

1

Epidemic spreading – Why?

Why is the spreading process important?



Network Science: Robustness Cascades (Nov 20, 2017)

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“Epidemic”

Epi + demos
upon people



Biological:

- Airborne diseases (flu, SARS, ...)
- Venereal diseases (HIV, ...)
- Other infectious diseases including some cancers (HPV, ...)
- Parasites (bedbugs, malaria, ...)

Digital:

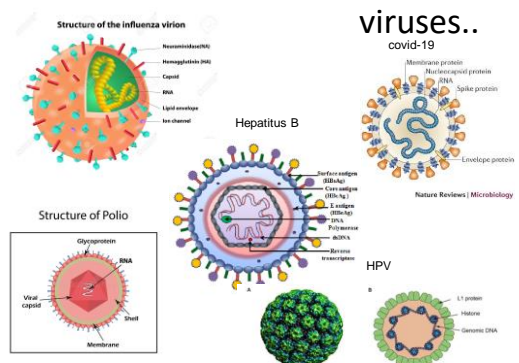
- Computer viruses, worms
- Mobile phone viruses

Conceptual/Intellectual:

- Diffusion of innovations
- Rumors
- Memes
- Business practices

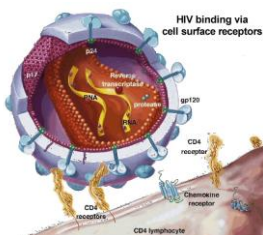
<http://en.wikipedia.org/wiki/Epidemic>

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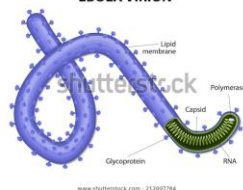


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RNA virus: HIV

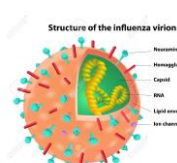


EBOLA VIRION



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viruses..



On the spikes of influenza virion: Hemagglutinin (H) and Neuraminidase (N)

H is being used for entering the cell, there are 16 types

N is being used for leaving the host cell, there are 9 types

Immune system can recognize H and N

RNA virus, mutates quickly

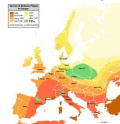
Avian flu (one of the variants) H5N1

Recombination of different influenza virions in different hosts (zoonose)

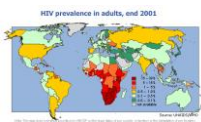
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Biological: Notable Epidemic Outbreaks

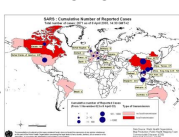
The Great Plague



HIV



SARS



1918 Spanish flu



H1N1 flu

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Epidemic spreading – Why does it matter now?

High population density



High mobility

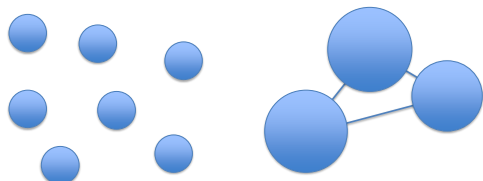


→ perfect conditions for epidemic spreading.

Airline figure: L. Hufnagel et al. *PNAS* 101, 15124 (2004)

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Large population can provide the “fuel”



Separate, small population
(hunter-gatherer society, wild animals)

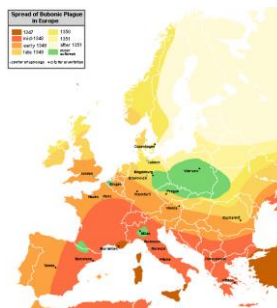
Connected, highly populated areas
(cities)

Human societies have “**crowd diseases**”, which are the consequences of large, interconnected populations (Measles, tuberculosis, smallpox, influenza, common cold, ...)

