Social and Technological Network Analysis

Lecture 8: Epidemics Spreading

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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.

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).

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 kxk=k^2 people.
- **Subsequent waves:** same process.

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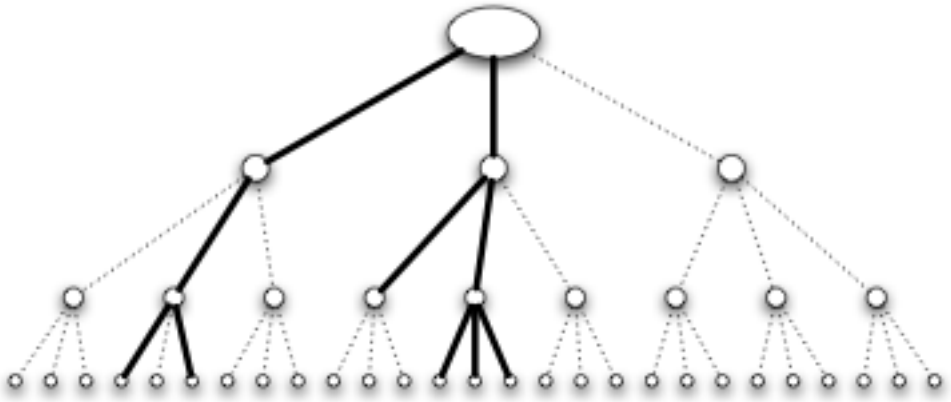
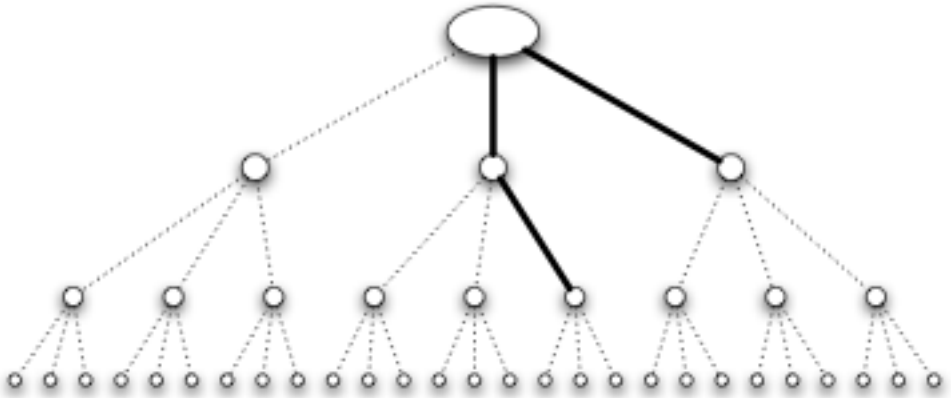
Example with k=3



High contagion probability:
The disease spreads

Low contagion probability:
The disease dies out



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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.

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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.

Formal Epidemics Models
The SI Model

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

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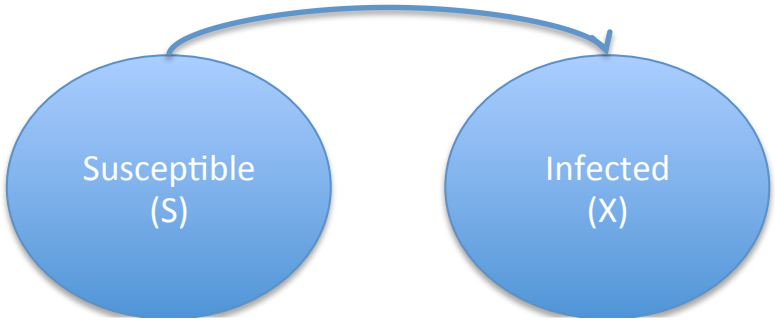


SI Model

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

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

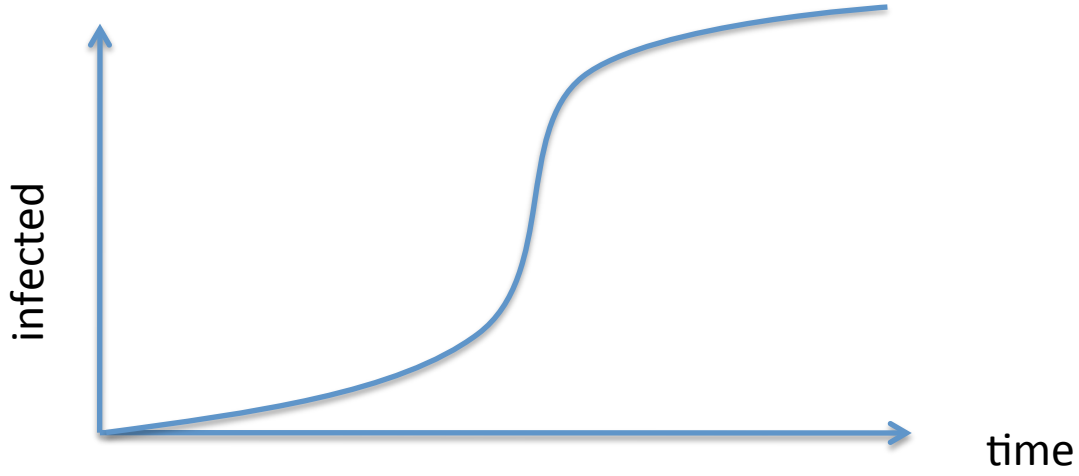
$$s = \frac{S}{n} \qquad x = \frac{X}{n}$$

