Social and Technological Network Data Analytics

Lecture 10: 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 various disciplines from different perspectives from theoretical models to simulations of real events.
  - But it also has important parallels and applications in information/idea diffusion in social and technological 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 transmits 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 $k*k=k^2$ people.
- **Subsequent waves:** same process.

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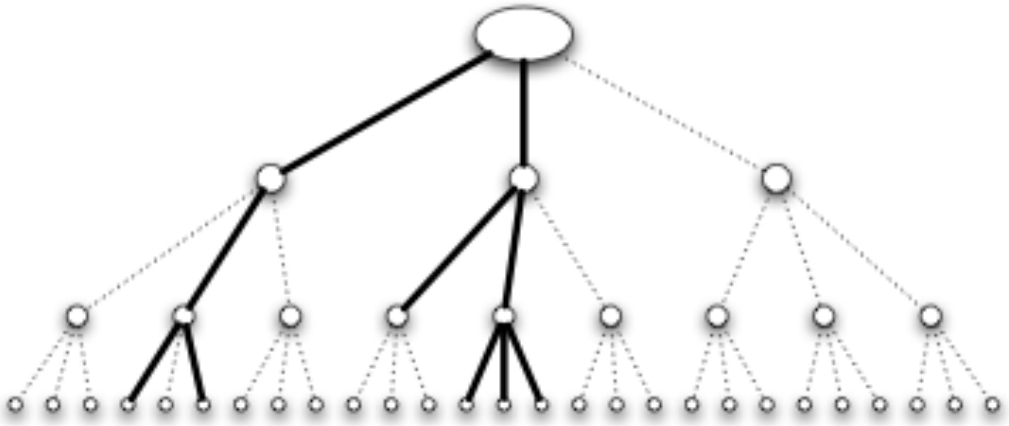
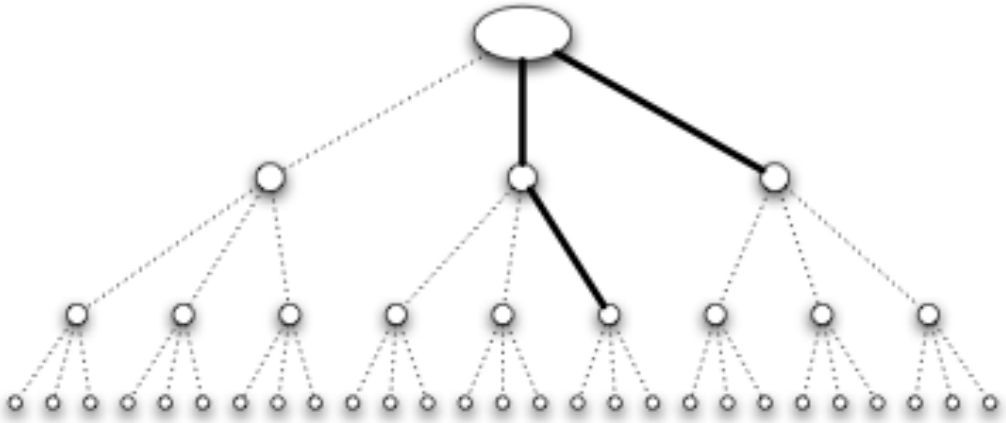
Example with k=3



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 if 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.

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.

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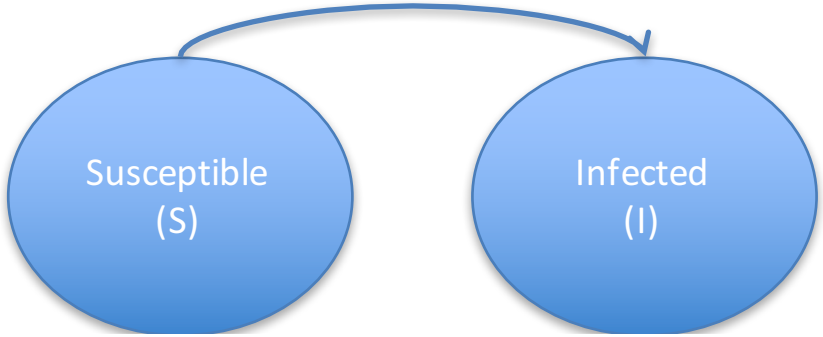
Formal Epidemics Models
The SI Model

- S: susceptible individuals.
- I: 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 $I\beta S/n$.



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SI Model

$$\frac{dI}{dt} = \beta \frac{SI}{n}$$

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

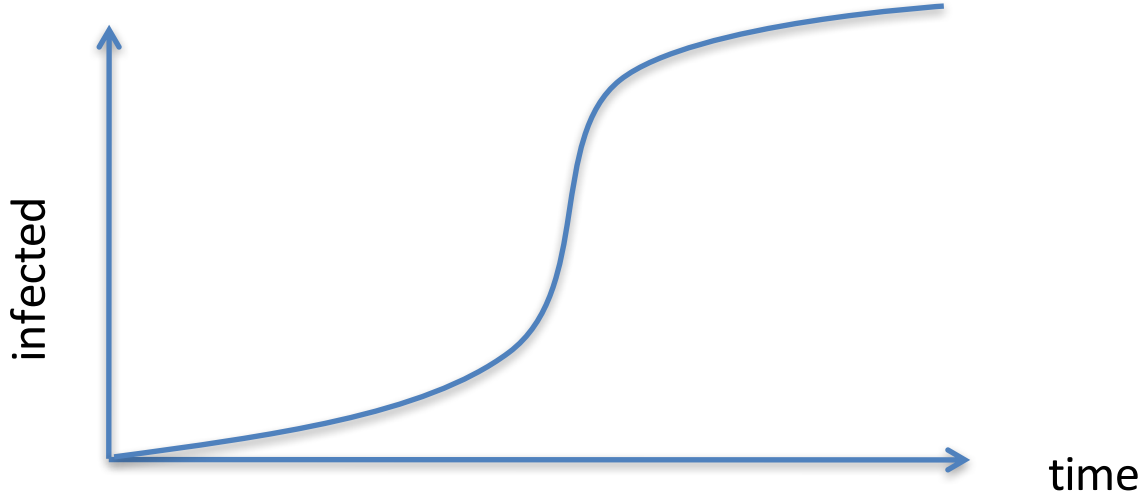
$$s = \frac{S}{n} \qquad i = \frac{I}{n}$$