Network Science: Robustness Cascades www.south-east.ac.uk

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14th Century – The Great Plague



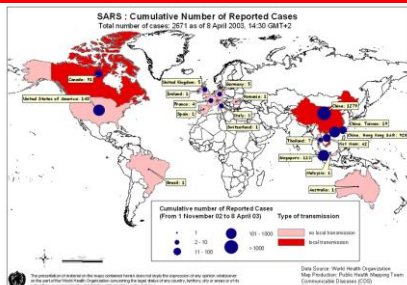
4 years from France to Sweden

Limited by the speed of human travel

http://en.wikipedia.org/wiki/Black_Death
http://de.wikipedia.org/wiki/Schwarzer_Tod

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21st Century – SARS

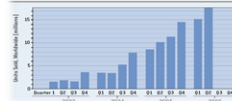


Source: World Health Organization

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Computer Viruses, Worms, Mobile Phone Viruses

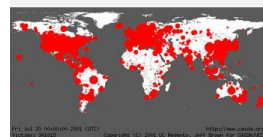
SMARTPHONES ON THE RISE



GROWTH IN MOBILE MALWARE



Code Red Worm paralyzed many countries' Internet

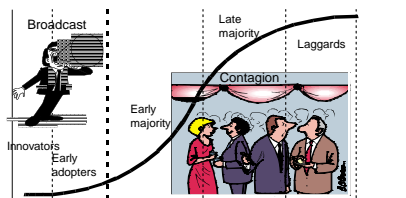


<http://www.caida.org/publications/visualizations/>

Hypponen M. *Scientific American* Nov. 70-77 (2006).

12

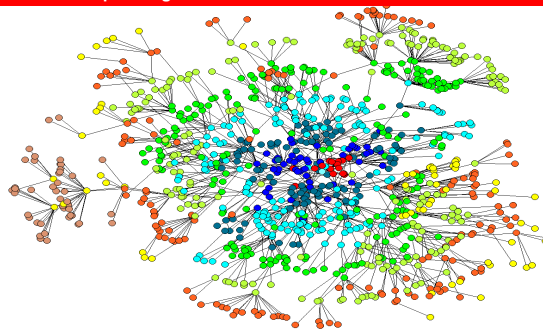
Diffusion of Innovation – The Adoption Curve



Reference unknown

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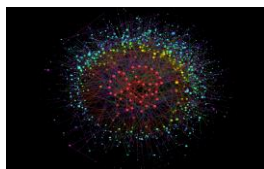
Information Spreading



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Diffusion and epidemic processes in real-world networks

- ✗ Birth-death processes
- ✗ Lattice gases
- ✗ Catalytic reactions
 - ✗ (Ziff-Gulari-Barshad model)
- ✗ Transport in random media
- ✗ Epidemic processes
- ✗ Packets routing
- ✗ Opinion spreading
- ✗ Stochastic data dissemination
- ✗ Pattern formation
- ✗

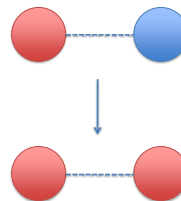


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Epidemic Spreading – Network

- Epidemic spreading always implies network structure!

Spreading happens only when the carries of the diseases/virus/idea are connected to each other.



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Epidemic Spreading – Network

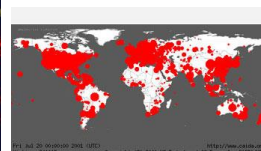


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Epidemic Spreading – Network



The transportation network

L. Hufnagel et al. *PNAS* **101**, 15124 (2004)

Internet

<http://www.caida.org/publications/visualizations/>

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Types of Spreading Phenomena and Networks

Phenomena	Network	Agent
Venereal disease	Sexual network	pathogens
Other infectious disease	Contact network, transport network	pathogens
Rumor spreading	Communication network	Information, memes
Diffusion of innovation	Communication network	Ideas
Internet worms	Internet	Malwares (binary strings)
Mobile phone virus	Social network / proximity network	Malwares (binary strings)
Bedbugs	Hotel – traveler network	Bedbugs
Malaria	Mosquito – Human network	<i>Plasmodium</i>

Network Science: Robustness Cascades (Nov 12, 2017)

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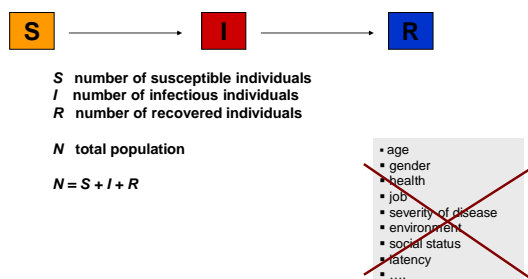
Classical Models of Epidemics

