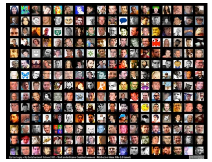


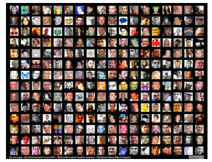
Social and Technological Network Analysis

Lecture 8: Epidemics Spreading

Dr. Vincenzo Nicosia
Dr. Cecilia Mascolo

UNIVERSITY OF CAMBRIDGE

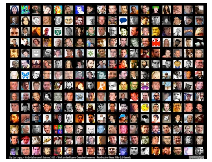
In This Lecture



- In this lecture we introduce the process of spreading epidemics in networks.
  - This has been studied widely in biology.
  - But it also has important parallels in information/idea diffusion in networks.

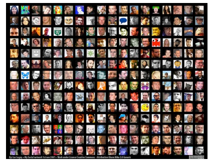
UNIVERSITY OF CAMBRIDGE

Epidemics vs Cascade Spreading



- In cascade spreading nodes make decisions based on pay-off benefits of adopting one strategy or the other.
- In epidemic spreading
  - Lack of decision making.
  - Process of contagion is complex and unobservable
    - In some cases it involves (or can be modeled as randomness).

UNIVERSITY OF CAMBRIDGE

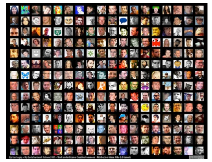


Branching Process

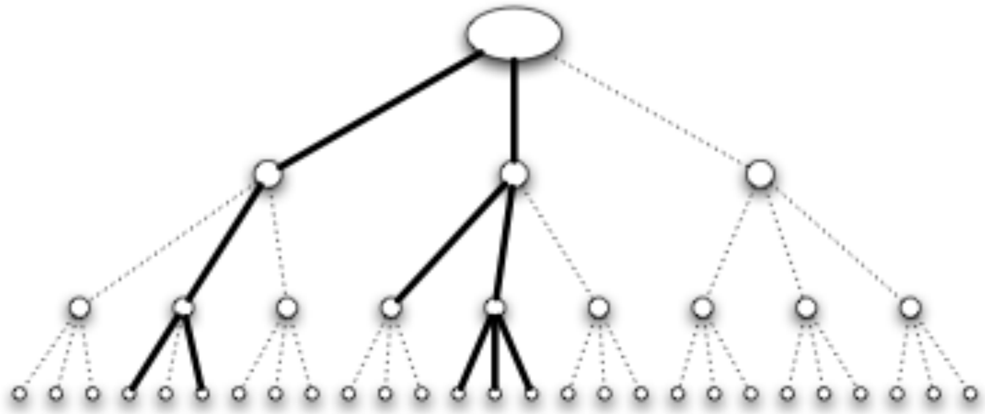
- Simple model.
- **First wave:** A person carrying a disease enters the population and transmit to all he meets with probability p. He meets k people: a portion of which will be infected.
- **Second wave:** each of the k people goes and meet k different people. So we have a second wave of $k \times k = k^2$ people.
- **Subsequent waves:** same process.

UNIVERSITY OF CAMBRIDGE

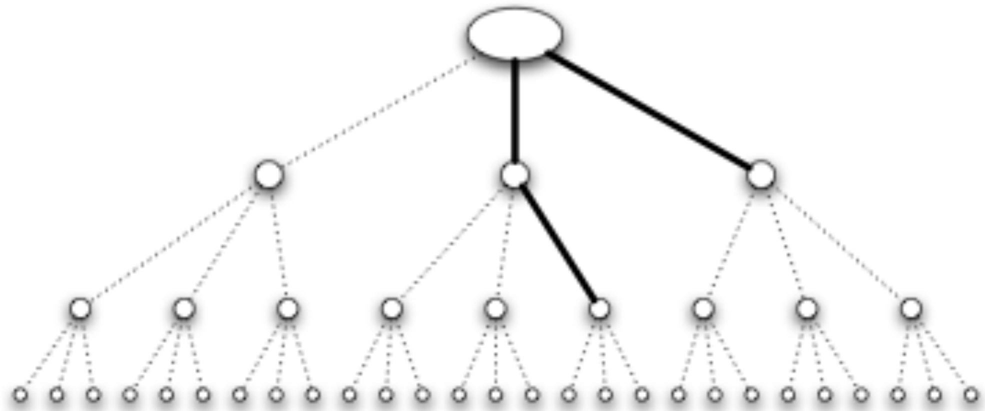
Example with k=3



High contagion probability:
The disease spreads

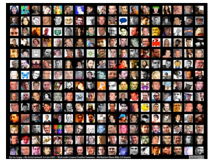


Low contagion probability:
The disease dies out



UNIVERSITY OF CAMBRIDGE

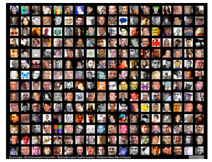
Basic Reproductive Number



- Basic Reproductive Number $R_0=p*k$
  - It determines it the disease will spread or die out.
- In the branching process model, if $R_0<1$ the disease will die out after a finite number of waves. If $R_0>1$, with probability >0, the disease will persist by infecting at least one person in each wave.

