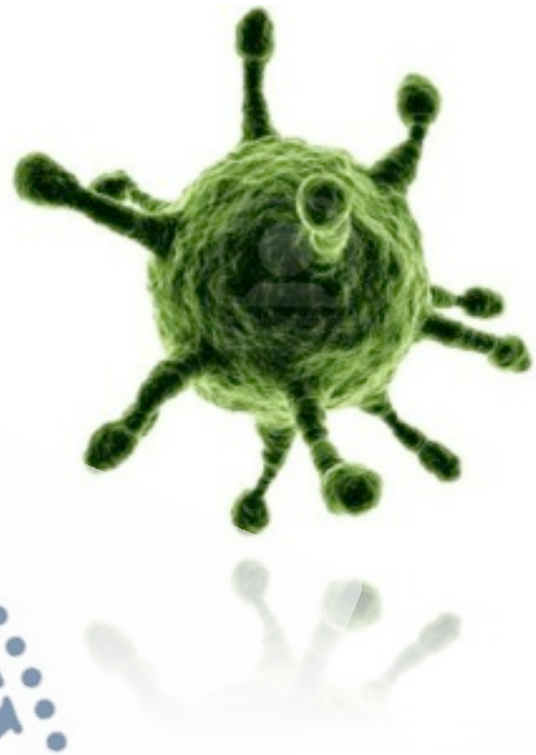
Epidemics & Networks



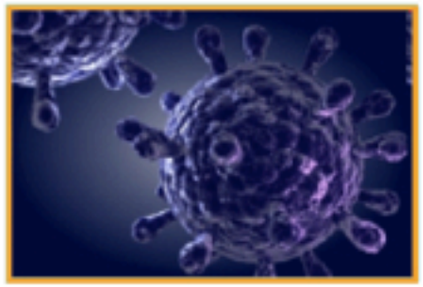
Jesús Gómez Gardeñes

Instituto de Biocomputación y Física de Sistemas Complejos (BIFI)

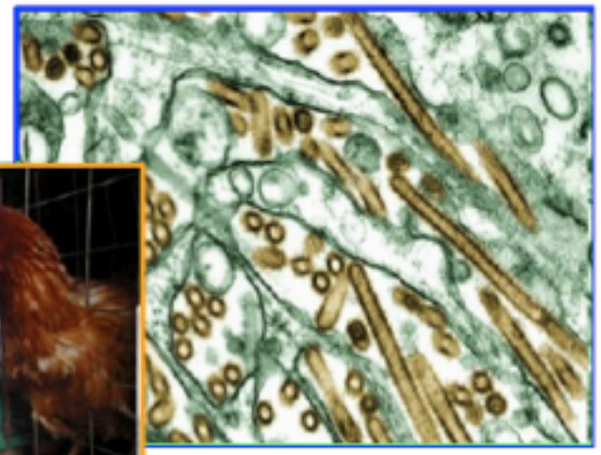
Universidad de Zaragoza

DO WE NEED A MOTIVATION?

SOS Epidemic Spreading (America, Asia & Africa)

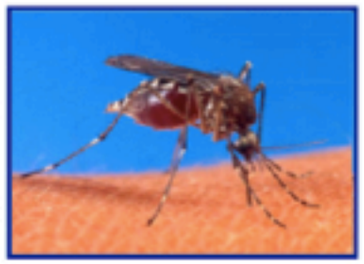


VIH In 2007, more than 33.2 millions of people all over the world were infected.