Epidemic Modeling
(classical models)

Network Science: Robustness Cascades (Nov 12, 2017)

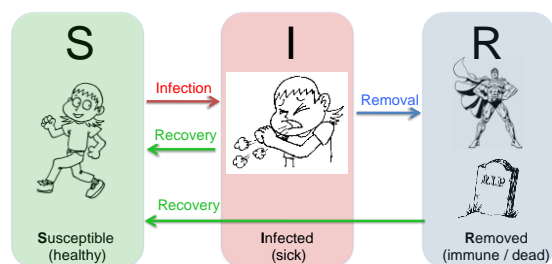
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SIR Model



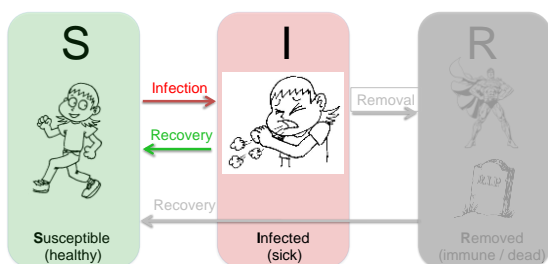
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Classical Epidemic Models – Basic States



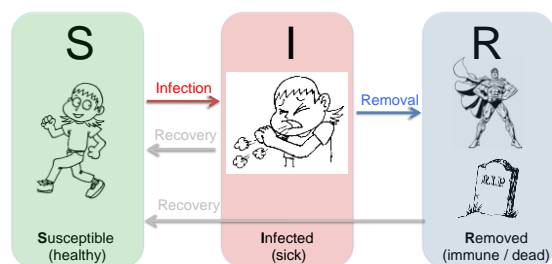
22

SIS Model: Common Cold



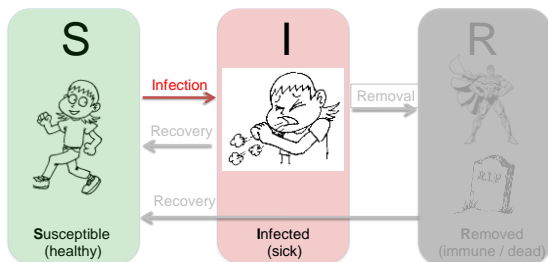
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Example 2: Flu, SARS, Plague, ...



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Simplest Model: SI



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SI Model: Homogeneous Mixing (No network)



Each individual has β infectious contacts with randomly chosen others individuals per unit time.

If there are I infected individuals and S susceptible individuals, the average rate of new infection is $b \frac{S}{N} I$
 with fraction of susceptible $s = S/N$,
 with fraction of infected $i = I/N$

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

M. E. J. Newman, Networks: an introduction

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SI Model: Dynamics

Susceptible + Infected \rightarrow more Infected

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

$$i(t) = \frac{i_0 \exp(bt)}{1 - i_0 + i_0 \exp(bt)}$$

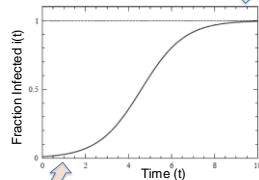
Logistic equation: a basic model of population growth. http://en.wikipedia.org/wiki/Logistic_function
<http://mathworld.wolfram.com/LogisticEquation.html>

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SI Model – Behavior

$$\frac{di}{dt} = bi(1 - i) \quad i(t) = \frac{i_0 \exp(bt)}{1 - i_0 + i_0 \exp(bt)}$$

If $i(t)$ is small,
 $\frac{di}{dt} \gg bi$
 $i \gg i_0 \exp(bt)$
 exponential outbreak

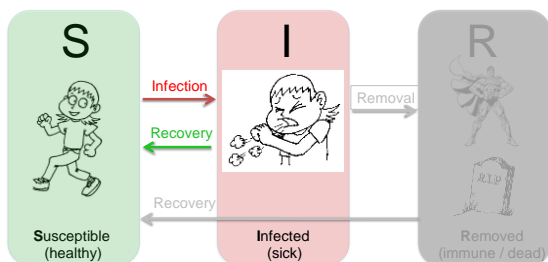


As $i(t) \rightarrow 1$,
 $\frac{di}{dt} \rightarrow 0$
 saturation

SI model: the fraction infected increases until everyone is infected.

