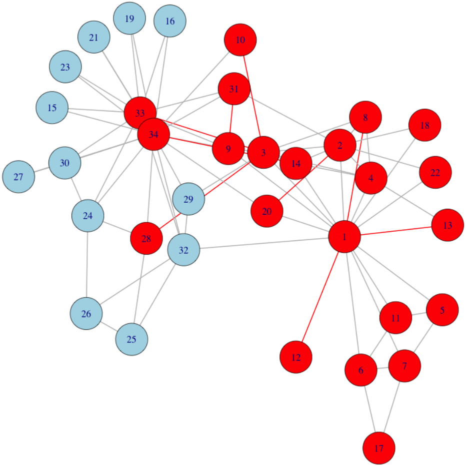
SI model simulation

$\beta = 0.5$



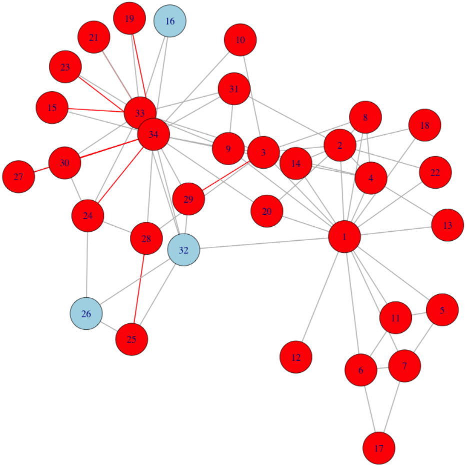
SI model simulation

$\beta = 0.5$



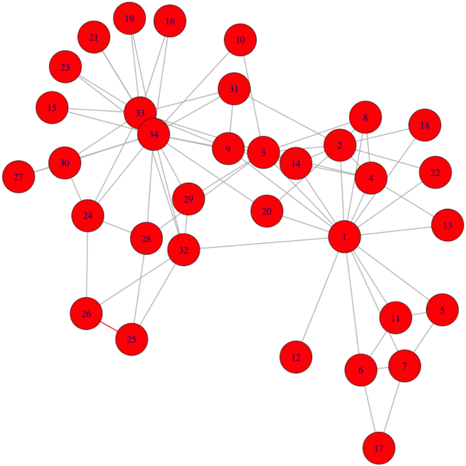
SI model simulation

$\beta = 0.5$

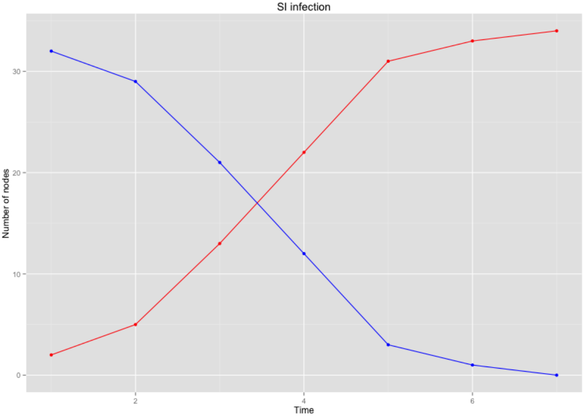


SI model simulation

$\beta = 0.5$



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, $x_i(t) \ll 1$

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

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

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

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

SIS model

- Eigenvector basis

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

- Solution

$$\mathrm{x}(t) = \sum_k a_k(t)\mathrm{v}'_k = \sum_k a_k(0)\mathrm{v}'_k e^{\lambda'_k \beta t} = \sum_k a_k(0)\mathrm{v}_k e^{(\beta\lambda_k - \gamma)t}$$

- $\lambda_1 \geq \lambda_k$, critical: $\beta\lambda_1 = \gamma$
  -if $\beta\lambda_1 > \gamma, \quad \mathrm{x}(t) \to \mathrm{v}_1 e^{(\beta\lambda_1 - \gamma)t}$ - growth
  -if $\beta\lambda_1 < \gamma, \quad \mathrm{x}(t) \to 0$ - 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