UNIVERSITY OF CAMBRIDGE

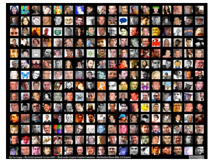
Measures to limit the spreading



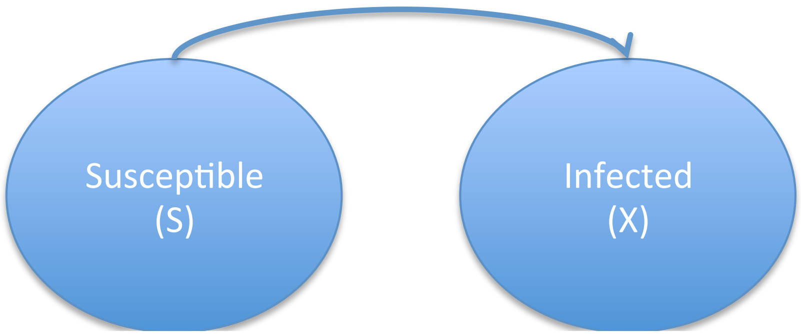
- When R_0 is close 1, slightly changing p or k can result in epidemics dying out or happening.
  - Quarantining people/nodes reduces k.
  - Encouraging better sanitary practices reduces germs spreading [reducing p].
- Limitations of this model:
  - No realistic contact networks: no triangles!
  - Nodes can infect only once.
  - No nodes recover.

UNIVERSITY OF CAMBRIDGE

Formal Epidemics Models
The SI Model



- S: susceptible individuals.
- X: infected individuals, when infected they can infect others continuously (different from before).
- n: total population.
- $<k>$ average contacts per individual
- $\beta=\lambda<k>$ is the infection rate per individual $(0\leq\lambda\leq1)$
- Susceptible contacts per unit of time $\beta S/n$.
- Overall rate of infection $X\beta S/n$.



UNIVERSITY OF CAMBRIDGE

SI Model

$$\frac{dX}{dt} = \beta \frac{SX}{n}$$

$$\frac{dS}{dt} = -\beta \frac{SX}{n}$$

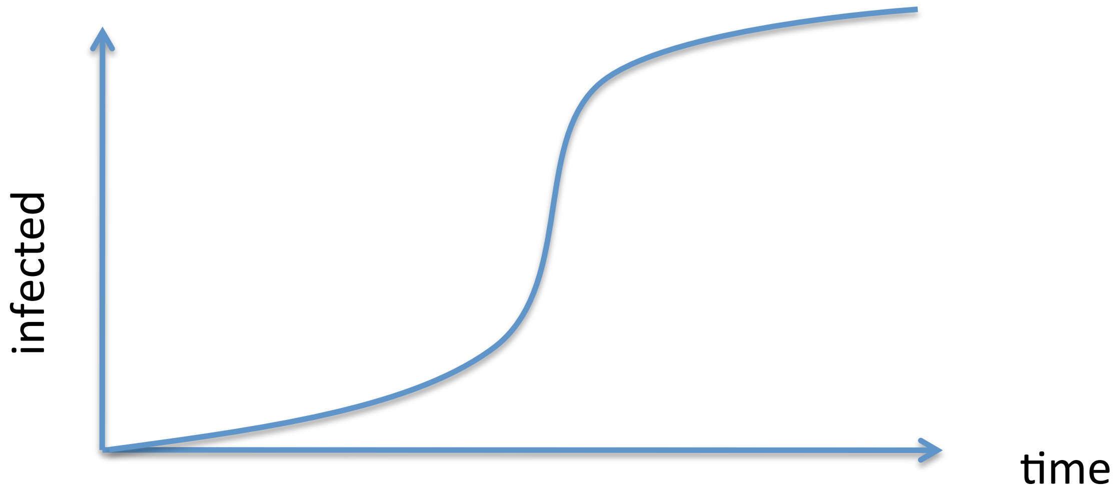
$$s = \frac{S}{n} \qquad x = \frac{X}{n}$$

$$s = 1 - x$$

$$\frac{dx}{dt} = \beta x(1 - x)$$

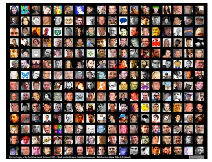
$$x(t) = \frac{x_0 e^{\beta t}}{1 - x_0 + x_0 e^{\beta t}}$$