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SIS Model: Common Cold



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SIS Model

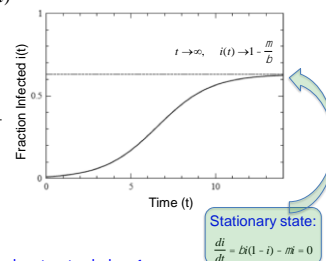
$$\frac{di}{dt} = bi(1 - i) - m\bar{i} = i(b - m - bi)$$

$$i(t) = \left(1 - \frac{m}{b}\right) \frac{Ce^{(b-m)t}}{1 + Ce^{(b-m)t}}$$

If $m \approx b$, $i \rightarrow 0$

"Epidemic threshold"

SIS model: fraction infected individuals saturates below 1.



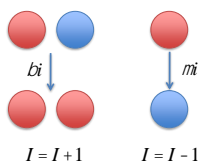
Stationary state:
 $\frac{di}{dt} = bi(1 - i) - m\bar{i} = 0$

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SIS Model: Epidemic Threshold and Basic Reproductive Number

$$\frac{di}{dt} = \underbrace{bi(1-i)}_{I \rightarrow S} - \underbrace{mi}_{I \rightarrow S}$$

If $m \approx b$, $i \rightarrow 0$
"Epidemic threshold"



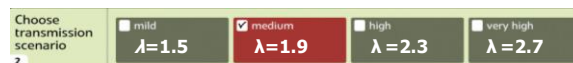
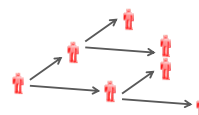
$I \propto \frac{b}{m}$ "Basic reproductive number"
On average, how many infected individuals will be infected by one infected individual?

$I > 1$: Outbreak, $I < 1$: Die out

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reproductive number λ : average # of infectious individuals generated by one infected in a fully susceptible population.

e.g. $\lambda = 2$



Vespignani

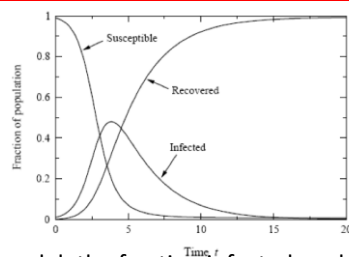
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R0 parameter

Disease	Transmission	R0
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)	Airborne droplet	2–3

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SIR Model



- SIR model: the fraction infected peaks and the fraction recovered saturates.

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Basic features of epidemic models

Early behavior:

Exponential growth of infected individuals

$$i(t) = \frac{i_0 \exp(bt)}{1 - i_0 + i_0 \exp(bt)} \quad i(t) = \left(1 - \frac{m}{b}\right) \frac{C e^{(b-m)t}}{1 + C e^{(b-m)t}}$$

Late behavior:

Saturation at $t \rightarrow \infty$

$$i(t) \rightarrow 1 \quad i(t) \rightarrow 1 - \frac{m}{b}$$

Epidemic threshold:

Disease does not always spread

$$\text{No threshold } I_c = 1 \quad I \propto \frac{b}{m}$$

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Epidemics on Networks

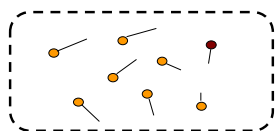
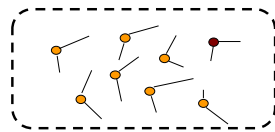
The approaches described above have not considered explicitly that the spreading takes place on a network – they assumed *homogenous mixing*, which means that each individual can infect *any* other individual.

In reality, epidemics spread along *links in a network* → we need to explicitly account for the role of the network in the epidemic process.