$$s = 1 - i$$

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

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

Logistic Growth Equation



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SIR Model

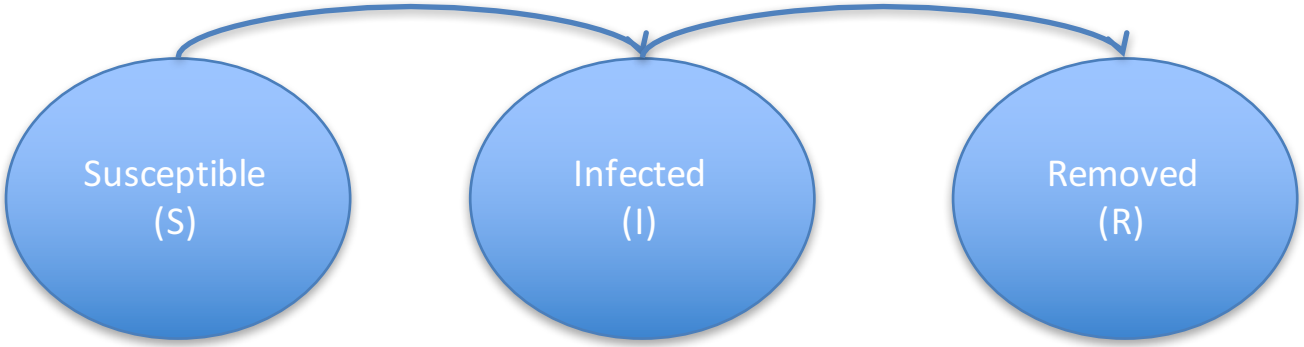
- Infected nodes recover at a rate γ.
- A node stays infected for τ time.
- Branching process is SIR with τ=1.

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

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

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

$$s + i + r = 1$$



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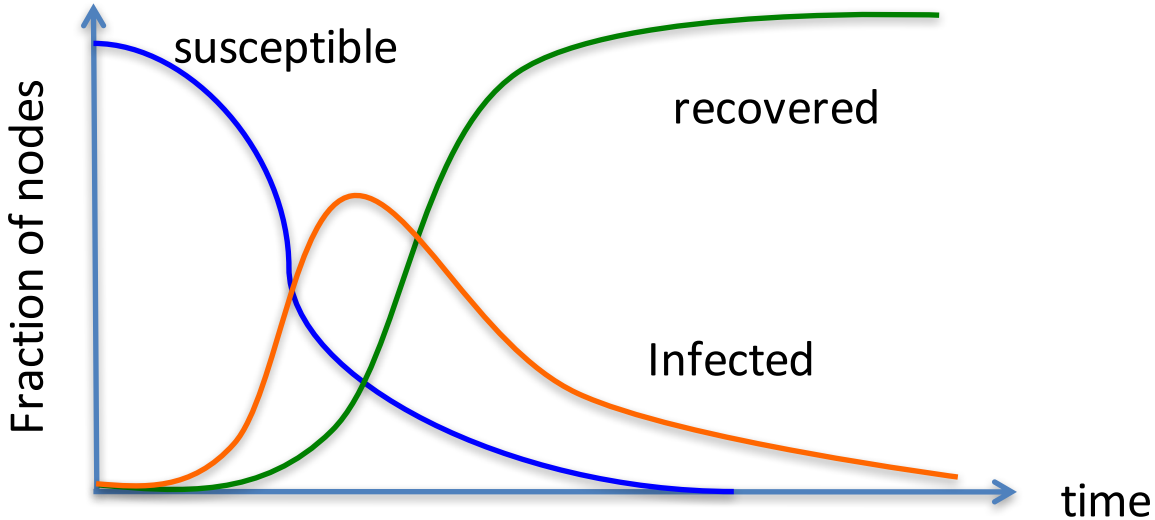
Example

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



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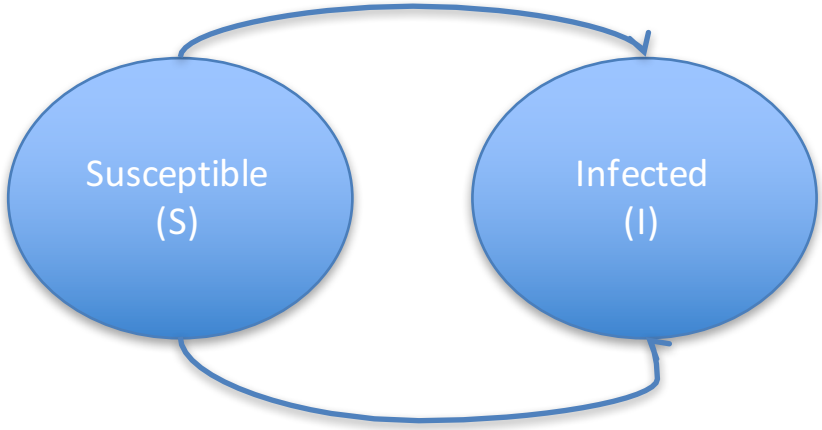
SIS Model

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

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

$$s + i = 1$$

- 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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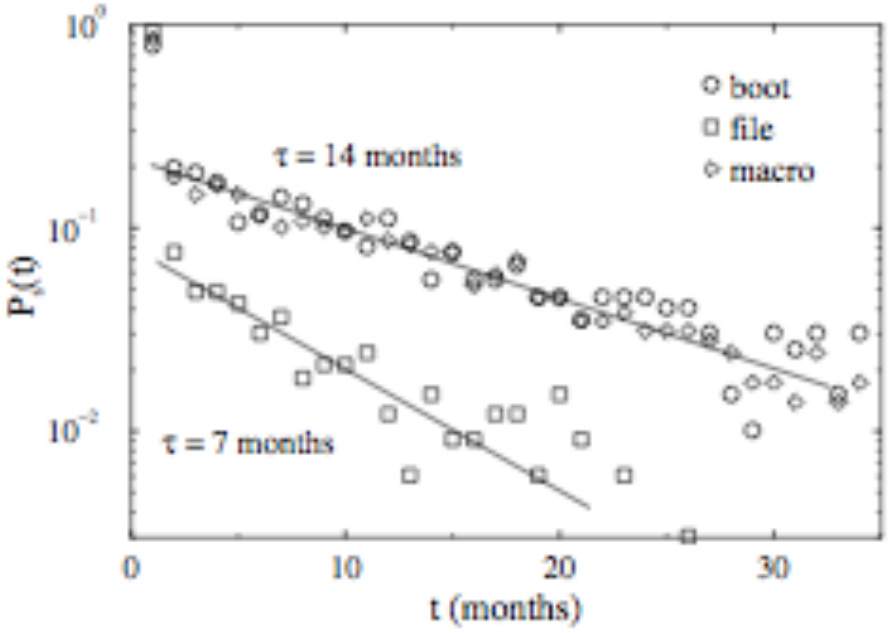
Relaxing Assumptions

- 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).