Logistic Growth Equation



UNIVERSITY OF CAMBRIDGE

Microscopic explanation



- Probability for a node to not be infected from each infected contact: $1 - \lambda$
- Number of infected contacts per node: $\langle k \rangle x$
- Probability for a susceptible node to avoid infection from all its $\langle k \rangle x$ infected contacts: $p = (1 - \lambda)^{\langle k \rangle x}$
- Probability to be infected from at least one infected contact: $1 - p = 1 - (1 - \lambda)^{\langle k \rangle x}$
- If $\lambda \ll 1$ then $p \approx \lambda \langle k \rangle x = \beta x$
- Therefore, the increase of infected nodes reads:

$$\frac{dx}{dt} = \beta x s = \beta x(1 - x)$$

UNIVERSITY OF CAMBRIDGE

SIR Model

- Infected nodes recover at a rate γ.
- A node stays infected for τ time.
- Branching process is SIR with τ=1.

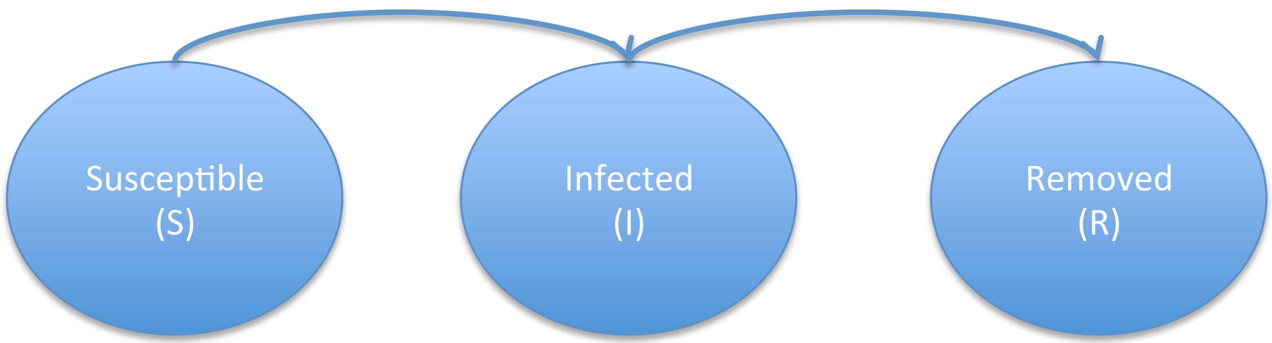
$$\frac{ds}{dt} = -\beta s x$$

$$\frac{dx}{dt} = \beta s x - \gamma x$$

$$\frac{dr}{dt} = \gamma x$$

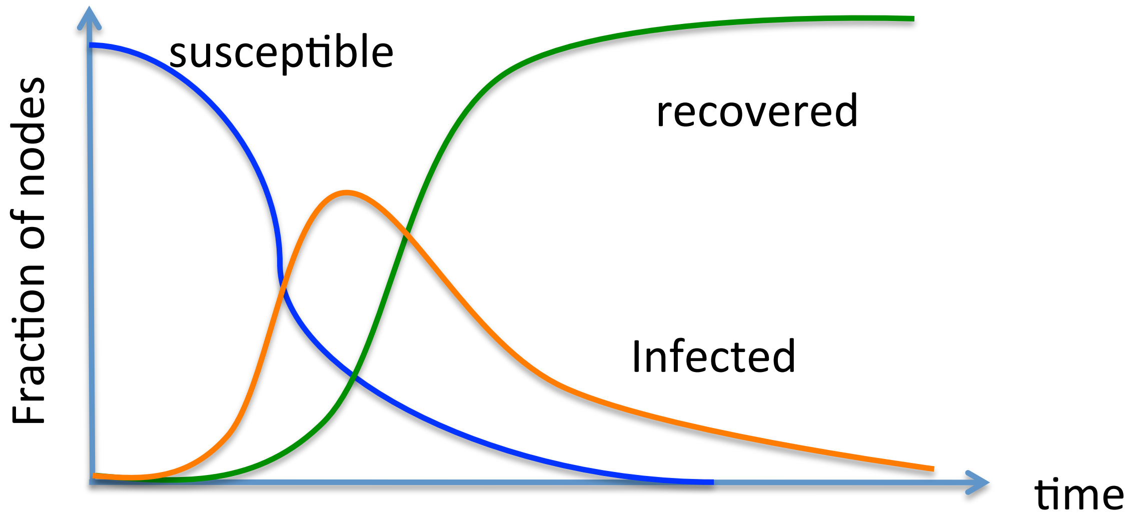
$$s + x + r = 1$$

UNIVERSITY OF CAMBRIDGE



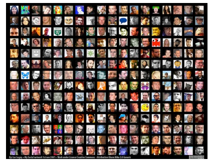
Example

- Numerical examples of solution:
- β=1, γ=0.4, s(at start)=0.99, x(at start)=0.01, r (at start)=0



UNIVERSITY OF CAMBRIDGE

Epidemic Threshold

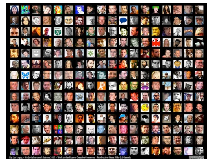


- When would the epidemic develop and when would it die out?