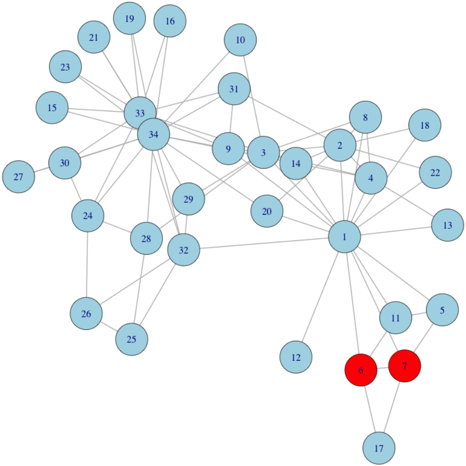
1. Every node at any time step is in one state $\{S, I\}$
2. Initialize c nodes in state I
3. Each node stays infected $\tau_\gamma = \int_0^\infty \tau e^{-\tau\gamma} d\tau = 1/\gamma$ time steps
4. On each time step each I node has a prabability β to infect its nearest neighbours (NN), $S \to I$
5.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

Model dynamics:

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

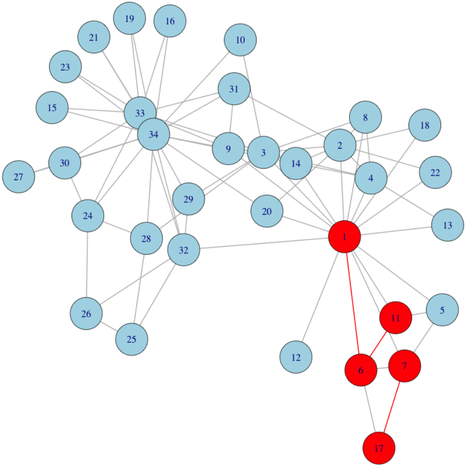
SIS model simulation

$\beta = 0.5, \tau = 2$



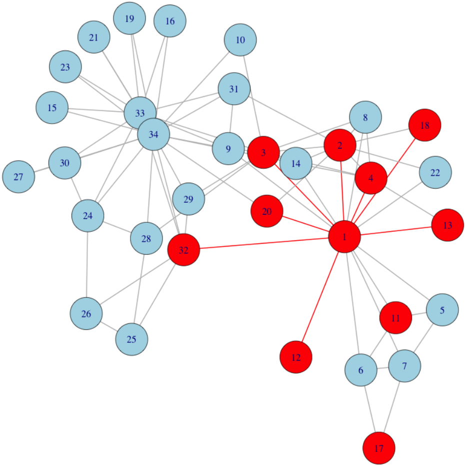
SIS model simulation

$\beta = 0.5, \tau = 2$



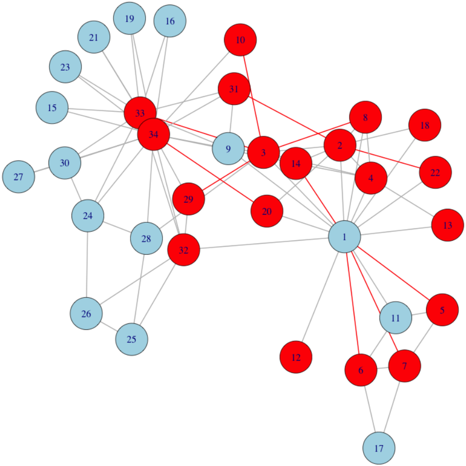
SIS model simulation

$\beta = 0.5, \tau = 2$



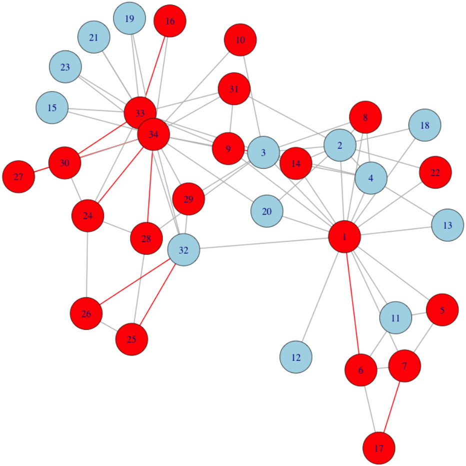
SIS model simulation

$\beta = 0.5, \tau = 2$



SIS model simulation

$\beta = 0.5, \tau = 2$



SIS model simulation

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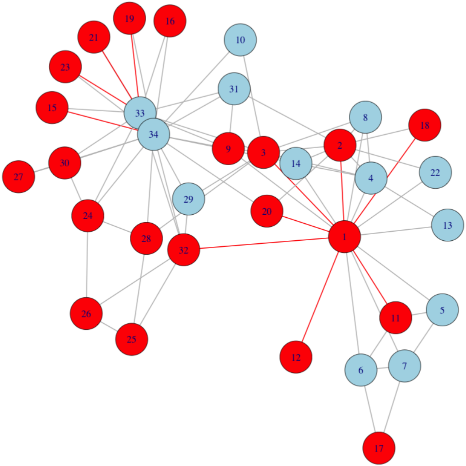
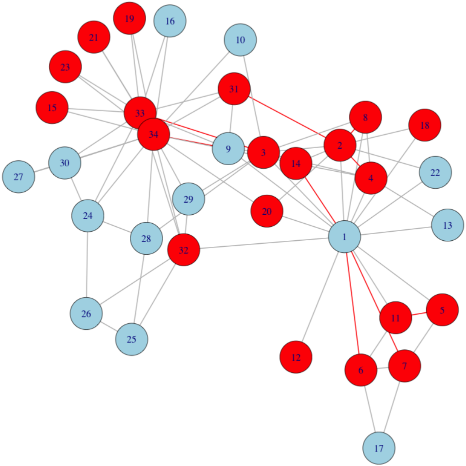
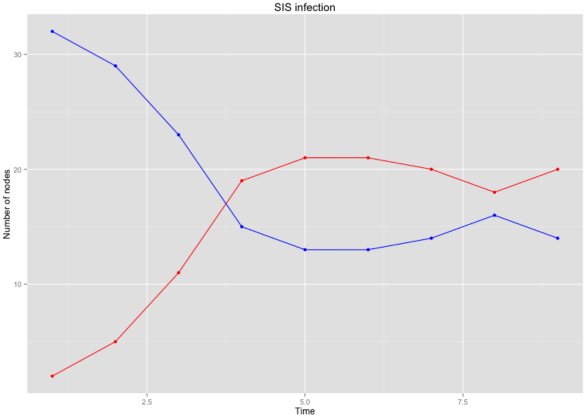