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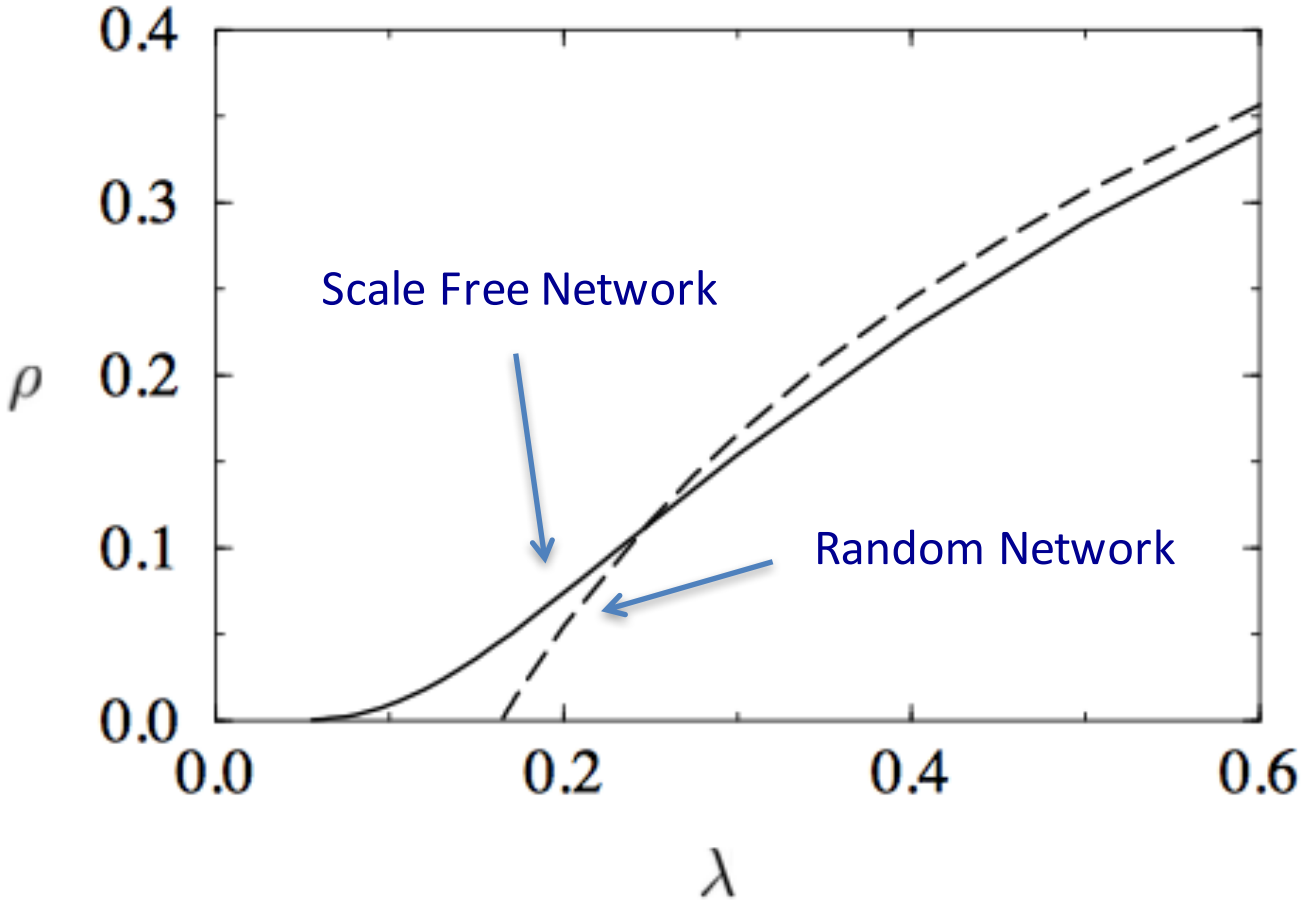
No Epidemic Threshold for SF!



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Infections proliferate in SF networks independently of their spreading rates!

Network Immunisation

- Random network can be immunized with some sort of uniform immunization process [oblivious of the characteristics of nodes].
- **Random immunisation does not work in SF networks** no matter how many nodes are immunized [unless it is all of them].
- Targeted immunization in SF must be used instead.
  - Keeping into account degree!

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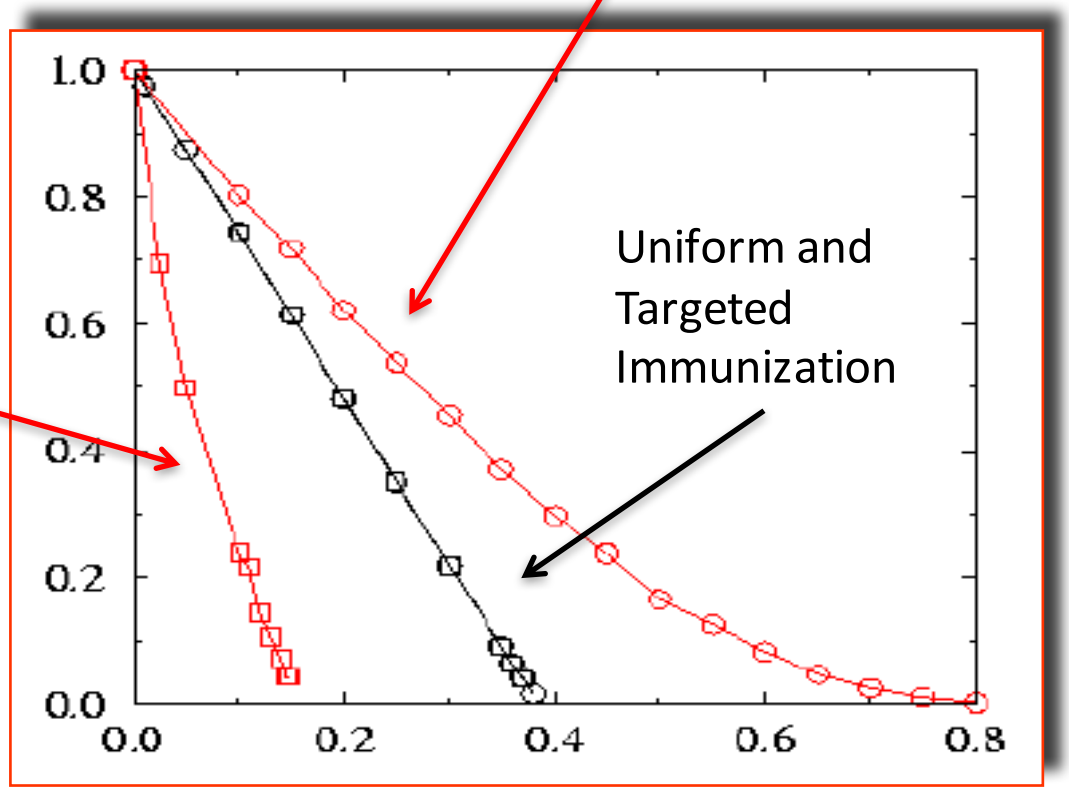
Immunization on SF Networks