$$s = 1 - x$$

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

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

Logistic Growth Equation



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SIR Model

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

$$\frac{ds}{dt} = -\beta sx$$

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

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

$$s + x + r = 1$$

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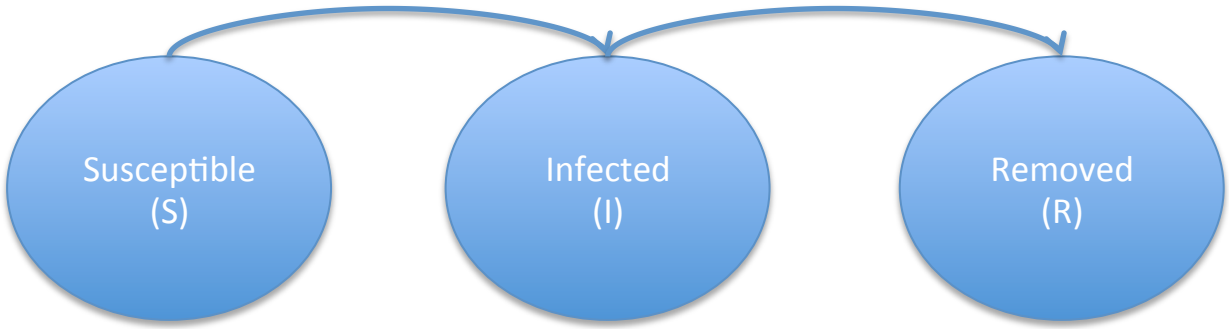
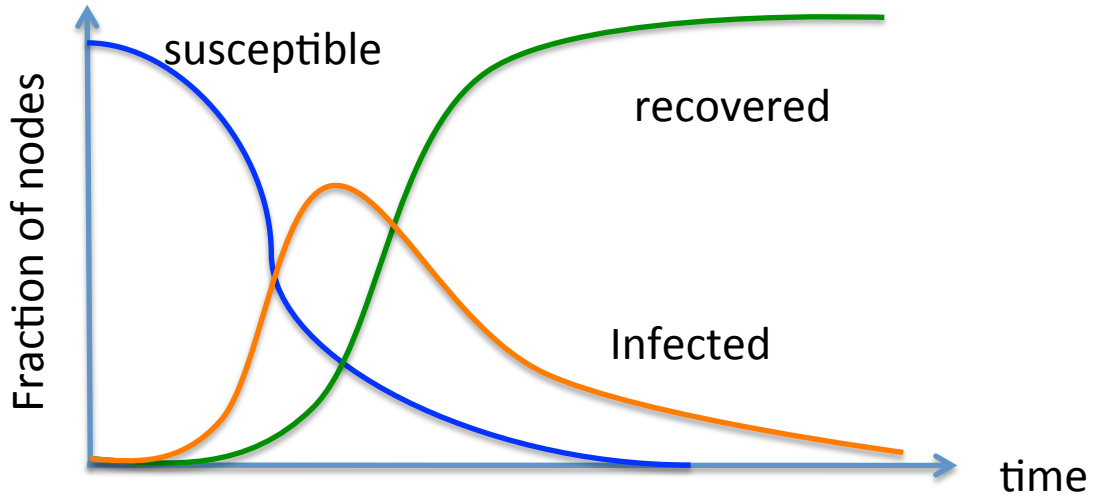


Example

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



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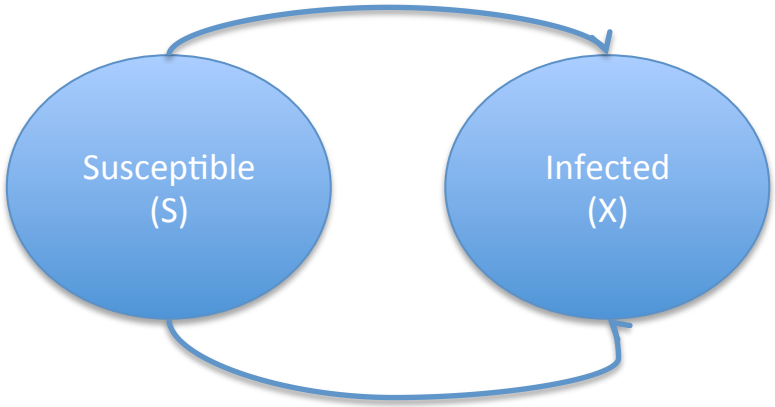
SIS Model

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

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

$$s + x = 1$$

- 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.



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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, γ=0 so the epidemics always happen.

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.

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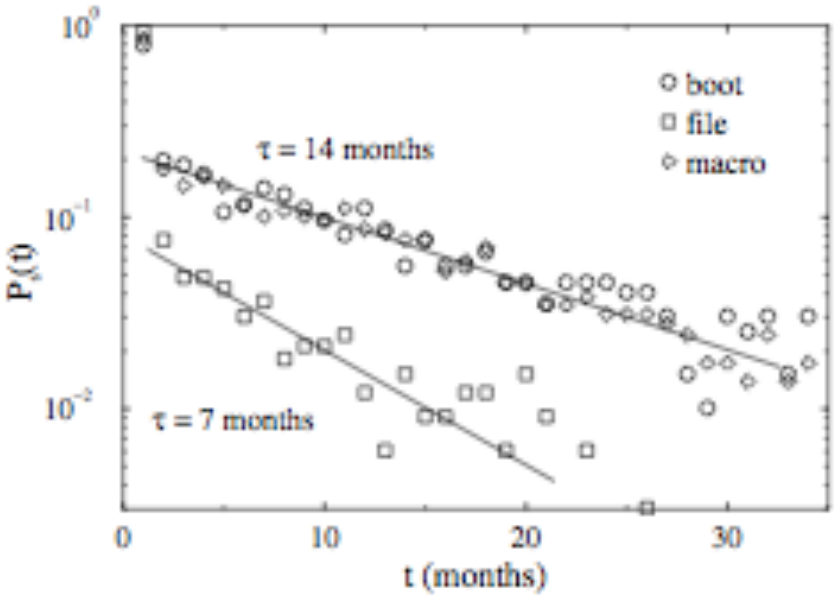
Relaxing Assumptions

- 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!