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SIS model on a network: Degree based representation

Class of nodes with degree $k=1$ Class of nodes with degree $k=2$

Split nodes by their degrees

$$i_k = \frac{I_k}{N_k}, \quad i = \sum_k P(k) i_k$$

SIS model:

$$\frac{di_k(t)}{dt} = b(1 - i_k(t))kQ_k(t) - m i_k(t)$$

Proportional to k Density of infected neighbors of nodes with degree k I am susceptible with k neighbors, and $Q_k(t)$ of my neighbors are infected.

(Vespignani)

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ROBUSTNESS IN COMPLEX SYSTEMS

Epidemics on Networks
(early time behavior)

Network Science: Robustness Cascades (Nov 20, 2017)

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Early time behavior of an epidemic

Why do we care about the early behavior of an epidemic?

- vaccines, cures, and other medical interventions take months to years to develop
- the best way to stop or slow down an epidemic:
 - early quarantine
 - early vaccination
- SI model is the most relevant for early stages

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Early time behavior – SI model

$t = \frac{\langle k \rangle}{b(\langle k^2 \rangle - \langle k \rangle)}$ The timescale it takes for an epidemics to grow. The smaller is τ , the faster it grows.

ER network:
 $\langle k^2 \rangle = \langle k \rangle (\langle k \rangle + 1)$ $t_{ER} = \frac{1}{b\langle k \rangle}$

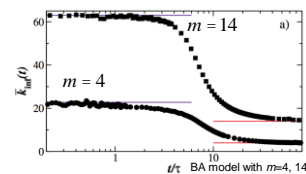
→ The more connected the network is, the faster does the epidemic spread.

SF network ($\gamma < 3$):
 $\langle k^2 \rangle \rightarrow \infty$ for $N \rightarrow \infty \rightarrow \tau \rightarrow 0$

For heterogeneous networks, the characteristic time vanishes, which means that the epidemic becomes instantaneous. The reason: the hubs get infected first, which then rapidly reach most nodes.

Numerical Test:
 The average degree of newly infected nodes at time t

$$\bar{k}_{new}(t) = \frac{\sum_k k (I_k(t) - I_k(t-1))}{I(t) - I(t-1)}$$



M. Barthélemy et al., PRL 92, 178701 (2004)

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Early time behavior – SIR model

SI model

$$t = \frac{\langle k \rangle}{b(\langle k^2 \rangle - \langle k \rangle)}$$

The timescale it takes for an epidemics to grow. The smaller is τ , the faster it grows.

SIR model

$$\tau = \frac{\langle k \rangle}{b(\langle k^2 \rangle - (\mu + \beta)\langle k \rangle)}$$

$$t_{ER} = \frac{1}{b\langle k \rangle}$$

ER network: $\langle k^2 \rangle = \langle k \rangle (\langle k \rangle + 1)$

$$t_{ER} = \frac{1}{b\langle k \rangle - m}$$

SF network ($\gamma < 3$):
 $\langle k^2 \rangle \rightarrow \infty$ for $N \rightarrow \infty \rightarrow \tau \rightarrow 0$

For heterogeneous networks, the characteristic time vanishes, which means that the epidemic becomes instantaneous.

M. Barthélemy et al., PRL 92, 178701 (2004)

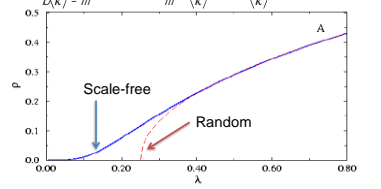
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SIR Model – Epidemic Threshold

In order to have an epidemic outbreak, we must have $\tau > 0$.

SIR for a random (ER) network:

$$t_{ER} = \frac{1}{b\langle k \rangle - m} > 0 \rightarrow l = \frac{b}{m} > \frac{1}{\langle k \rangle} \quad l_c = \frac{1}{\langle k \rangle} \quad \text{Epidemic threshold}$$



SIR for a SF network: $t = \frac{\langle k \rangle}{b(\langle k^2 \rangle - (m + b)\langle k \rangle)} > 0 \rightarrow l = \frac{b}{m} > l_c = \frac{1}{\langle k \rangle} - 1$

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ROBUSTNESS IN COMPLEX SYSTEMS