- It depends on the relationship of β and γ:
  - Basic Reproductive Number $R_0=\beta/\gamma$
  - If the infection rate [per unit of time] is higher than the removal rate the infection will survive otherwise it will die out.
  - In SI, $\gamma=0$ so the epidemics always happen.

UNIVERSITY OF CAMBRIDGE

Limitations of SIR



- Contagion probability is uniform and “on-off”

- Extensions

  – Probability q of recovering in each step.
  – Infected state divided into intermediate states (early, middle and final infection times) with varying probability during each.
  – **We have assumed homogenous mixing :** assumes all nodes encounter each others with same probability: we could assume different probability per encounter.

UNIVERSITY OF CAMBRIDGE

SIS Model

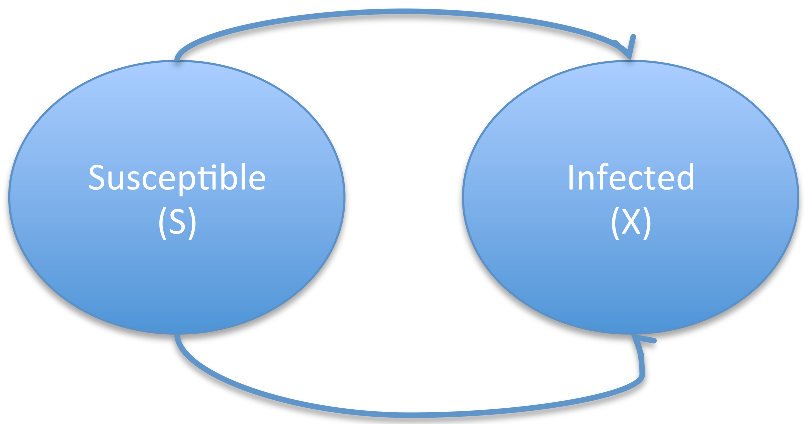
$$\frac{ds}{dt} = \gamma x - \beta s x$$

$$\frac{dx}{dt} = \beta s x - \gamma x$$

$$s + x = 1$$

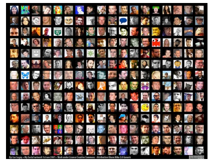
$$\frac{dx}{dt} = (\beta - \gamma - \beta x)x$$

- If $\beta > \gamma$ growth curve like in SI but never reaching all population infected. The fraction of infected->0 as β approaches γ.
- If $\beta < \gamma$ the infection will die out exponentially.
- SIS has the same R_0 as SIR.



UNIVERSITY OF CAMBRIDGE

Relaxing Assumptions



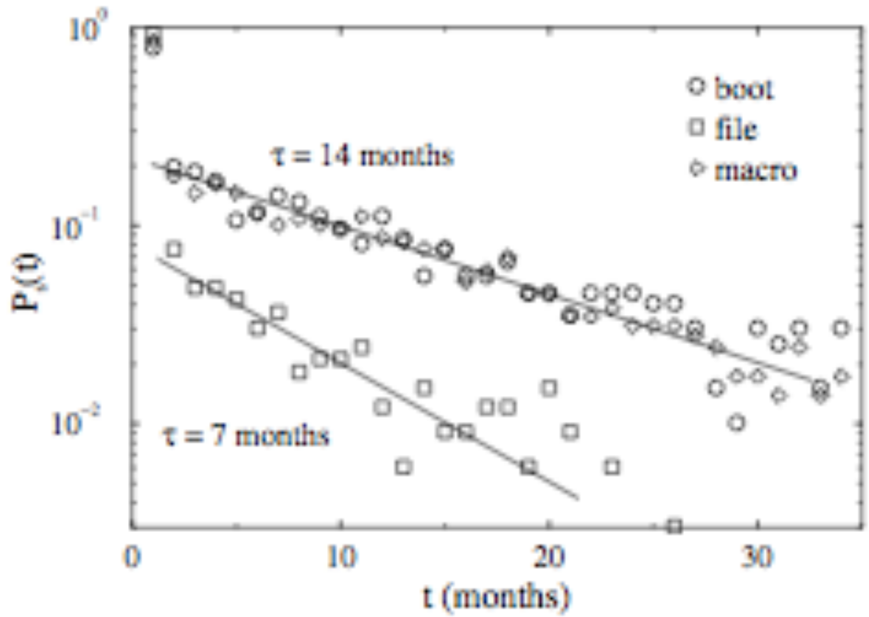
- Homogeneous Mixing: a node connects to the same average number of other nodes as any other.
- Most real networks are not Erdos-Renyi random networks (for which the homogeneous mixing assumption holds).
- Most networks have heterogeneous degree distributions.
  - Scale free networks!