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

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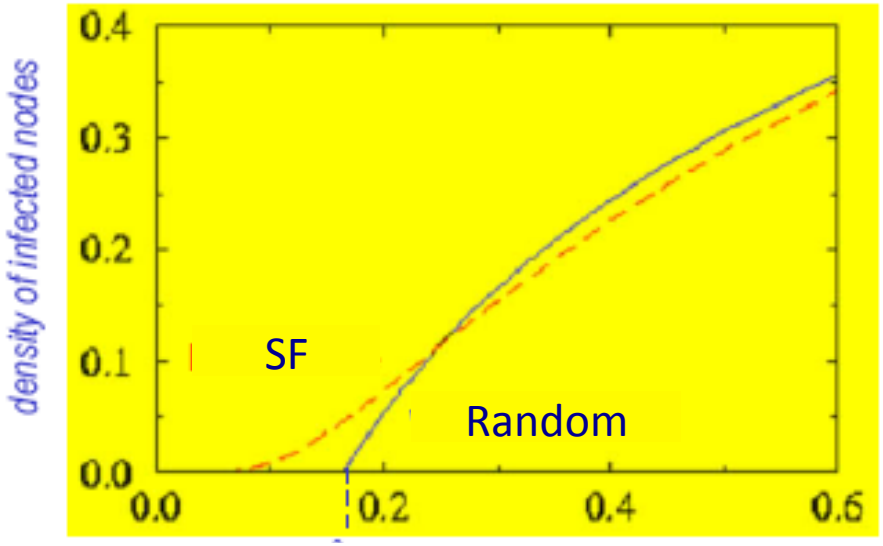
How to justify this survival time?

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

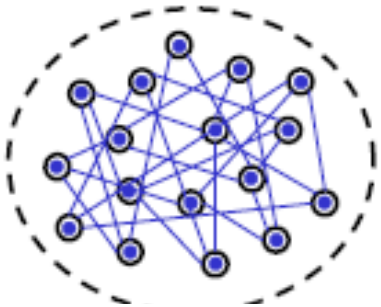
- Experiment: SIS over a generated Scale Free network (exponent -3).

No Epidemic Threshold for SF!

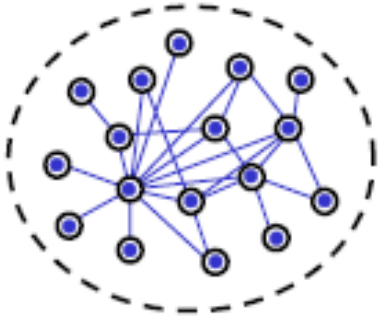


threshold

Infections proliferate in SF networks independently of their spreading rates!



Random Network



Scale Free Network

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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!

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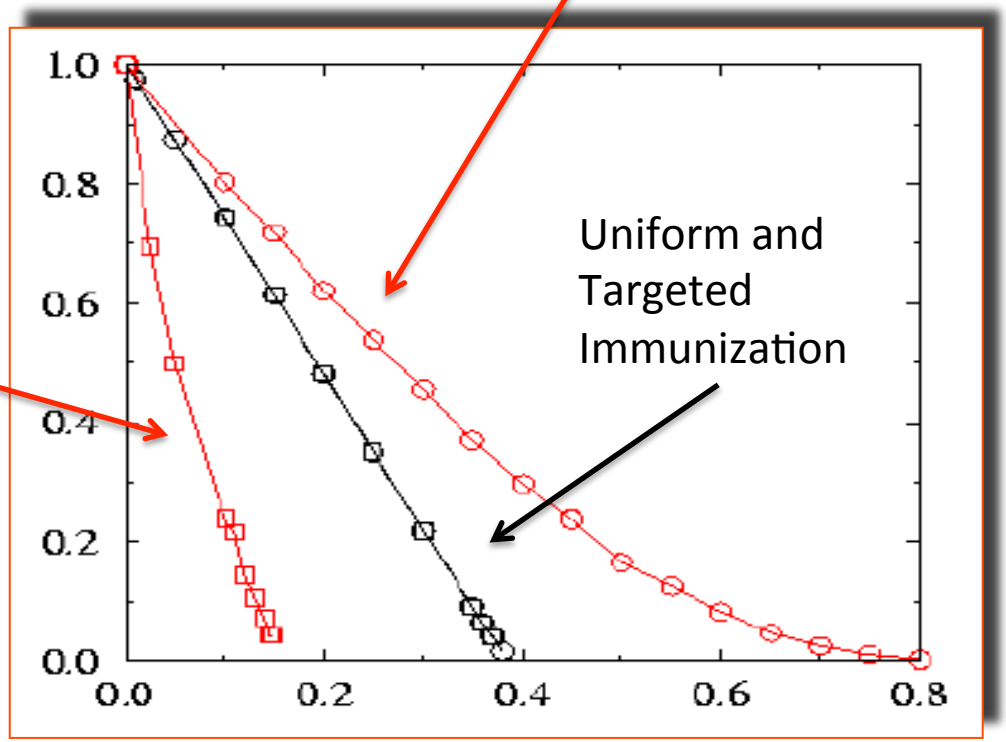
Immunization on SF Networks

- Red=SF
- Black= Random

Uniform Immunization

Targeted Immunization

Density of Infected



Fraction of immunized nodes

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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!)