SIS model simulation

$\beta = 0.5, \tau = 2$

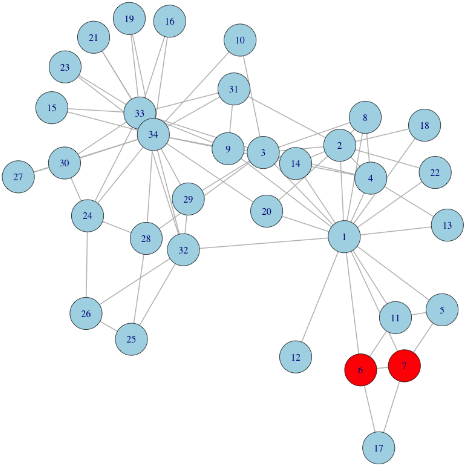


SIS model



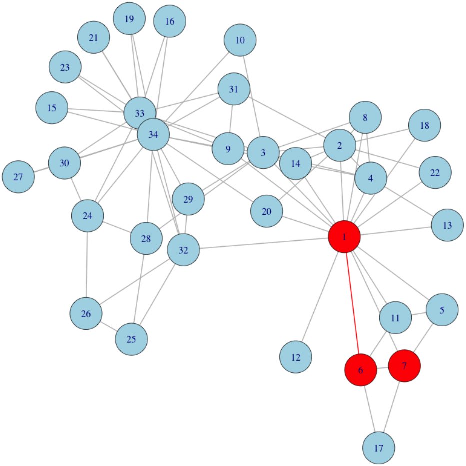
SIS model simulation

$\beta = 0.2, \tau = 2$



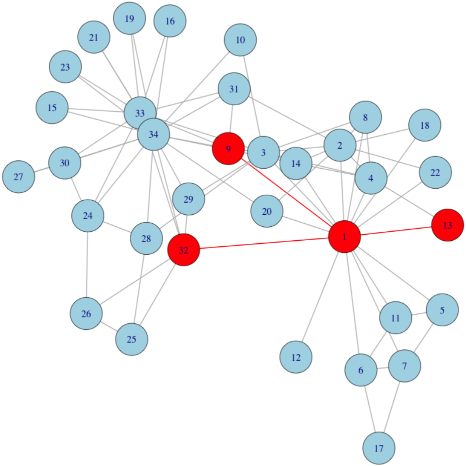
SIS model simulation

$\beta = 0.2, \tau = 2$



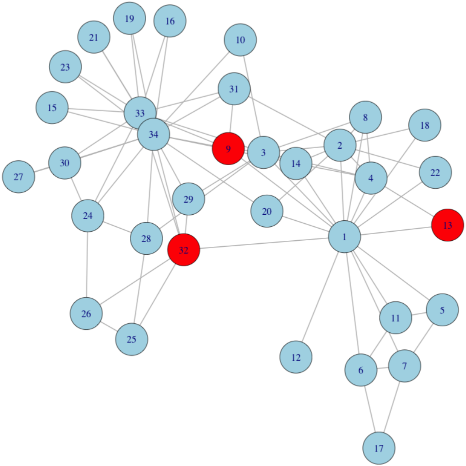
SIS model simulation

$\beta = 0.2, \tau = 2$



SIS model simulation

$\beta = 0.2, \tau = 2$



SIS model simulation

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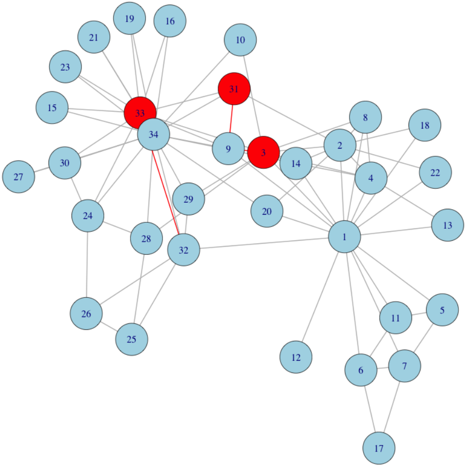

SIS model simulation

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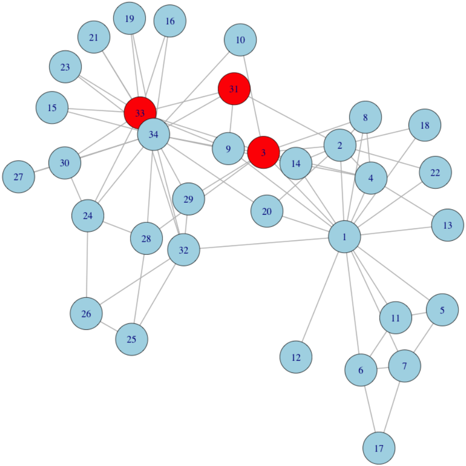

SIS model simulation

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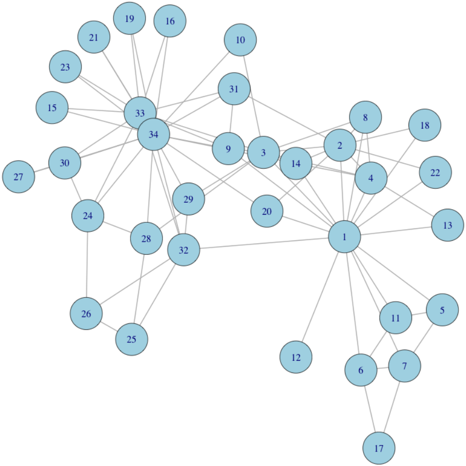
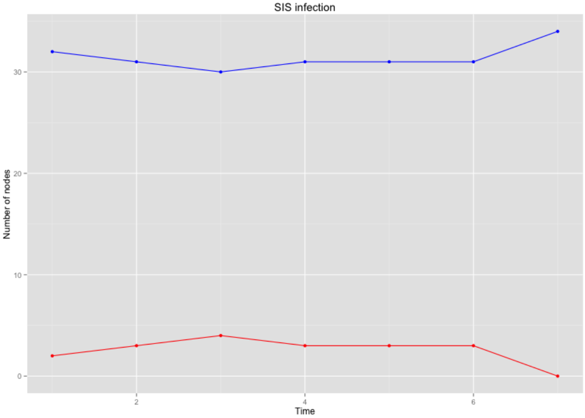