UNIVERSITY OF CAMBRIDGE

Would the model apply to SF?

- Pastor-Satorras and Vespignani [2001] have considered the life of computer viruses over time on the Internet:

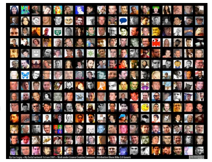
Surviving probability of virus



Virus survived on average 6-9/14 months depending on type

UNIVERSITY OF CAMBRIDGE

How to justify this survival time?

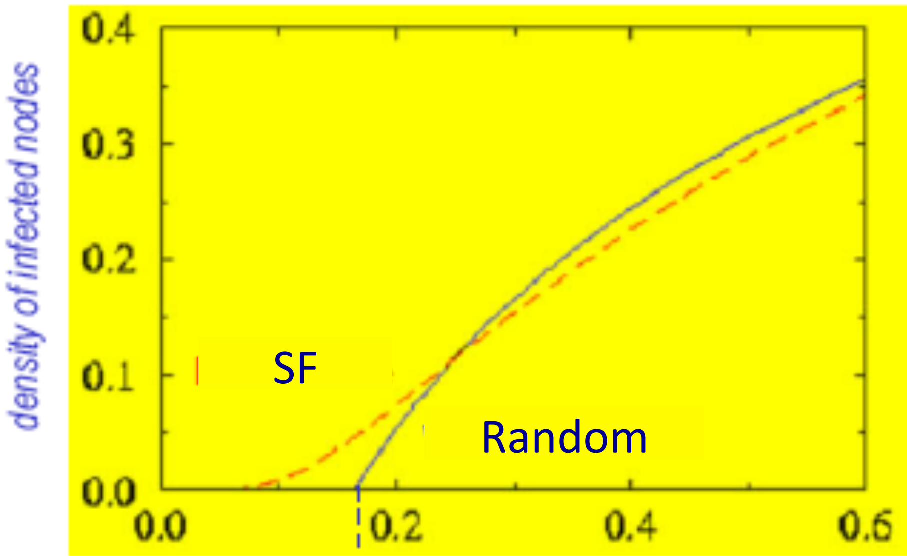


- The virus survival time is considerably high with respect to the results of epidemic models of spreading/recovering:
  - Something wrong with the epidemic threshold!

- Experiment: SIS over a generated Scale Free network (exponent -3).

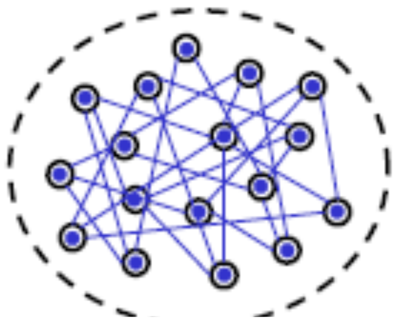
UNIVERSITY OF CAMBRIDGE

No Epidemic Threshold for SF!

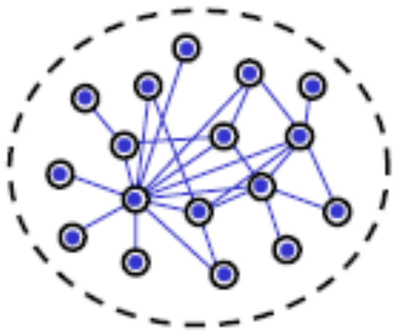


threshold

Infections proliferate in SF networks independently of their spreading rates!

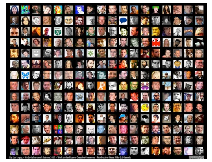


Random Network



Scale Free Network

UNIVERSITY OF CAMBRIDGE



The vanishing threshold

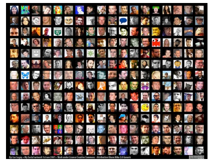
- Percentage of infected of degree k:

$$x_k(t) = i_0(1 + ck(e^{t/\tau} - 1))$$

$$\tau = \frac{\langle k \rangle}{\beta\left(\langle k^2 \rangle - \langle k \rangle\right)}$$

- Larger degree nodes are infected with higher probability
- In scale-free networks with $2<\gamma\leq 3$ $<k^2>$ diverges as $N \to \infty$, so the epidemic spreads very fast