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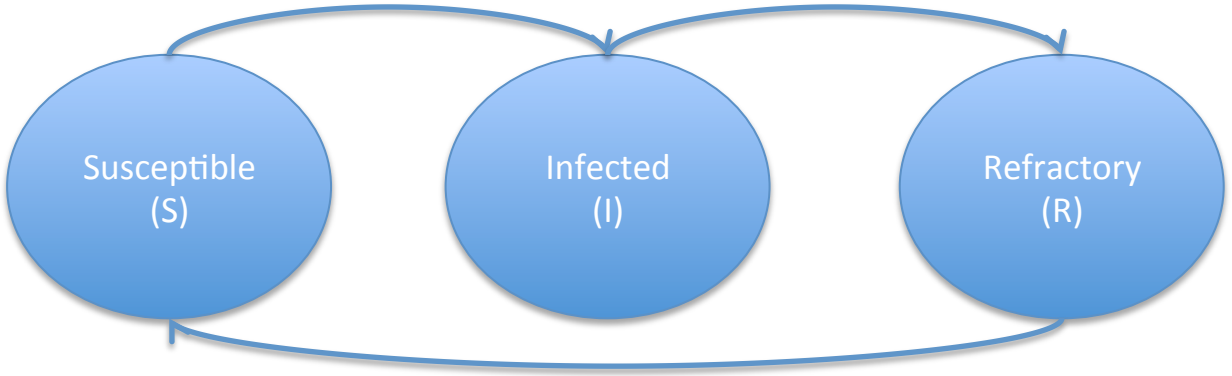
SIRS Model

- 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).



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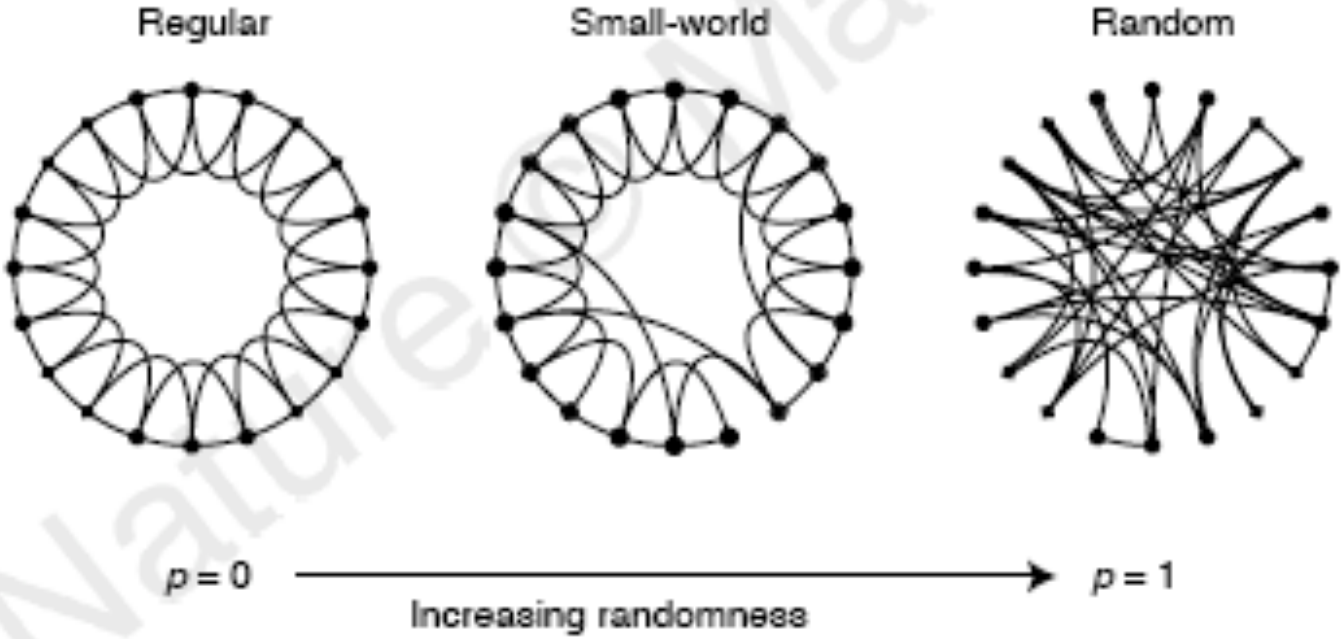
Application of SIRS to Small World Models