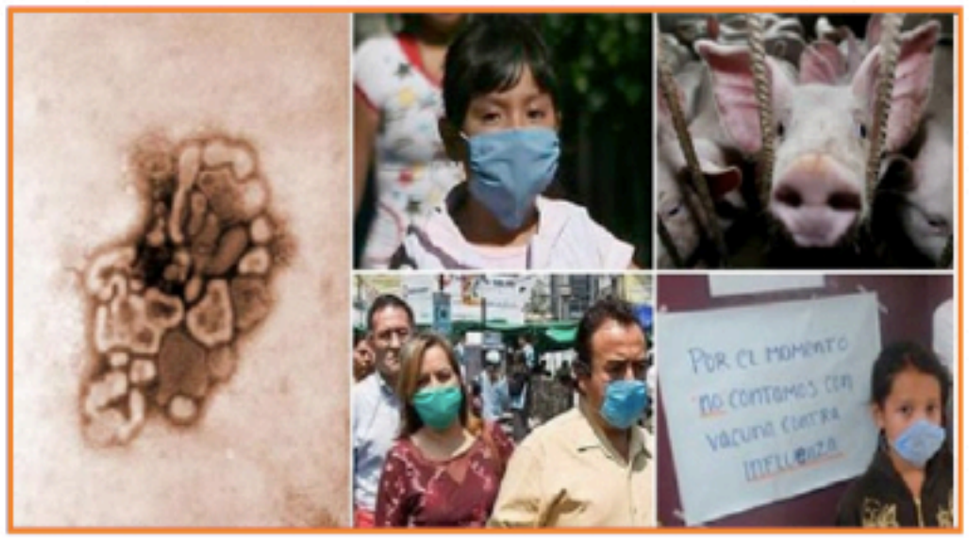


Avian Influenza Virus H5N1 *(REUTERS & EFE)*

Dengue Epidemics in Bolivia 2009
Aedes aegypti

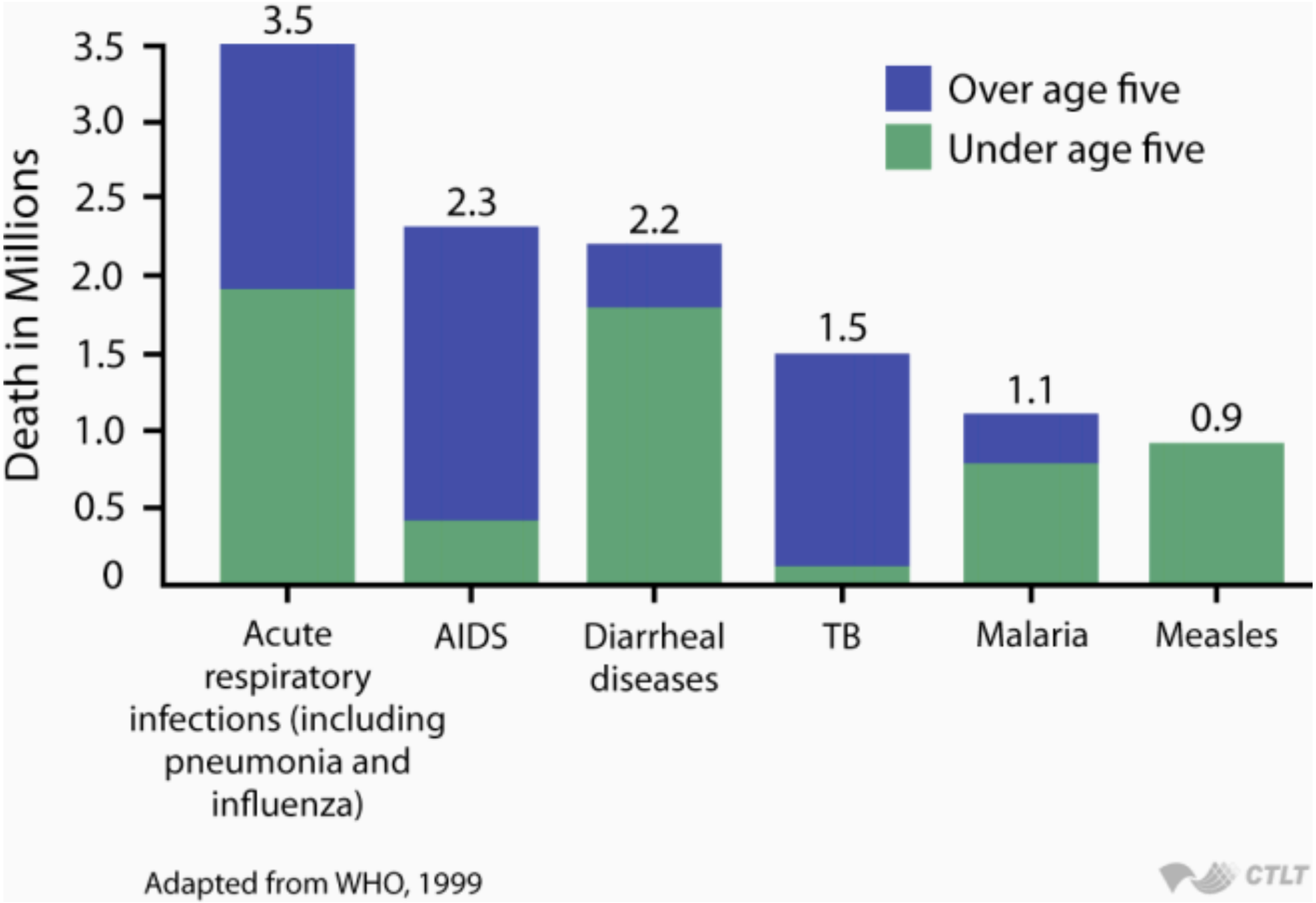


Swine Fever Epidemics in Mexico