UNIVERSITY OF CAMBRIDGE

Following result on Immunization 

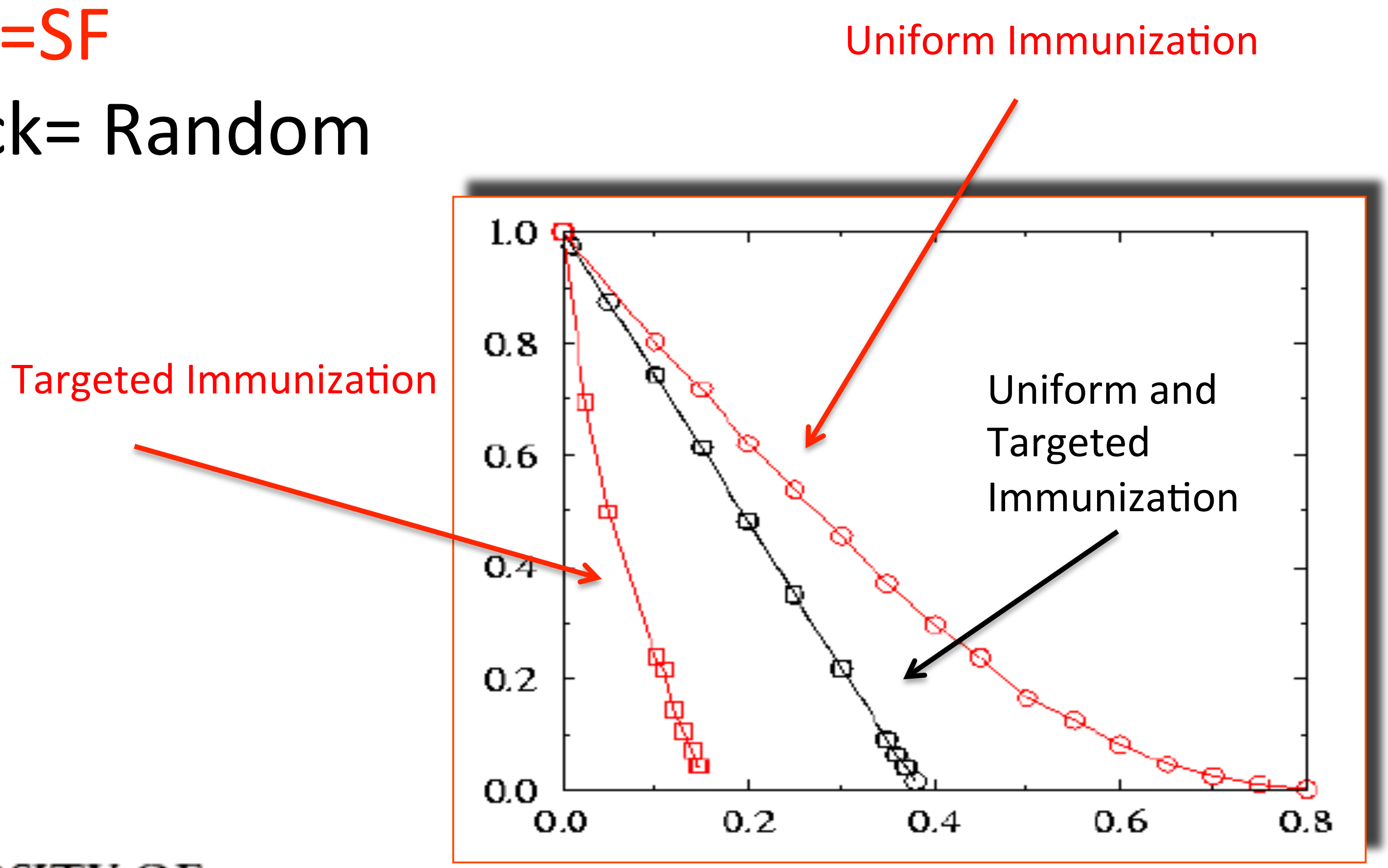
- Random network can be immunized with some sort of uniform immunization process [oblivious of the characteristics of nodes].

- **This does not work in SF networks** no matter how many nodes are immunized [unless it is all of them].
- Targeted immunization needs to be applied
  - Keeping into account degree!