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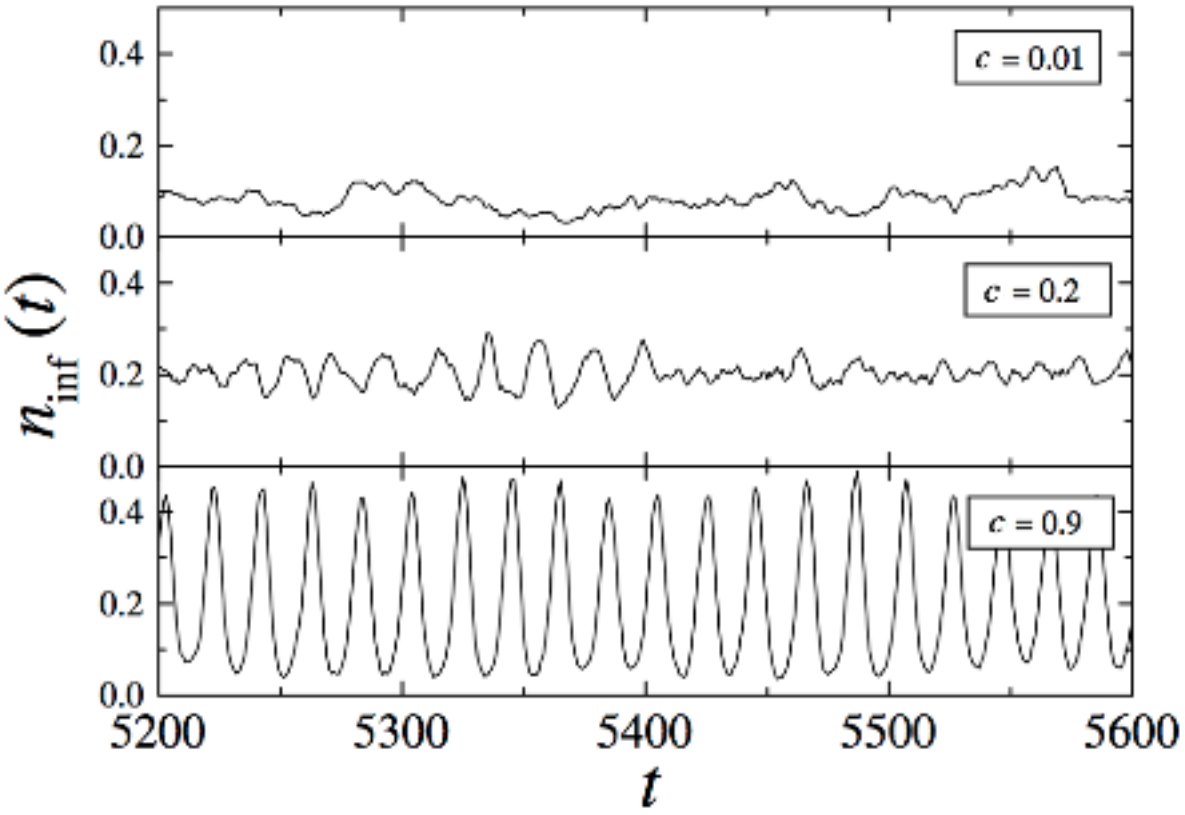
Numerical Results

- c is the rewiring probability



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SARS Prediction

- SARS: severe acute respiratory syndrome
- SIR like model with more parameters and homogenous mixing
- Travel data and census data
- WHO data about SARS spreading to evaluate the model
- Outbreak starts in Hong Kong

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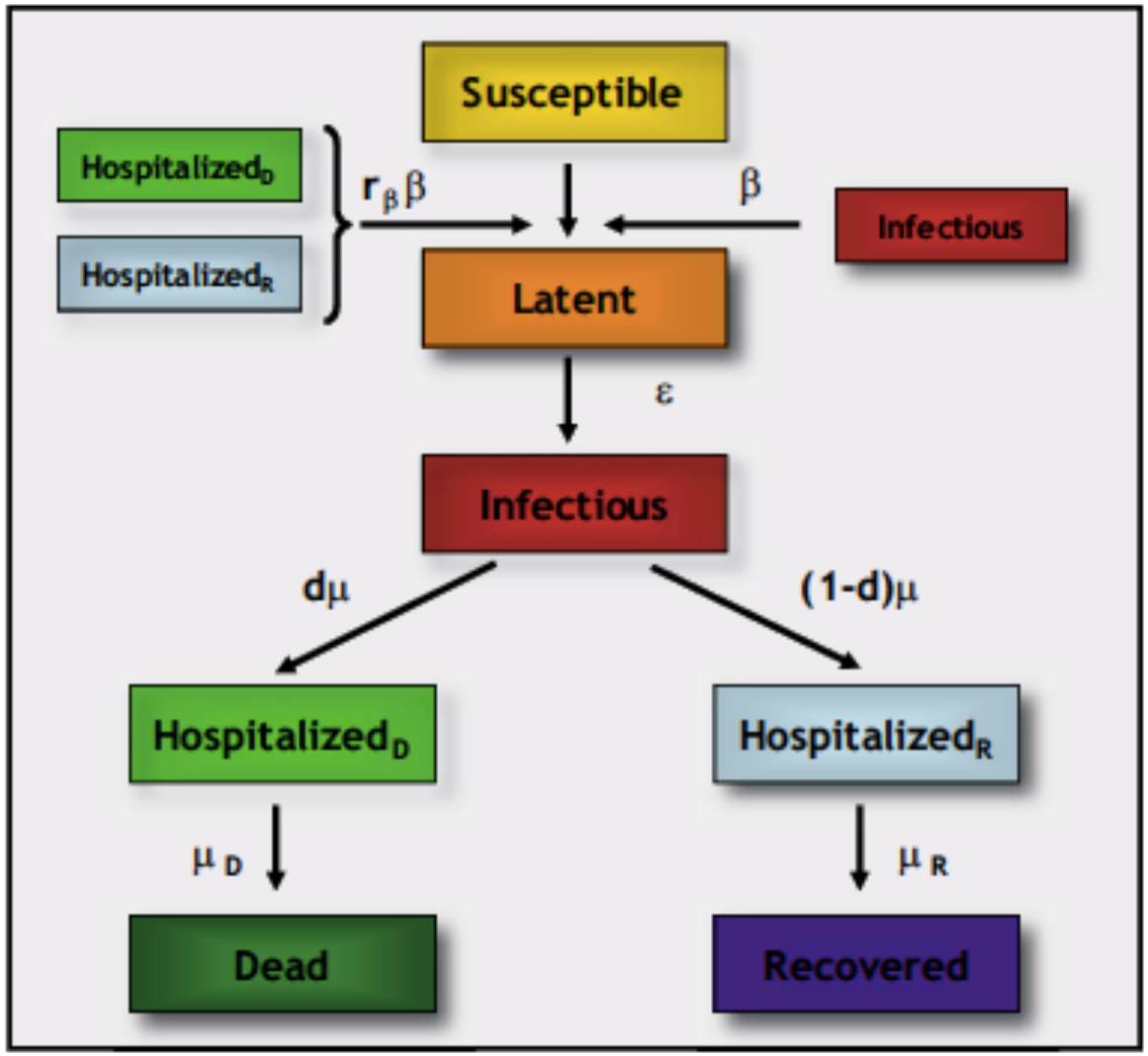
Epidemics Flow