SIS model



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

$$\mathrm{x}(t) \sim \mathrm{v}_1 e^{(\beta\lambda_1 - \gamma)t}$$

SIR model

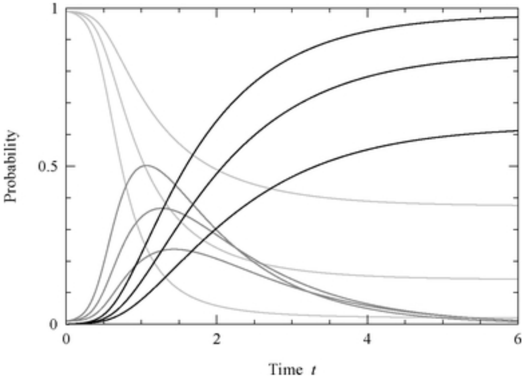


image from M. Newman, 2010

SIR simulation

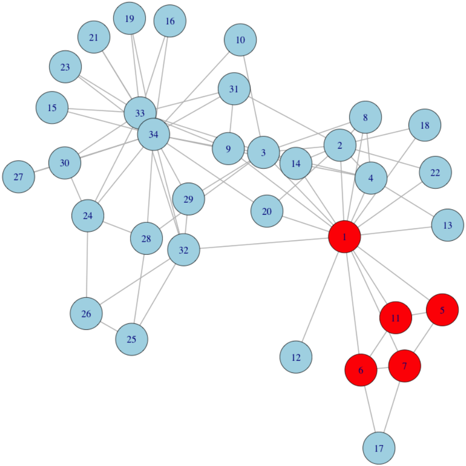
1. Every node at any time step is in one state $\{S, I, R\}$
2. Initialize c nodes in state I
3. Each node stays infected $\tau_\gamma = 1/\gamma$ time steps
4. On each time step each I node has a prabability β to infect its nearest neighbours (NN), $S \to I$
5. After τ_γ time steps node recovers, $I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

Model dynamics:

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

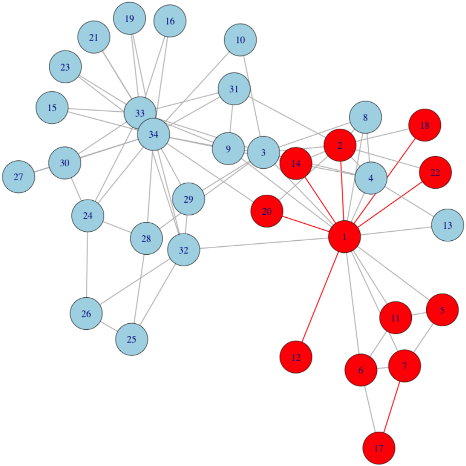
SIR model

$\beta = 0.5, \tau = 2$



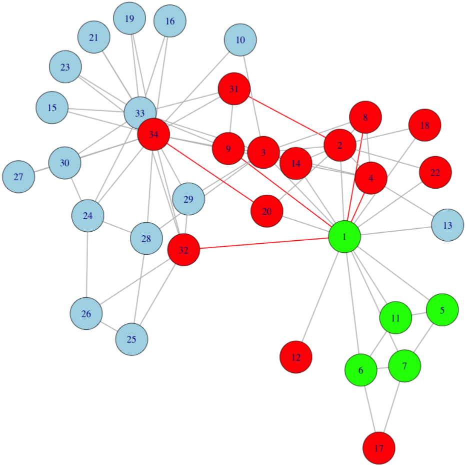
SIR model

$\beta = 0.5, \tau = 2$



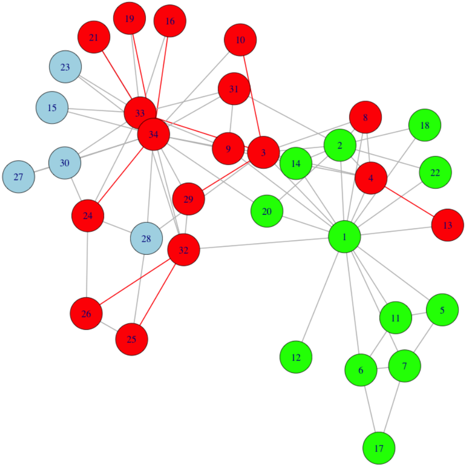
SIR model

$\beta = 0.5, \tau = 2$



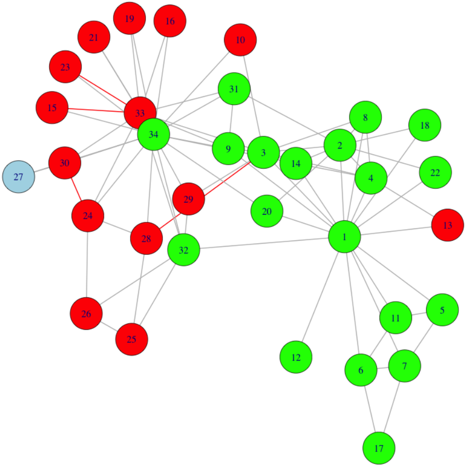
SIR model

$\beta = 0.5, \tau = 2$



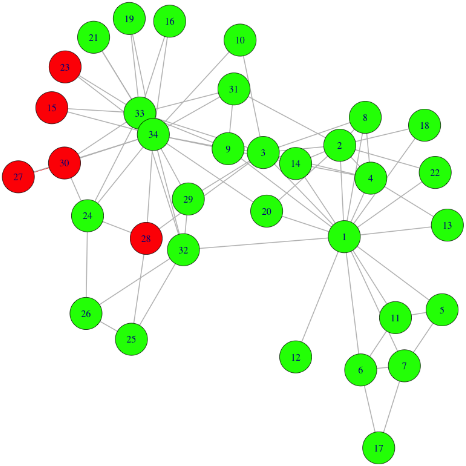
SIR model