UNIVERSITY OF CAMBRIDGE

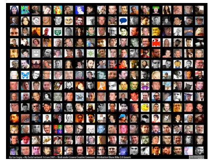
Immunization on SF Networks

- Red=SF
- Black= Random



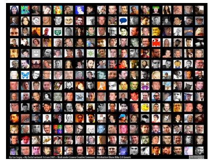
UNIVERSITY OF CAMBRIDGE

Local Immunization



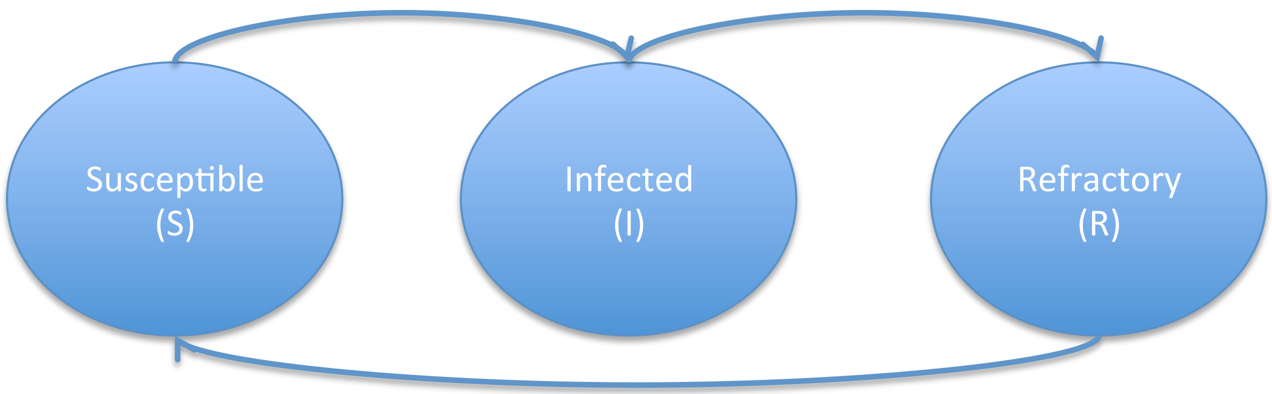
- Global knowledge on the network structure is rarely (or never) available
- Local immunization strategy:
  - Select *g* nodes at random
  - Ask to each of them to pass over the vaccine to one of their neighbors
  - As a result, a node with degree k is immunized with a probability kP(k) (hubs are immunized with higher probability!)

UNIVERSITY OF CAMBRIDGE



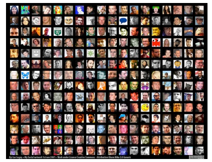
SIRS Model

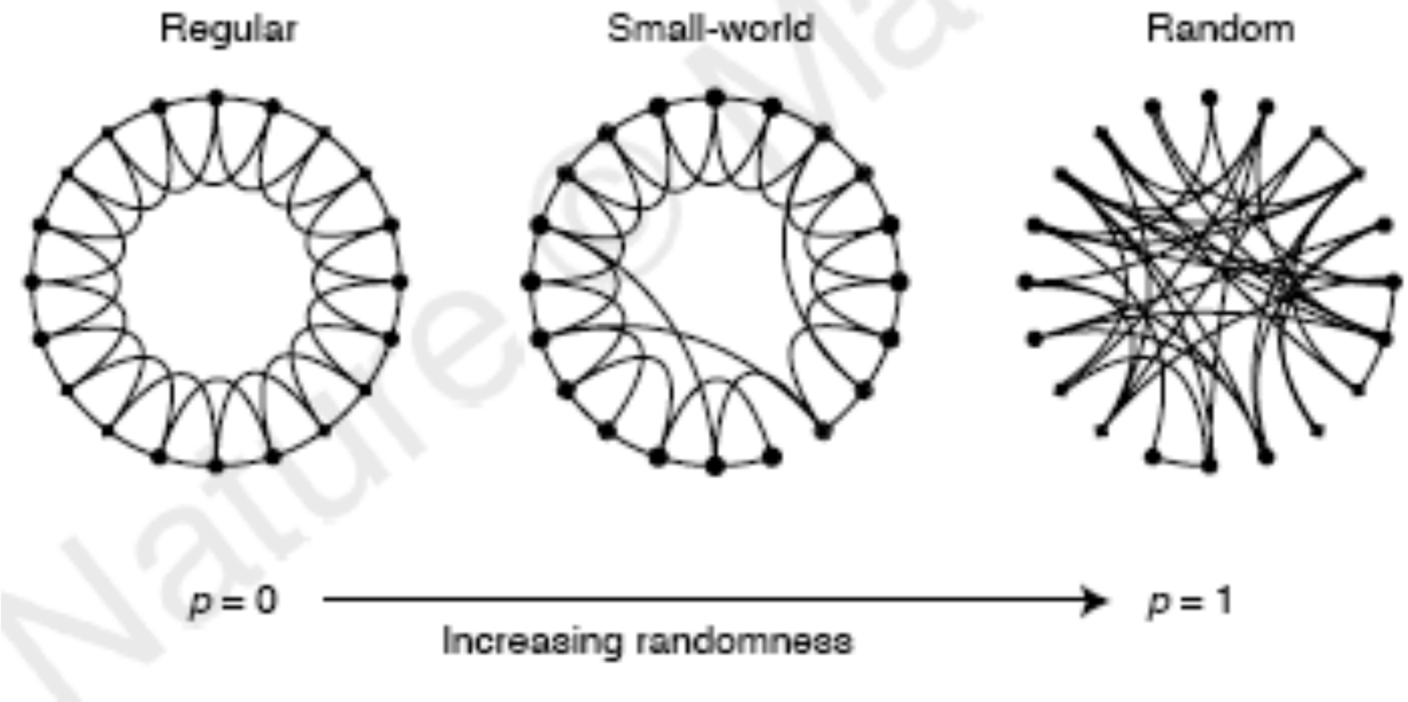
- SIR but after some time an R node can become susceptible again.
- A number of epidemics spread in this manner (remaining latent for a while and having bursts).