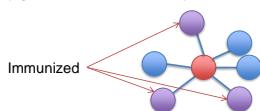
Immunization Strategies

Network Science: Robustness Cascades 10/11/12, 2017

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Immunization strategies

A density g individuals are randomly chosen to be immunized.



$$b \rightarrow b(1 - g)$$

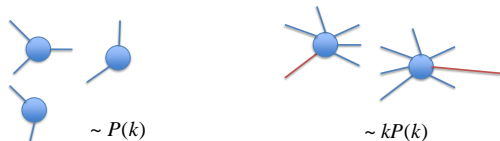
If $\langle k^2 \rangle \rightarrow \infty$, Random immunization cannot prevent the outbreak.

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Immunization strategies – without global knowledge

In many cases, you cannot figure out who are the hubs.

Can we effectively immunize the population when we don't know the node degrees?



If you follow an edge, you are likely to meet high-degree nodes!

Select a random individual, then immunize one of its RANDOMLY CHOSEN FRIENDS.

R. Cohen et al., PRL 91, 247901 (2003)

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How to control the epidemic?

- Transmission-reducing interventions: face masks, gloves, washing hands – may reduce the transmission rate below the epidemic-causing critical rate
- Contact-reducing interventions: quarantining a patient, closing schools – make the network sparser, may increase the critical transmission rate
- Vaccinations: remove nodes from the network
- Q: Who should be vaccinated for most effective control?

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Vaccination strategies in scale-free networks

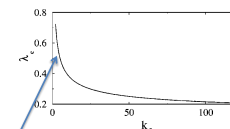
As hubs are responsible for the spread of the disease \rightarrow cure the hubs.

Targeted immunization – immunize all nodes with degree $k > k_0$.

$$\lambda_c = \frac{\langle k \rangle}{\langle k^2 \rangle} = \frac{k_0 - m}{k_0 m} \left(\frac{k_0}{m} \right)^{-1}$$

As the hubs are removed, the $\langle k^2 \rangle$ term decreases, hence the epidemic threshold will go to higher values

With increasing critical point increases, it is harder for a virus to spread.



Z. Dezso and A.-L. Barabási, Phys. Rev. E 65, 055103 (2002);
R. Pastor-Satorras and A. Vespignani, Phys. Rev. E 65, 036104 (2002)

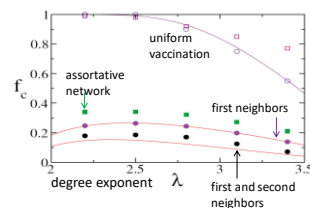
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A local method for vaccination effective in scale-free networks

Contact network described by scale-free random graph

Immunization strategy: select a node randomly, immunize a randomly selected neighbor of it.

Use theory and simulations to determine the critical immunization fraction for each transmissibility value



R. Cohen et al, Phys. Rev. Lett 91, 247901 (2003)

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Modelling Outbreaks

Plotting the pandemic

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Modelling the outbreak



<http://www.aaronkoblin.com/work/flightpatterns/interactiveMap.html>

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Modelling the outbreak

The real-time prediction of an epidemic outbreak is a very recent development. The ground was set by the development of the epidemic modeling framework in the 1980s and by the 2003 SARS epidemic, which resulted in worldwide reporting guidelines that allows the collection and sharing of real time data pertaining to a pandemic, serving as input to modeling efforts.

The **2009 H1N1** outbreak was the first test of this new framework, also becoming the first pandemic whose spread was predicted by modeling efforts in real time.

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Modelling the outbreak

The discovery of a new pathogen raises several key questions:

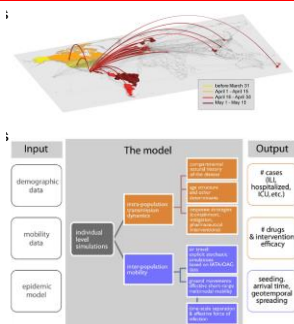
- Where did the pathogen originate?
- Where do we expect new cases?
- When will the epidemic arrive at various densely populated areas?
- How many infections are to be expected?
- What can we do to slow it down, offering local agencies time to prepare for it?