$\beta = 0.5, \tau = 2$



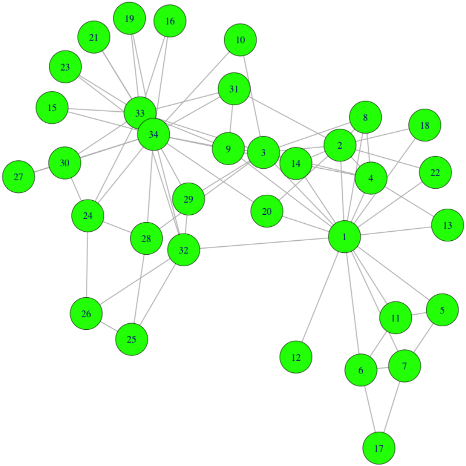
SIR model

$\beta = 0.5, \tau = 2$

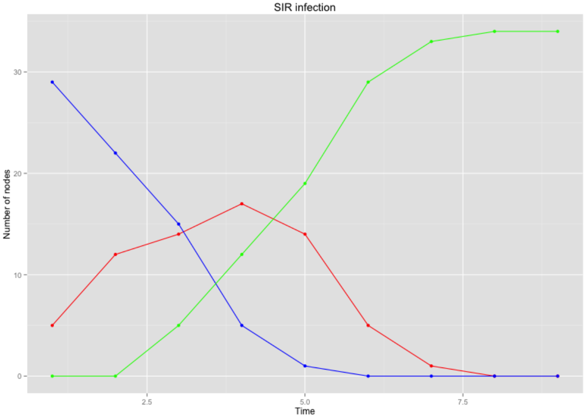


SIR model

$\beta = 0.5, \tau = 2$

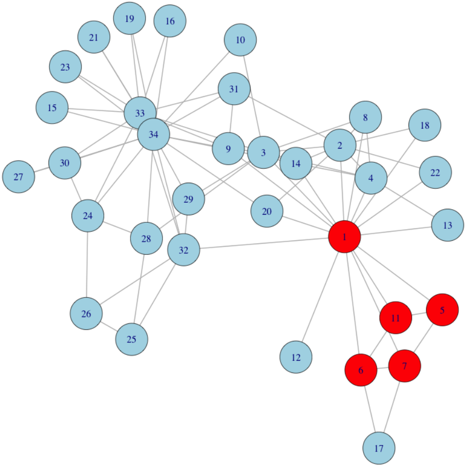


SIR model



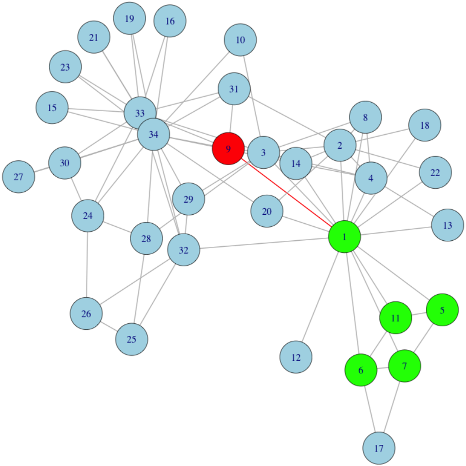
SIR model

$\beta = 0.2, \tau = 2$



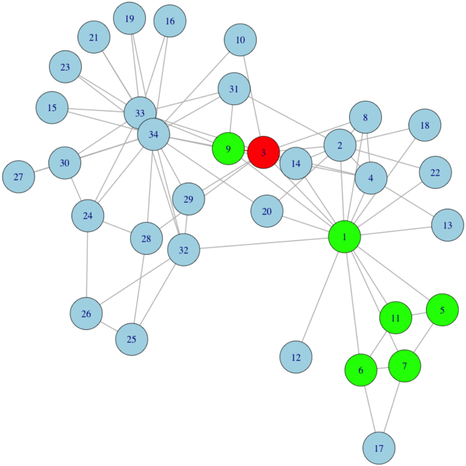
SIR model

$\beta = 0.2, \tau = 2$



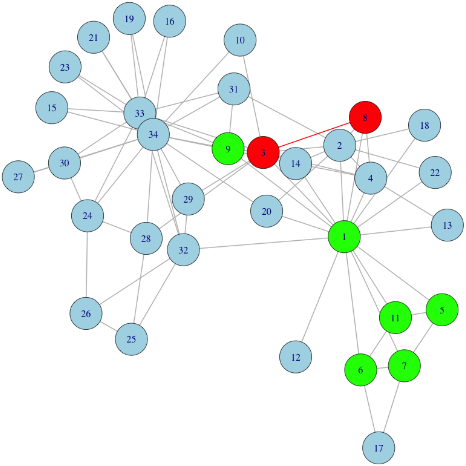