- 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 available (more on this later)
- 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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Modelling SARS Spreading

- 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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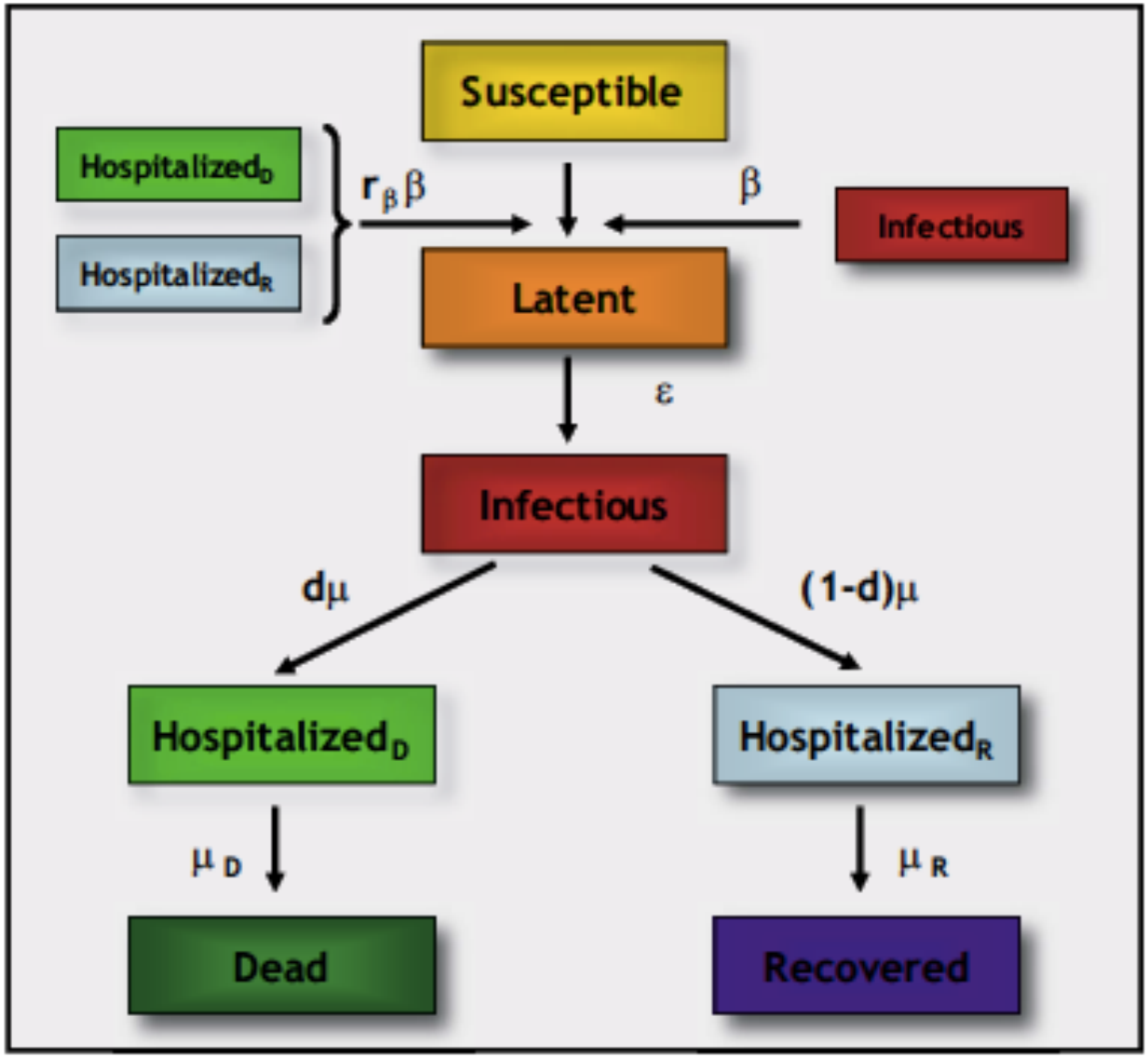
Epidemics Flow



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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
$\mu^{-1}(t)$	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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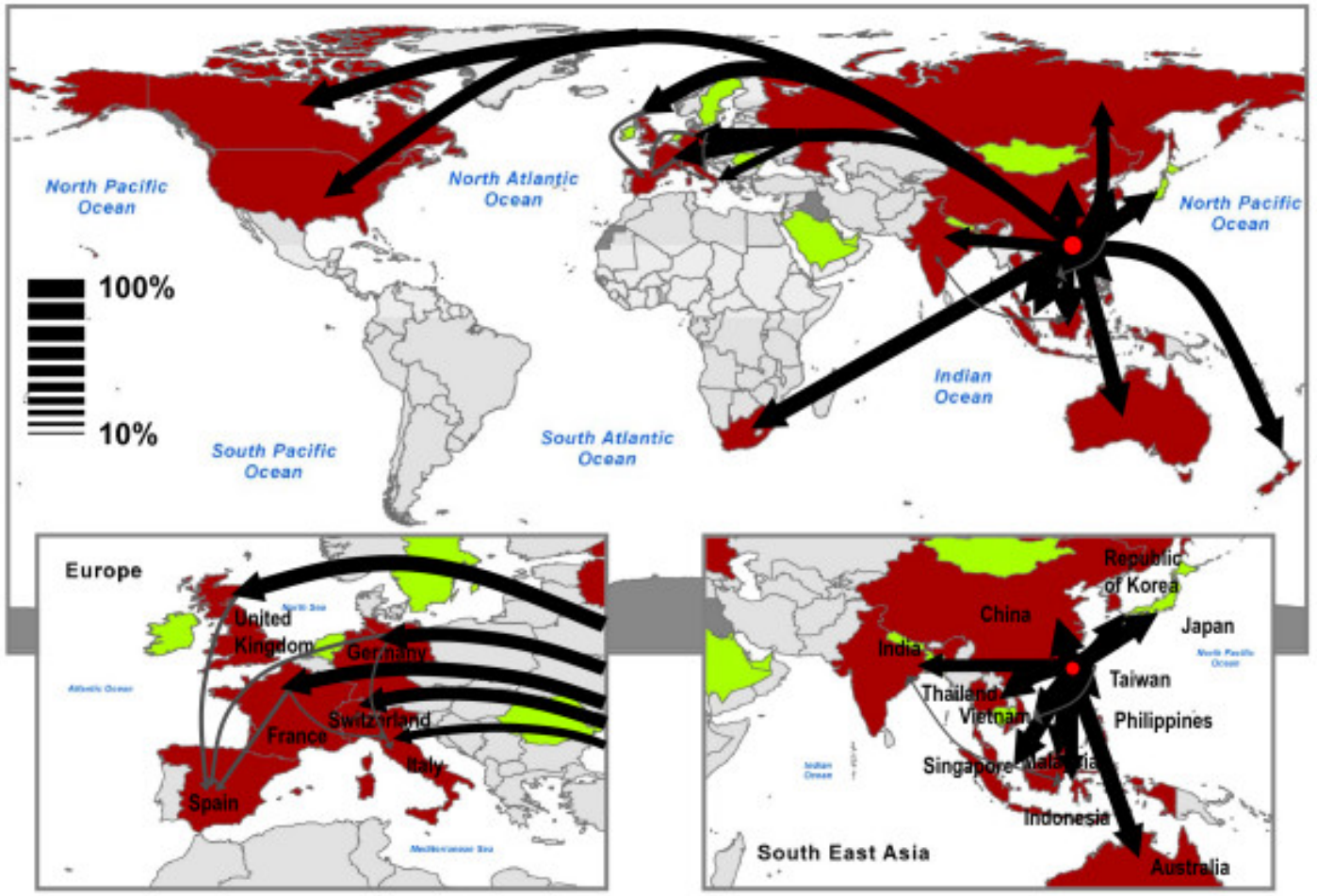
Adding Travel and Geography