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The Parameters of the Model

- Parameters used:

Parameter	Description		Baseline value
T_0	Initial offset from 21 February (days)		3*
β	Rate of transmission		0.57*
$L(t = 0)$	Number of initial latent individuals		10*
$s_f(t)$	Scaling factor for the rate of transmission	21 February + T_0-20 March	1.00
		21 March – 9 April	0.37
		10 April – 11 July	0.06
r_β	Relative infectiousness of patients at the hospital		0.2
ε^{-1}	Average latency period (days)		4.6
$\mu_I^{-1}(t)$	Average period from onset of symptoms to admission (days)	21 February + T_0-25 March	4.84
		25 March – 1 April	3.83
		2 April – 11 July	3.67
μ_R^{-1}	Average period from admission to recovery (days)		23.5
μ_D^{-1}	Average period from admission to death (days)		35.9
d	Case fatality rate		0.2

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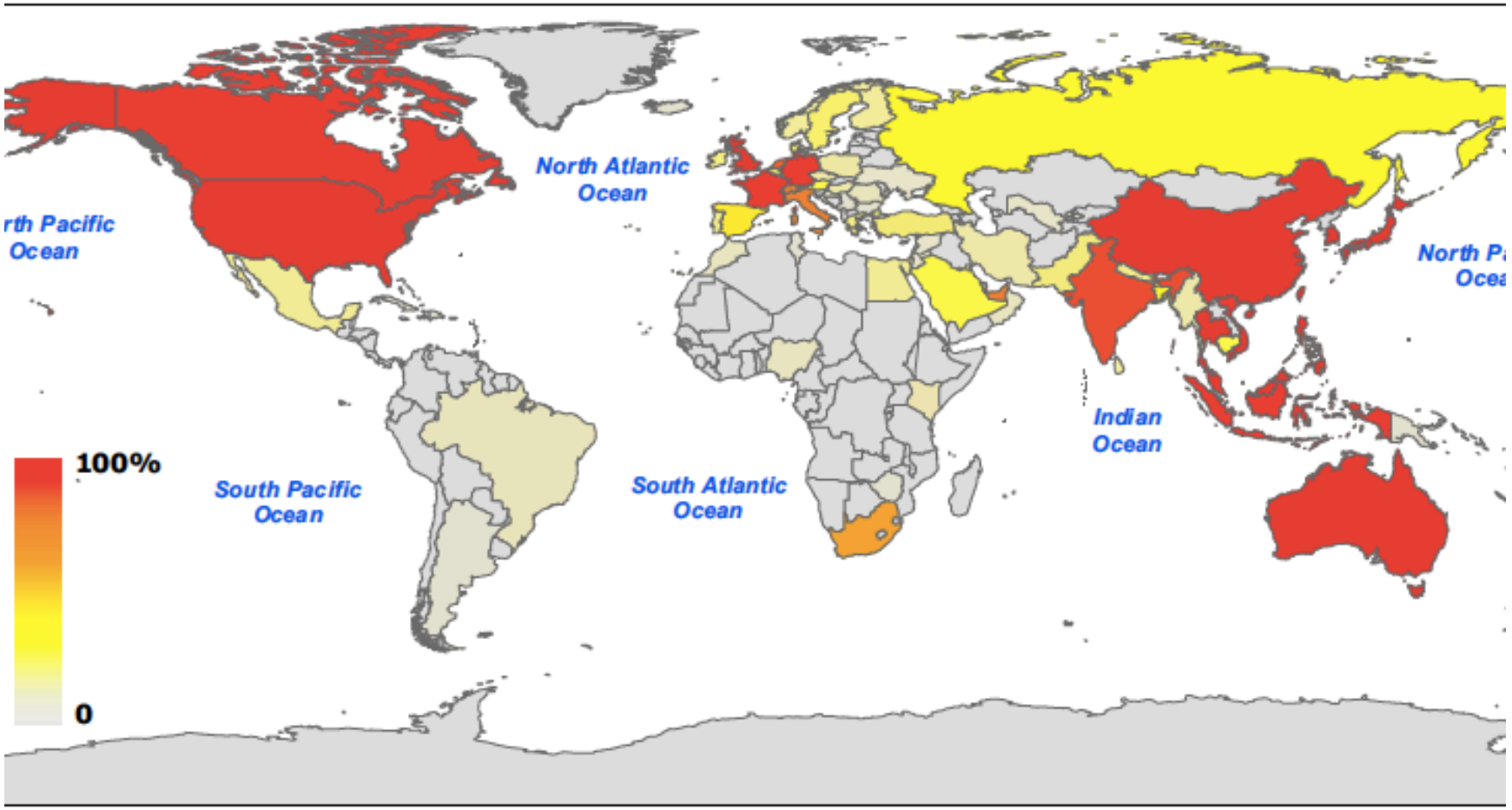
Adding Travel and Geography

- A model per city
- Probabilities of an individual of moving from one city to the next follows proportions of traffic observed in the air travel data