Cholera Outbreak in Zimbabwe
2008

Infectious Disease Impact



Lets Model!

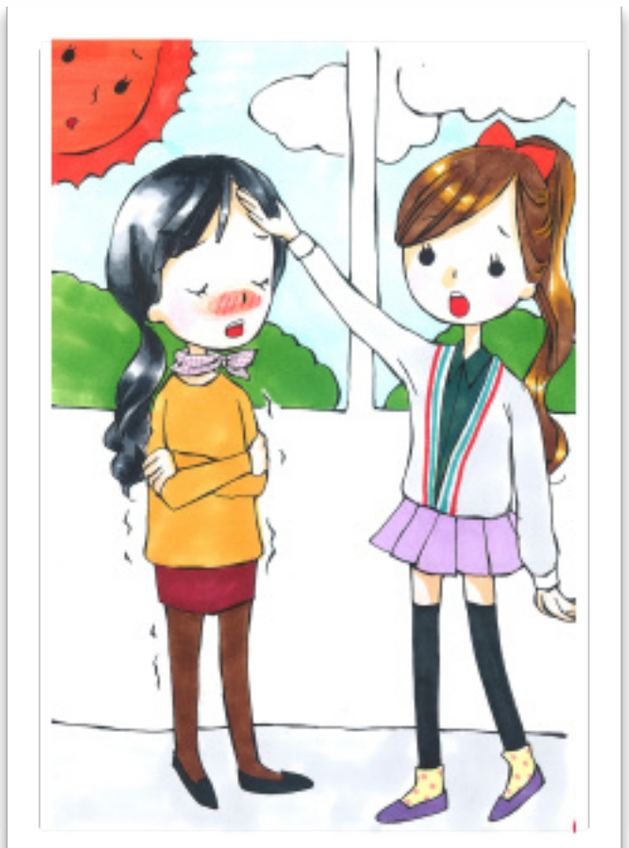
Compartmental models

Aimed at capturing the global (population-level) dynamics from the microscopic contagion processes