- A model per city ("meta-population model")
  - Each compartmental model describes the epidemics in a given city.
  - Models per city are coupled using information from air travel
    - Possible simplification of the reality but effective abstraction.
- Stochastic model
  - Probabilities of an individual of moving from one city to the next follows proportions of traffic observed in the air travel data.

Epidemic Pathways



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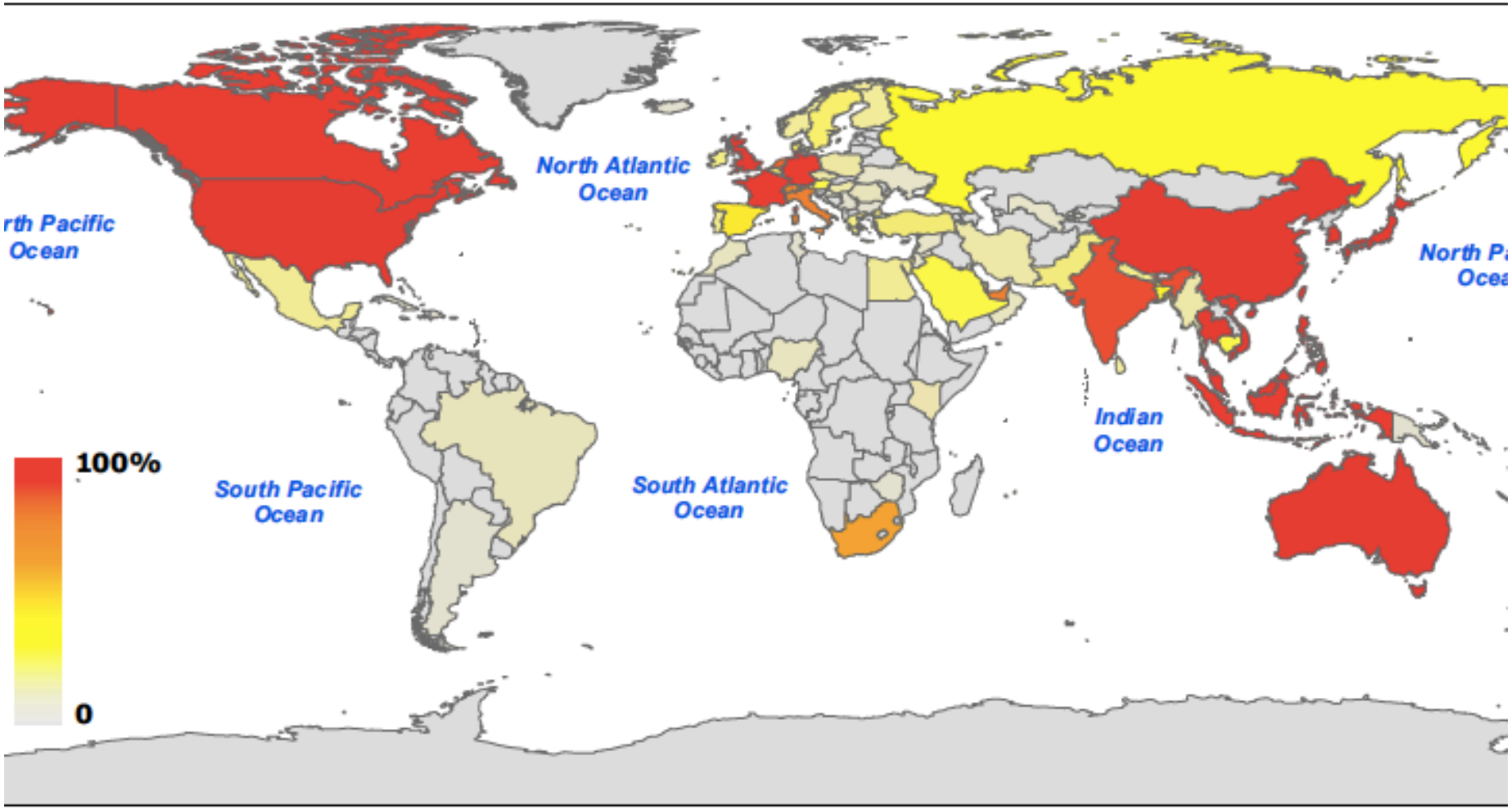
Predicted Outbreak Likelihood