UNIVERSITY OF CAMBRIDGE

Application of SIRS to Small World Models

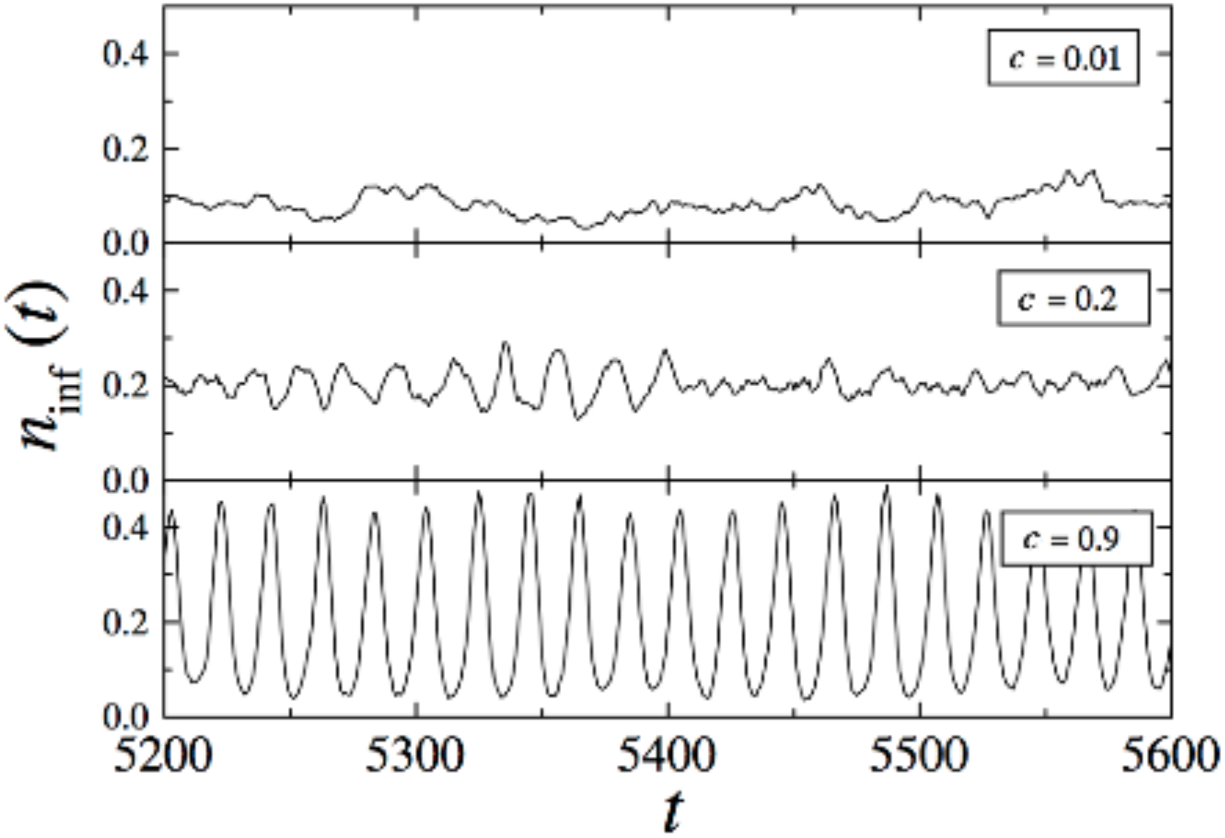




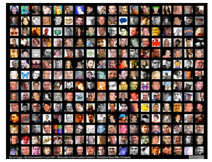
UNIVERSITY OF CAMBRIDGE

Numerical Results

- c is the rewiring probability



UNIVERSITY OF CAMBRIDGE

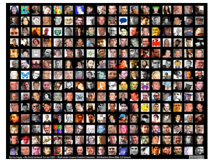


Summary

- Epidemics are very complex processes.
- Existing models have been increasingly capable of capturing their essence.
- However there are still a number of open issues related to the modelling of real disease spreading or information dissemination.

UNIVERSITY OF CAMBRIDGE

References



- Chapter 21
- Pastor-Satorras, R. and Vespignani, A. Epidemic Spreading in Scale-Free Networks. Phys. Rev. Lett. (86), n.14. Pages = 3200--3203. 2001.
- Pastor-Satorras, R. and Vespignani, A. Immunization of Complex Networks. Physical Review E 65. 2002.
- Marcelo Kuperman and Guillermo Abramson. Small world effect in an epidemiological model. Physical Review Letters, 86(13):2909–2912, March 2001.

UNIVERSITY OF CAMBRIDGE