SIR model

$\beta = 0.2, \tau = 2$



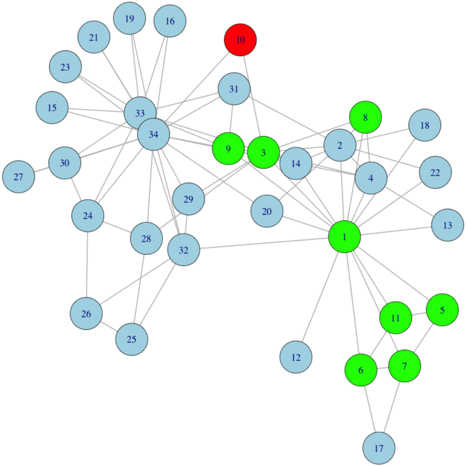
SIR model

$\beta = 0.2, \tau = 2$



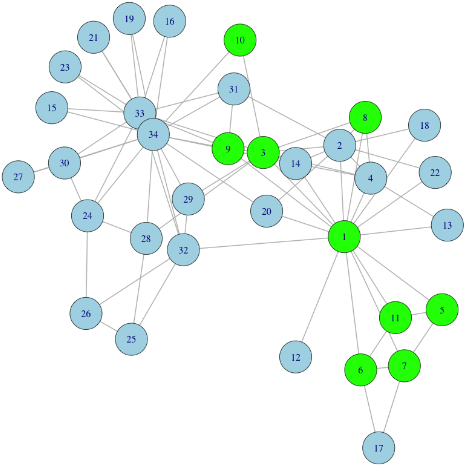
SIR model

$\beta = 0.2, \tau = 2$

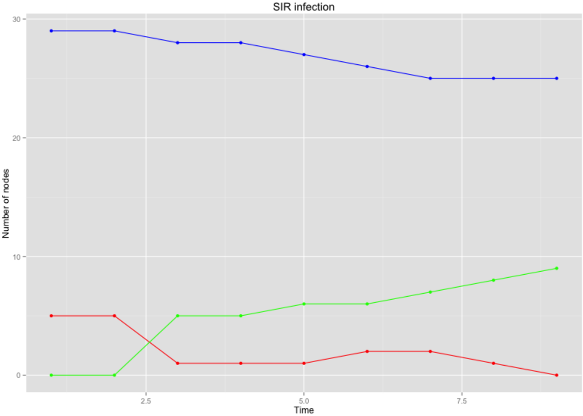


SIR model

$\beta = 0.2, \tau = 2$

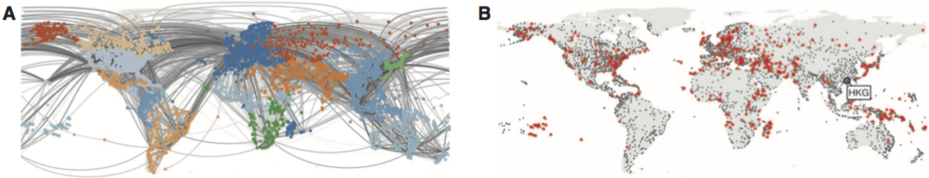


SIR model



Modeling SARS outbreak

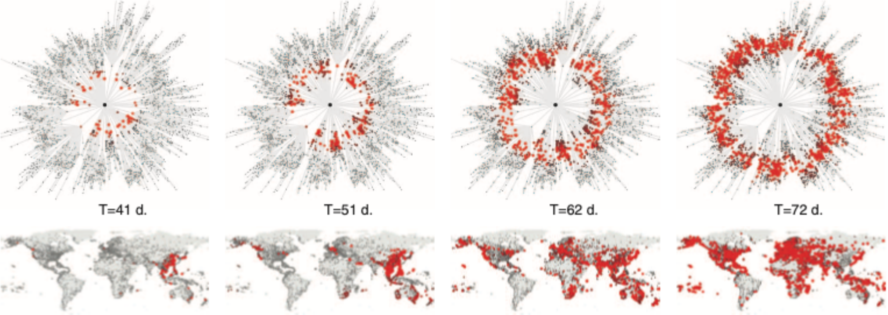
SARS 2003: $> 8,000$ cases, 37 countries