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Modelling the outbreak

The flowchart of the Global Epidemic and Mobility (GLEAM) computational model, used to predict the real-time spread of the H1N1 virus.

- The **left column** (Input) represents the input databases capturing demographic, mobility and epidemiological information.
- The **center column** (model) describes the dynamic processes that are modeled at each time step.
- The **right column** (Output) offers examples of quantities the model can predict.



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Modelling the outbreak

GLEAM implements the network-based epidemic framework encountered in the previous sections, generating a large number of potential outcomes of the pathogen's global progression for the coming months. The predictions for H1N1 were later compared with data collected from surveillance and virologic sources in 48 countries during the full course of the pandemic, resulting in several key findings:

Peak Time: Peak time denotes the week when the largest number of individuals are infected in a particular country. Knowing the peak time can help decision makers decide the timing and the quantity of the vaccines or treatments they need to distribute. The observed peak time fell within the prediction interval for 87% of the countries (Figure 10.30). In the remaining cases the difference between the real and the predicted peak was at most two weeks.

Early Peak: The forecast predicted that the H1N1 epidemic will peak out in November, rather than in January or February, the typical peak time of most influenza-like viruses. This unexpected prediction turned out to be correct, confirming the model's predictive power.

The impact of vaccination: Several countries implemented vaccination campaigns to accelerate the decline of the pandemic. The simulations indicated that these mass vaccination campaigns had only negligible impact on the course of the epidemic. The reason is that the timing of these campaigns was guided by the expectation of a January peak time, prompting the deployment of

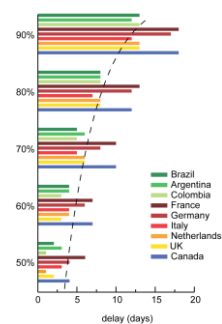


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Modelling the outbreak

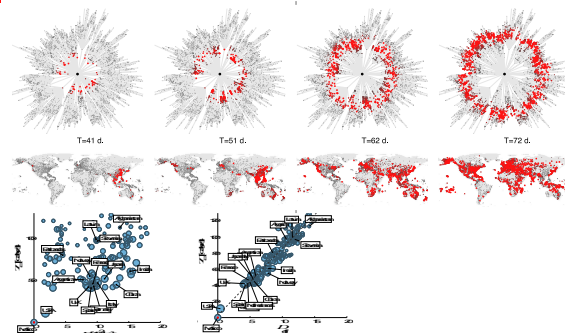
H1N1

Delay in arrival for
different levels of travel
restriction



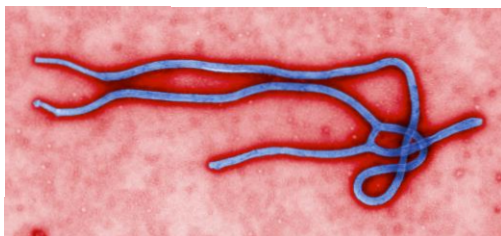
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Modelling the outbreak – effective distance



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Worlds deadliest outbreak



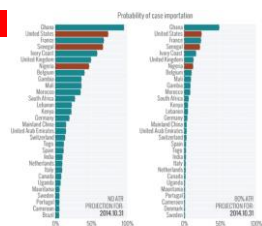
60

Worlds deadliest outbreak

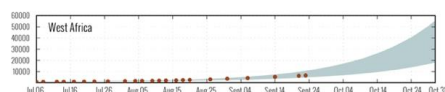


61

Worlds deadliest outbreak



Overestimation of risk: Underestimation of probability of reporting a case of Ebola by 10 October. But there are nations that have already experienced case importation. GDP (in our right column) GDP reflects travel before the case appeared in West Africa. GDP (in our left column) reflects the current reduction in air traffic in and from countries with Ebola. (Image: Alessandro Vespignani / www.mohs-lab.org)



Projection for the total number of Ebola cases in West Africa by 31 October. Red circles are reported cases. Gray area is the range of projected cases, based on a worst-case scenario where the epidemic continues to grow exponentially. (Image: Alessandro Vespignani / www.mohs-lab.org)

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The end

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