Predicted Outbreak Likelihood



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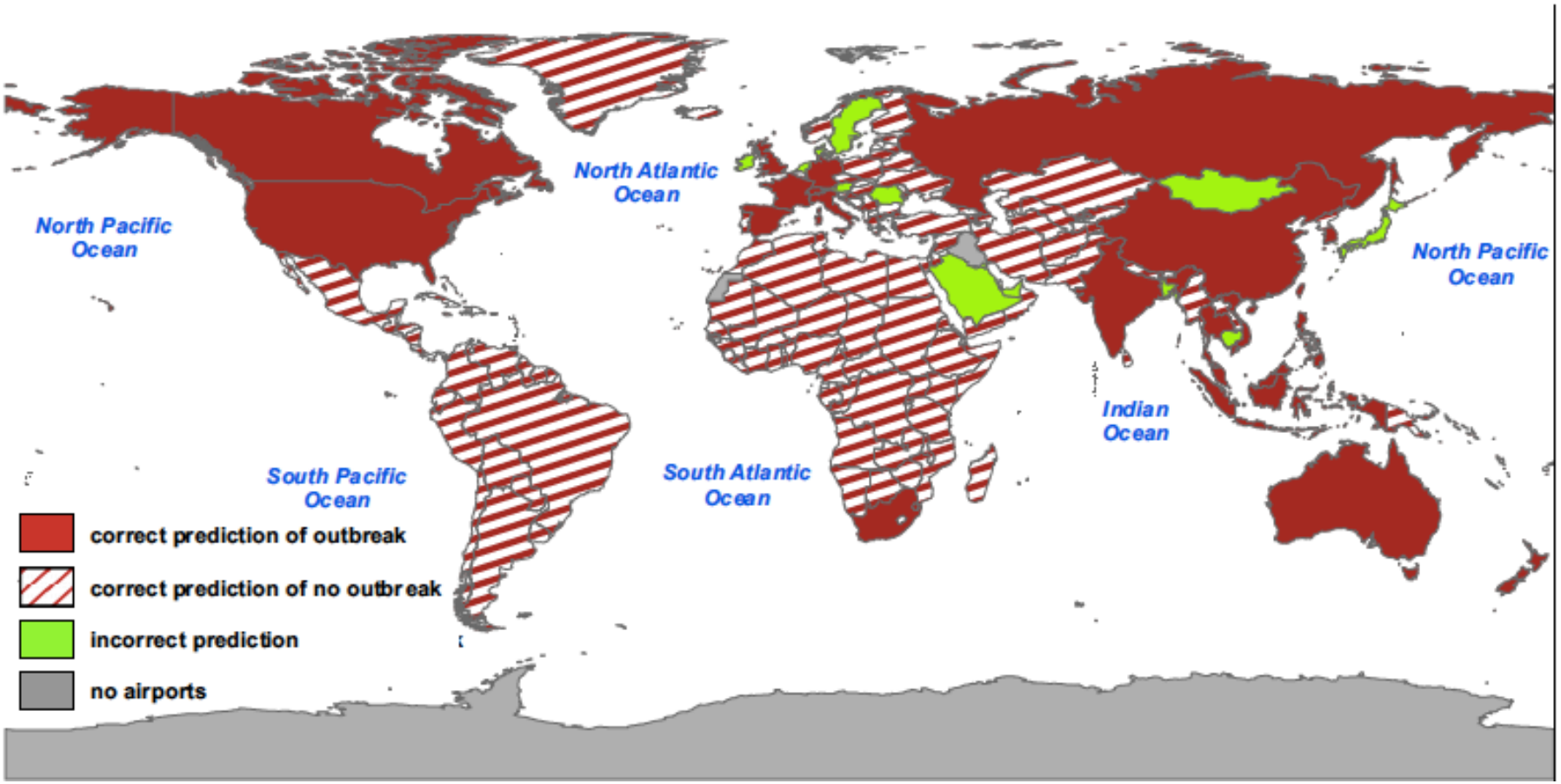
Comparison with Data



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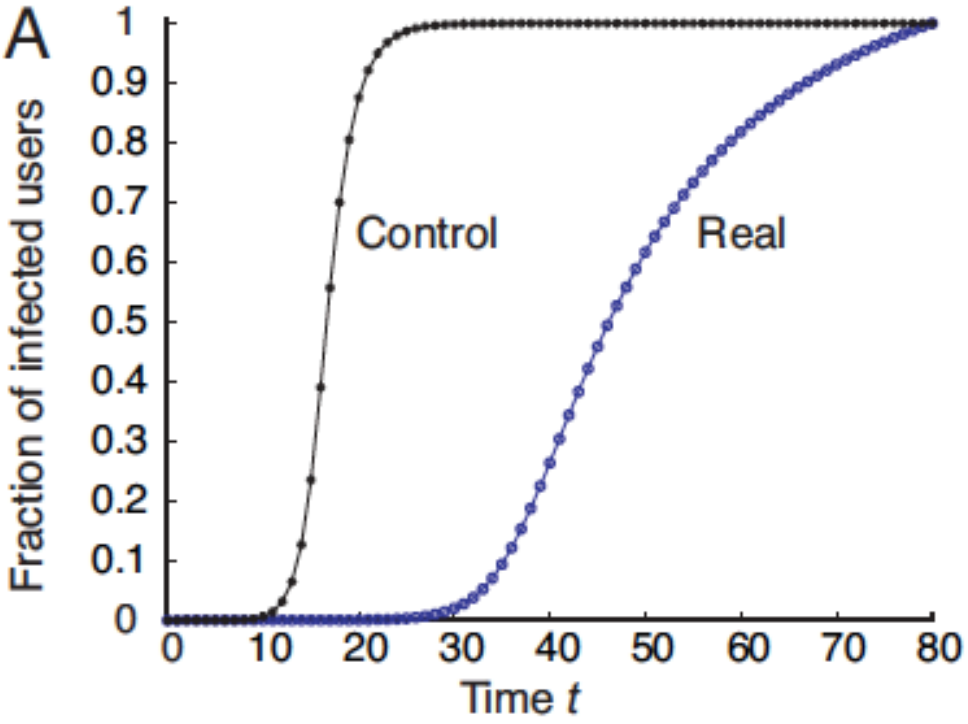
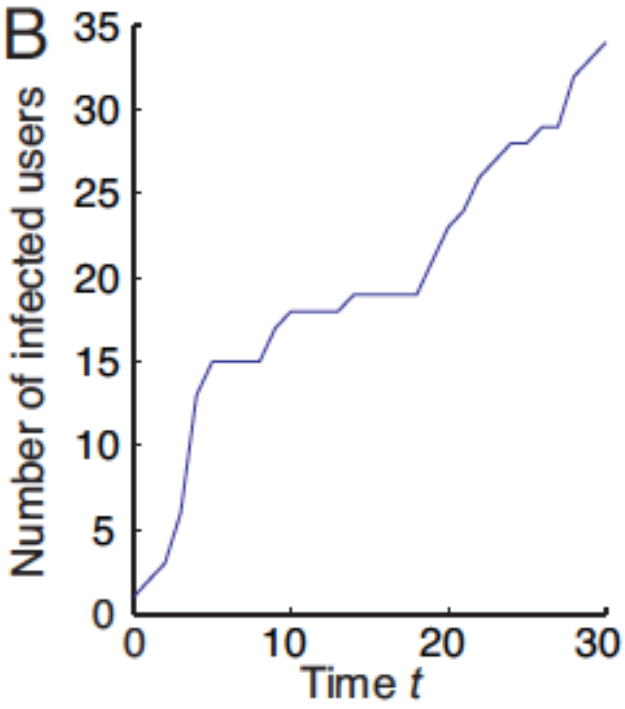
SI and Weak Ties (Onnela 2007)