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

D. Brockmann, D. Helbing, 2013

Modeling SARS outbreak

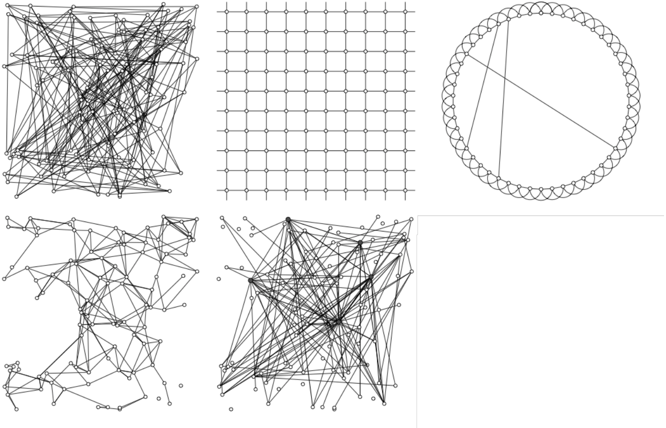


T=41 d. T=51 d. T=62 d. T=72 d.

Shortest path tree from Hong Kong

D. Brockmann, D. Helbing, 2013

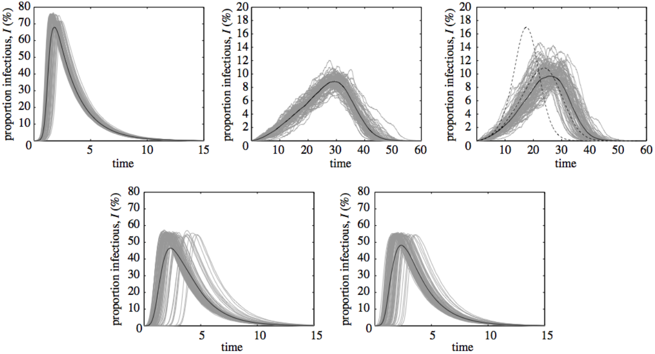
5 Networks, SIR



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

image from Keeling et al, 2005

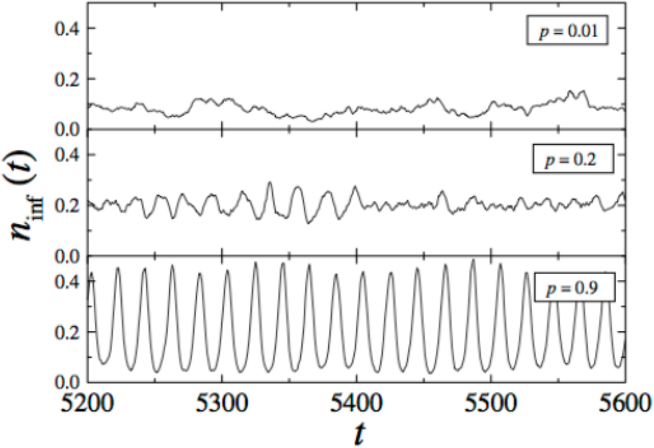
5 Networks, SIR



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

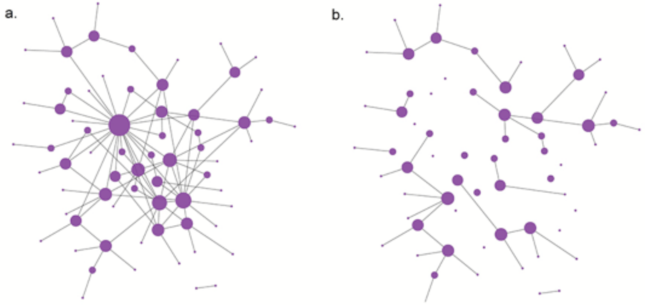
$$R = \frac{\langle k \rangle}{\langle k^2 \rangle}$$

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

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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