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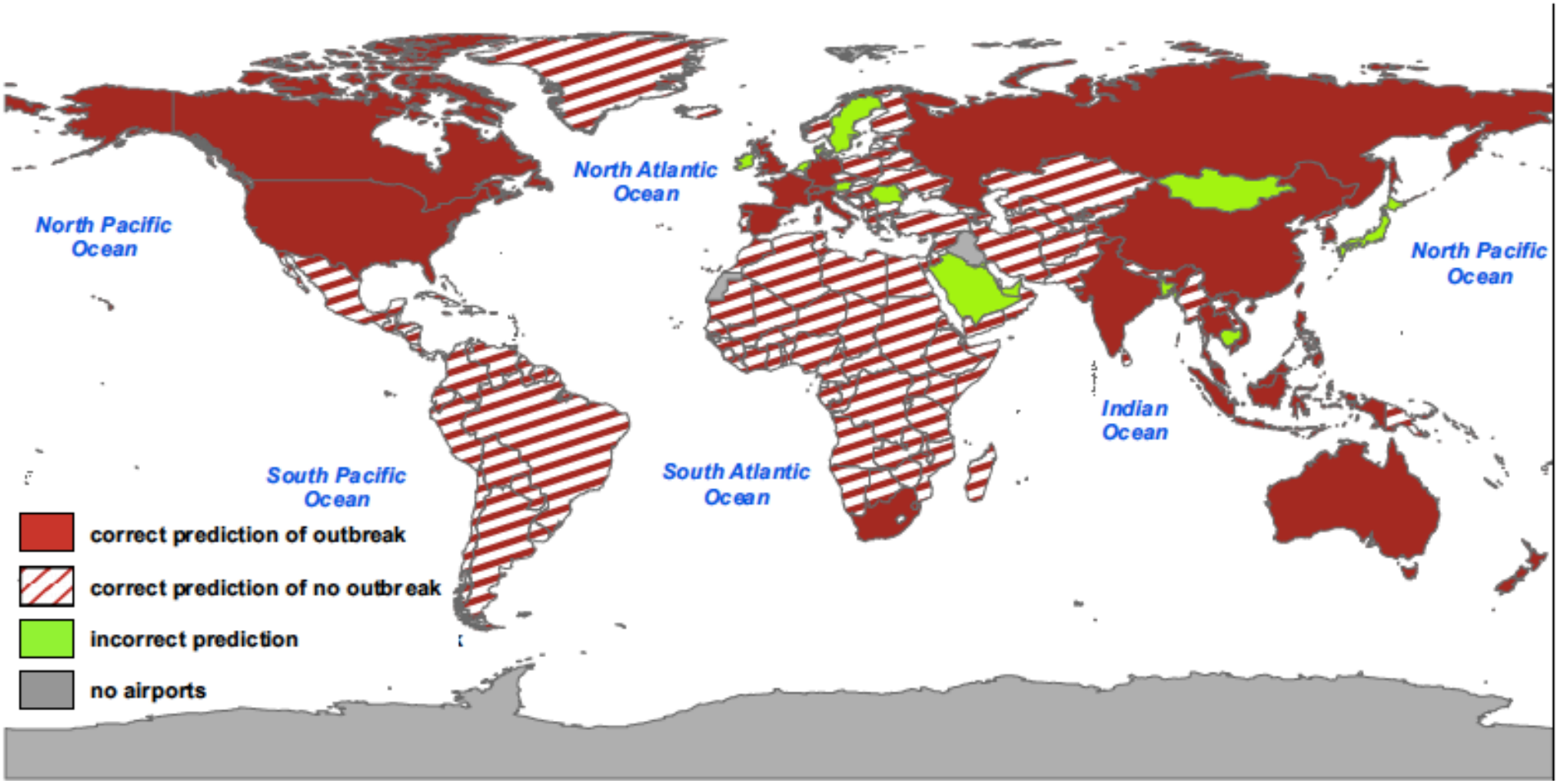
Comparison with Data



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Epidemic Spreading Models and Real Data

- A key problem is how to extract information for modelling the spreading the disease from real data.
- One possibility is to use information coming from the cellular network:
  - Transitions between base-stations for modelling the mobility;
  - Phone calls graph for modelling the underlying social networks between callers and callees.

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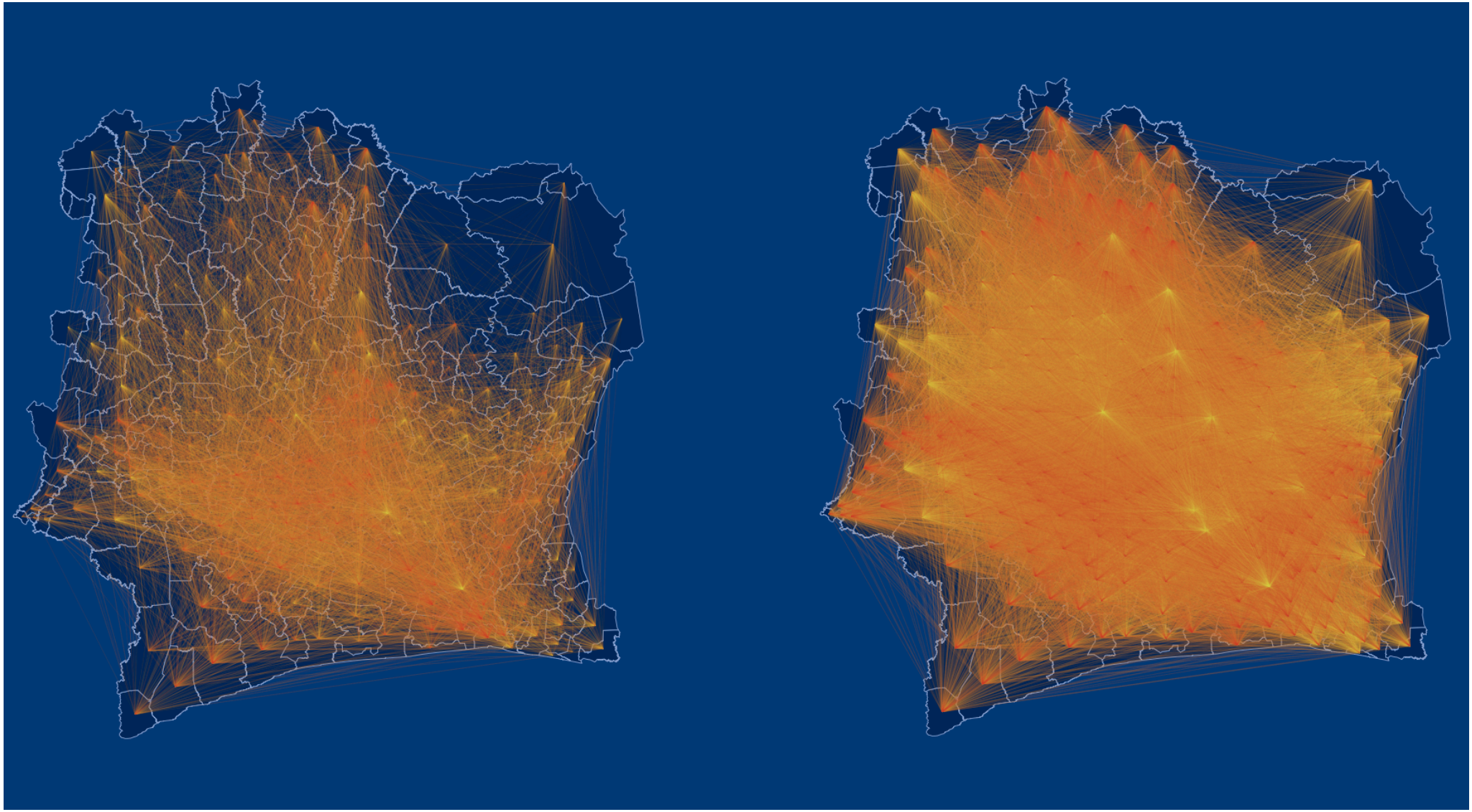
Epidemic Spreading Models and Real Data