- What is the role of tie strength in information diffusion/epidemic spreading?

- Let us remember the findings in Lecture 2…

SI over Communication Network





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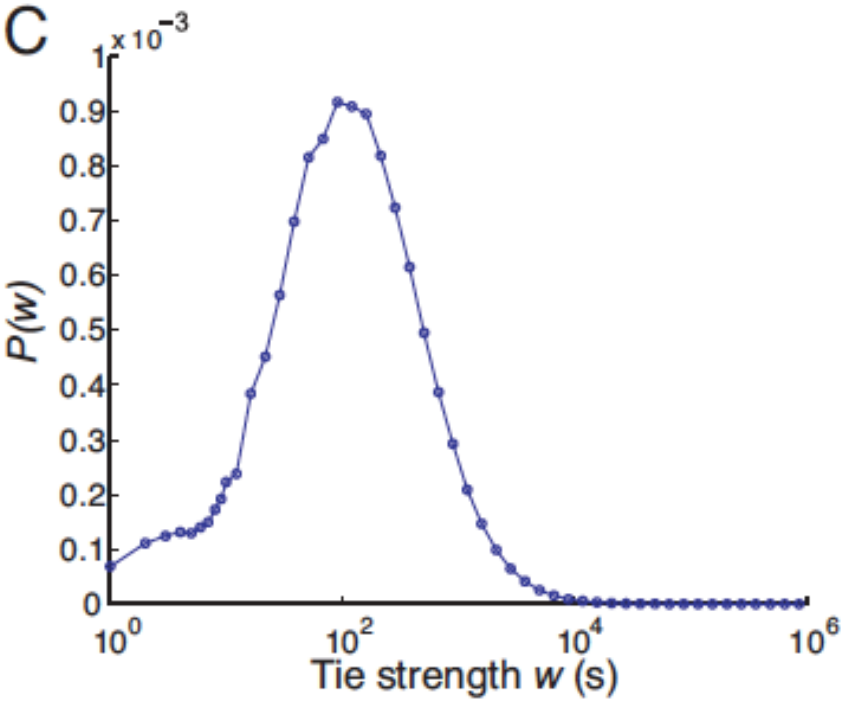
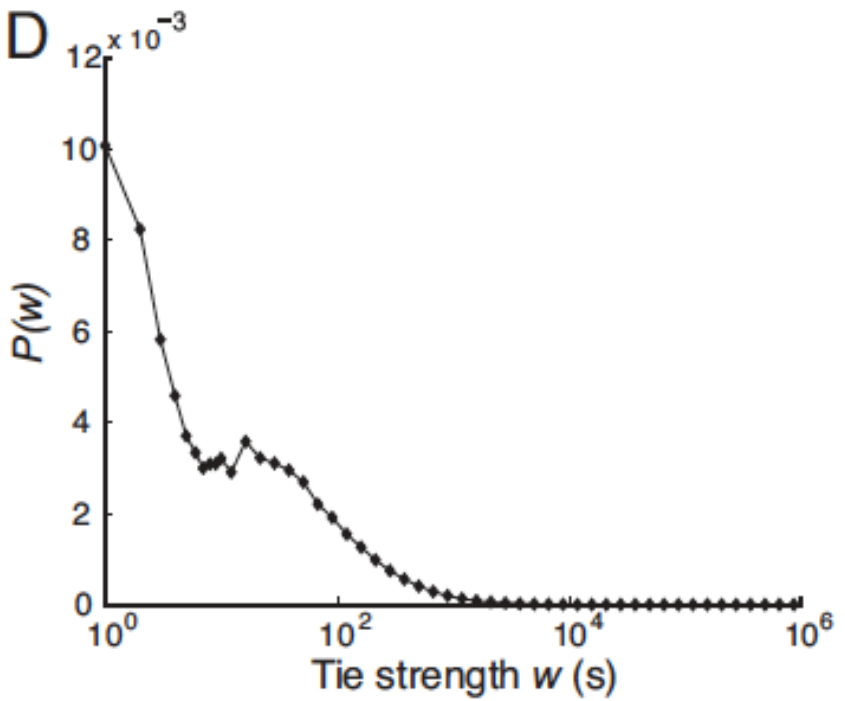
SI and tie strength

Medium ties are the most used:
Weak ties: not enough time to communicate
Strong ties: stuck inside a community

Time t



Time t



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.
- Mixing geographic factors with epidemics model is very relevant and important.
- Tie strength add another perspective.

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.
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