Compartmental models

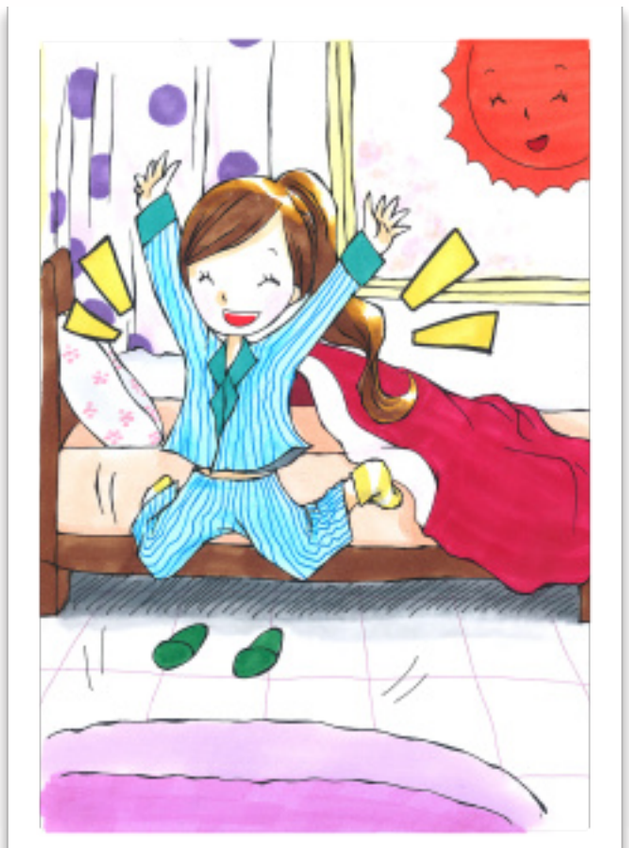
Aimed at capturing the global (population-level) dynamics from the microscopic contagion processes

Each individual can be in one of *n* states at time *t*



S - Susceptible (Healty)

I - Infected (and infectious)

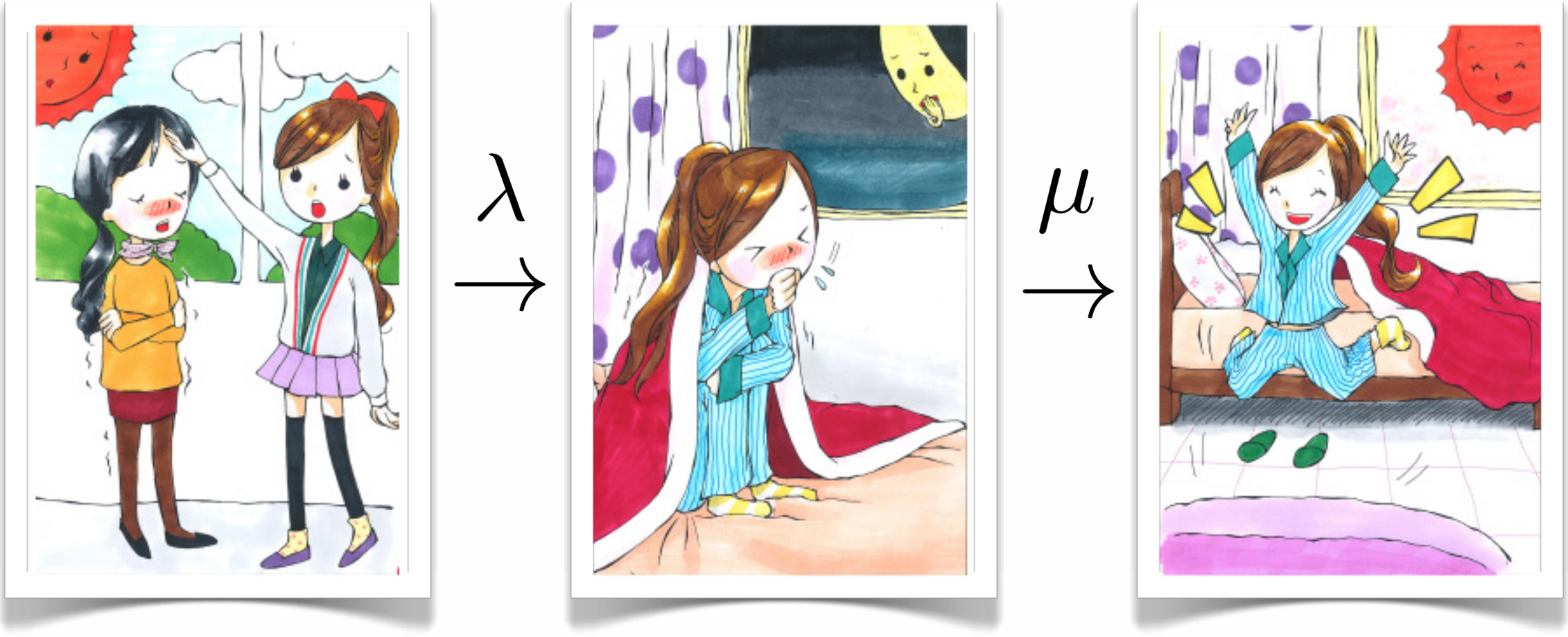


R - Recovered (immune/dead)

(From Petter Holme's blog)

Compartmental models

The transitions (e.g. S$\rightarrow$I) is mediated by some rates (λ) and the encounters between individuals.