- In order to study possible strategies of containment of epidemics, an important aspect is how to model information campaigns for example for mass vaccination.
- Vaccination can happen through the population by exploiting the “strong” ties between them (family ties or friendships, etc.)
- Presence of two concurrent processes:
  - Epidemic spreading
  - Information diffusion (spreading of “immunising information”)



Mobility

Calls

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Data for Development Challenge

- Data mining competition using a data set containing movement and call data of 5 million individuals in Ivory Coast in order to help to address society development questions in novel way
- Information extracted from the Call Data Records (CDRs) of the Orange network in Ivory Coast

Massachusetts Institute of Technology

orange™

Call Data Records

- A Call Data Record (CDR) entry contains information about a specific phone call (usually called “metadata”), including:
  - The phone number of the subscriber originating the call;
  - The phone number of the called party;
  - The identification of the equipment writing the record (base station).
    - From this information it is possible to extract the geographic location of the caller.

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Mobility Matrix

- Movement data extracted from the registration patterns to the cellular infrastructure (i.e., CDRs) are used to evaluate the influence of human mobility on the spreading of the disease in a given geographic area.
- From the data it is possible to extract the probability of transitions between different areas, in this case “sub-prefectures” (counties) of Ivory Coast.
- Using this information, we build a mobility matrix representing movement in the country as a Markov process.

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Mobility Matrix

Number of times a user *u* moves from the sub-prefecture *i* to the sub-prefecture *j*

$$m_{ij} = \frac{\sum_u \mathcal{M}_{ij}^u}{\sum_k \sum_u \mathcal{M}_{ik}^u}$$

Probability that an individual moves from the sub-prefecture *i* to the sub-prefecture *j*

Number of times a user *u* moves from the sub-prefecture *i* to the sub-prefecture *k*

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Call Graph

Number of phone calls initiated from the sub-prefecture *i* and directed to the sub-prefecture *j*

$$c_{ij} = \frac{C_{ij}}{\sum_k C_{ik}}$$

Probability of a call being established between sub-prefectures *i* and *j*

Number of phone calls initiated from the sub-prefecture *i* and directed to the sub-prefecture k

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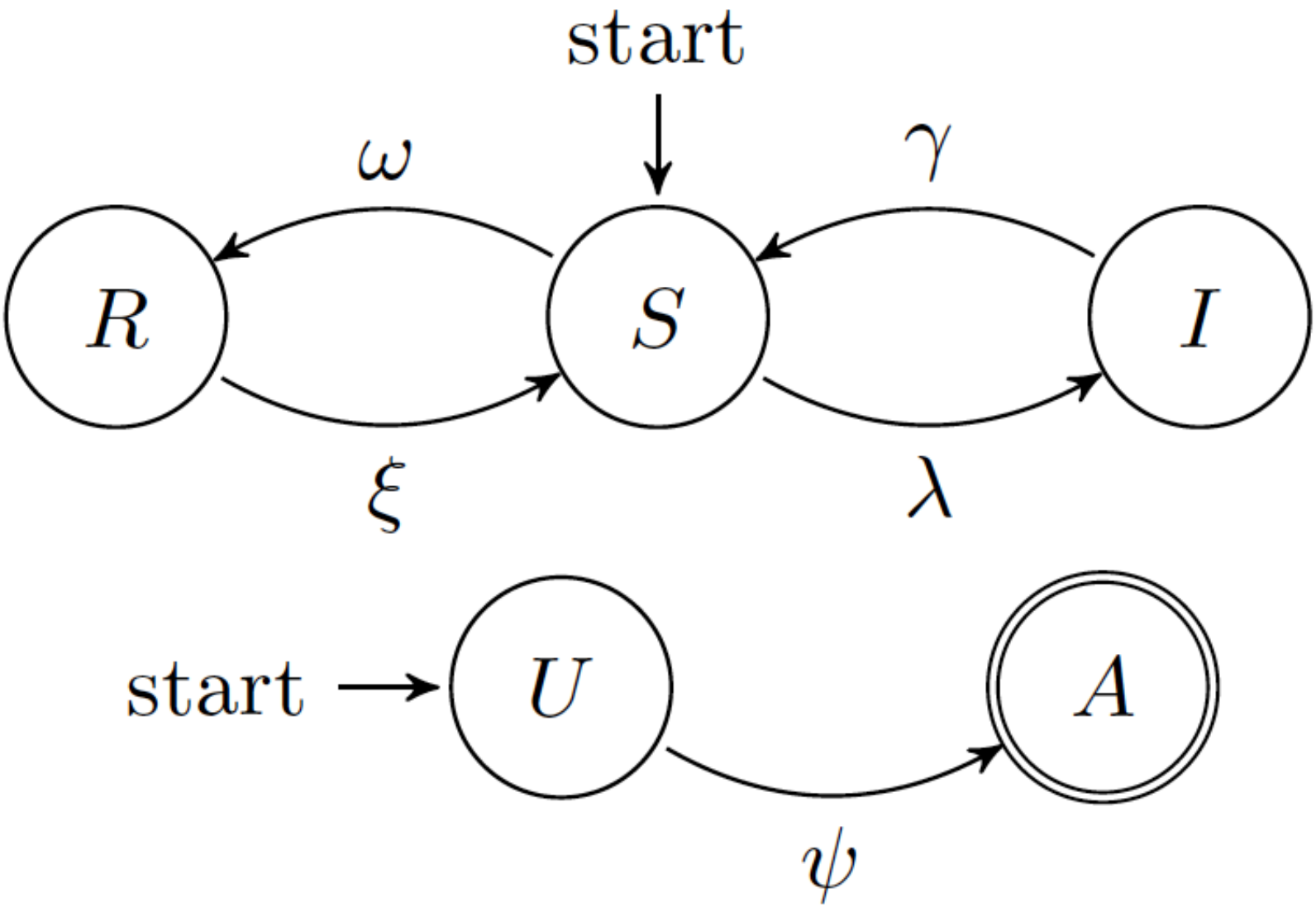
States

- Disease spreading process:
  - S: Susceptible
  - I: Infected
  - R: Resistant/recovered
- Information spreading process:
  - U: unaware
  - A: aware
- $N(t)=S(t)+I(t)+R(t)=U(t)+A(t)$


start
ω
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$$
\begin{aligned}
I_i[t+1] &= \sum_{j=1}^{n} m_{ji} \left[I_j[t] \ + \lambda \frac{S_j[t]}{N_j[t]} I_j[t] - \gamma I_j[t] \right] \\
S_i[t+1] &= \sum_{j=1}^{n} m_{ji} \left[S_j[t] \ - \lambda \frac{S_j[t]}{N_j[t]} I_j[t] + \gamma I_j[t] + \xi R_j[t] + \right. \\
&\qquad \left. - \omega S_j[t] \frac{\sum_{k=1}^{n} c_{kj} A_k[t]}{\sum_{k=1}^{n} c_{kj} N_k[t]} \right] \\
R_i[t+1] &= \sum_{j=1}^{n} m_{ji} \left[R_j[t] - \xi R_j[t] + \omega S_j[t] \frac{\sum_{k=1}^{n} c_{kj} A_k[t]}{\sum_{k=1}^{n} c_{kj} N_k[t]} \right] \\
A_i[t+1] &= \sum_{j=1}^{n} m_{ji} \left[A_j[t] + \psi U_j[t] \frac{\sum_{k=1}^{n} c_{kj} A_k[t]}{\sum_{k=1}^{n} c_{kj} N_k[t]} \right] \\
U_i[t+1] &= \sum_{j=1}^{n} m_{ji} \left[U_j[t] - \psi U_j[t] \frac{\sum_{k=1}^{n} c_{kj} A_k[t]}{\sum_{k=1}^{n} c_{kj} N_k[t]} \right] \qquad (3)
\end{aligned}
$$

Mobility Matrix

$$I_i[t+1] = \sum_{j=1}^{n} m_{ji} \left[I_j[t] + \lambda \frac{S_j[t]}{N_j[t]} I_j[t] - \gamma I_j[t] \right]$$

$$S_i[t+1] = \sum_{j=1}^{n} m_{ji} \left[S_j[t] - \lambda \frac{S_j[t]}{N_j[t]} I_j[t] + \gamma I_j[t] + \xi R_j[t] + - \omega S_j[t] \frac{\sum_{k=1}^{n} c_{kj} A_k[t]}{\sum_{k=1}^{n} c_{kj} N_k[t]} \right]$$

$$R_i[t+1] = \sum_{j=1}^{n} m_{ji} \left[R_j[t] - \xi R_j[t] + \omega S_j[t] \frac{\sum_{k=1}^{n} c_{kj} A_k[t]}{\sum_{k=1}^{n} c_{kj} N_k[t]} \right]$$

$$A_i[t+1] = \sum_{j=1}^{n} m_{ji} \left[A_j[t] + \psi U_j[t] \frac{\sum_{k=1}^{n} c_{kj} A_k[t]}{\sum_{k=1}^{n} c_{kj} N_k[t]} \right]$$

$$U_i[t+1] = \sum_{j=1}^{n} m_{ji} \left[U_j[t] - \psi U_j[t] \frac{\sum_{k=1}^{n} c_{kj} A_k[t]}{\sum_{k=1}^{n} c_{kj} N_k[t]} \right] \qquad (3)$$

Mobility Matrix

$$I_i[t+1] = \sum_{j=1}^{n} m_{ji} \left[I_j[t] + \lambda \frac{S_j[t]}{N_j[t]} I_j[t] - \gamma I_j[t] \right]$$

$$S_i[t+1] = \sum_{j=1}^{n} m_{ji} \left[S_j[t] - \lambda \frac{S_j[t]}{N_j[t]} I_j[t] + \gamma I_j[t] + \xi R_j[t] + \right.$$

Call Matrix

$$\left. - \omega S_j[t] \frac{\sum_{k=1}^{n} c_{kj} A_k[t]}{\sum_{k=1}^{n} c_{kj} N_k[t]} \right]$$

$$R_i[t+1] = \sum_{j=1}^{n} m_{ji} \left[R_j[t] - \xi R_j[t] + \omega S_j[t] \frac{\sum_{k=1}^{n} c_{kj} A_k[t]}{\sum_{k=1}^{n} c_{kj} N_k[t]} \right]$$

$$A_i[t+1] = \sum_{j=1}^{n} m_{ji} \left[A_j[t] + \psi U_j[t] \frac{\sum_{k=1}^{n} c_{kj} A_k[t]}{\sum_{k=1}^{n} c_{kj} N_k[t]} \right]$$

$$U_i[t+1] = \sum_{j=1}^{n} m_{ji} \left[U_j[t] - \psi U_j[t] \frac{\sum_{k=1}^{n} c_{kj} A_k[t]}{\sum_{k=1}^{n} c_{kj} N_k[t]} \right] \qquad (3)$$

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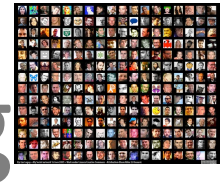
Real-time Predictive Modelling



- By using a model like this one, real-time predictive modelling might be possible
- Policy-makers might extract the parameters of the model, such as the mobility matrix, in real-time.
- Transmission models ha been widely used for assessing potential strategies for containing diseases such as influenza.
- “Mobile big data” might help in developing more accurate models.

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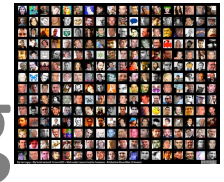
Real-time Predictive Modelling



- One of the key problems is understanding the uncertainty associated to the model.
- It is difficult to understand the contribution of many factors such as:
  - Climatic factors
  - Transmission seasonality
  - Long-term immunity of a population
  - …
- Scenario-based modelling is routinely used in order to predict future evolution of epidemics.

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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.
- The availability of “big data” might help in building more realistic and possibly real-time epidemic models.

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References

- Chapter 21
- Romualdo Pastor-Satorras and Alessandro Vespignani. Epidemic Spreading in Scale-Free Networks. Phys. Rev. Lett.(86), n.14. Pages = 3200--3203. 2001.
- Romualdo Pastor-Satorras and Alessandro Vespignani. 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.
- Vittoria Colizza, Alain Barrat, Marc Barthélemy and Alessandro Vespignani. Predictability and epidemic pathways in global outbreaks of infectious diseases: the SARS case study. BMC Medicine 2007, 5:34

References

- Antonio Lima, Manlio De Domenico, Veljko Pejovic and Mirco Musolesi. Exploiting Cellular Data for Disease Containment and Information Dissemination Campaigns Strategies in Country-wide Epidemics. In *Proceedings of NetMob'13*. Boston, MA, USA. May 2013.
- Marc Lipsitch, Lyn Finelli, Richard T. Heffernan, Gabriel M. Leung, and Stephen C. Redd. Improving the Evidence Base for Decision Making during a Pandemic: The Example of 2009 Influenza A/H1N1. In Biosecurity and Bioterrorism: Biodefense Strategy, Practice and Science. Volume 9, Number 2, 2011.
- Matt J. Keeling and Pejman Rohani. Modeling Infectious Diseases in Humans and Animals. Princeton University Press. 2007

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