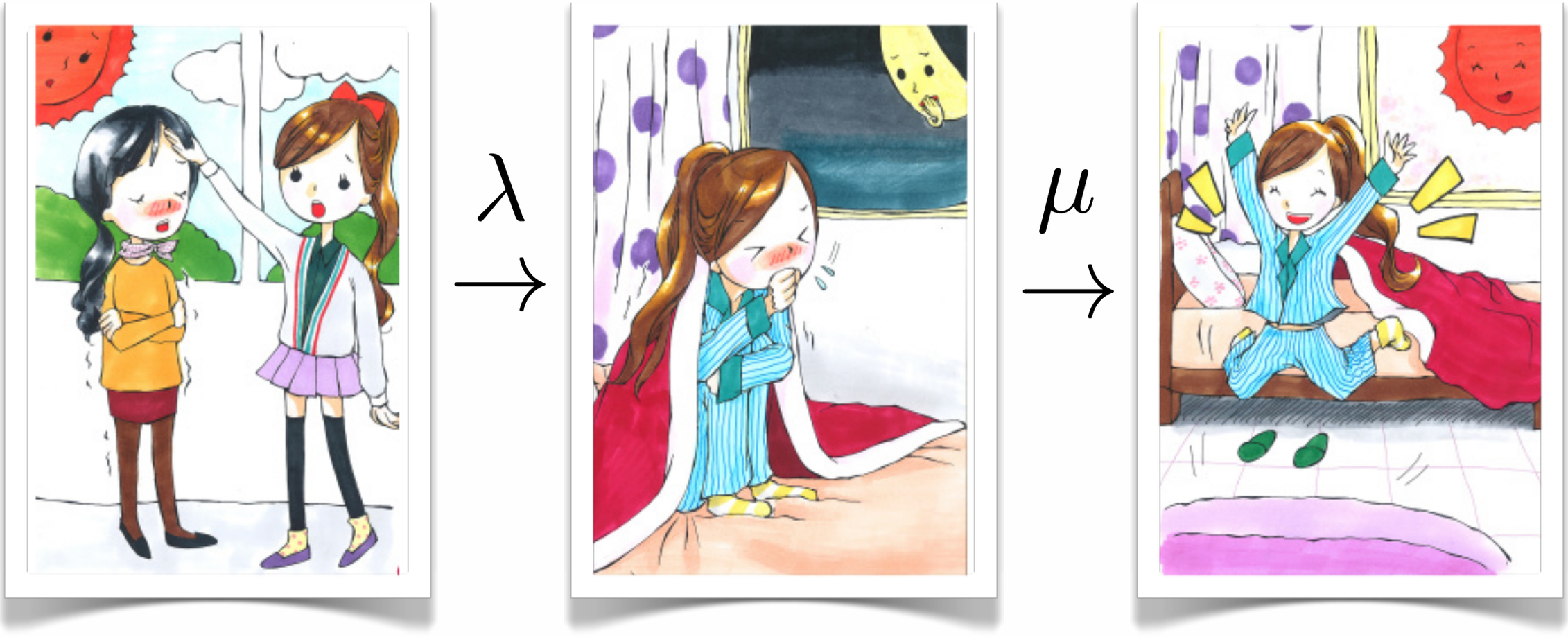
S - Susceptible (Healty) **I** - Infected (and infectious) **R** - Recovered (immune/dead)

(From Petter Holme's blog)

Compartmental models

The transitions (e.g. S$\rightarrow$I) is mediated by some rates (λ) and the encounters between individuals.

The final impact of an SIR epidemic is given by the fraction of affected (Recovered) individuals

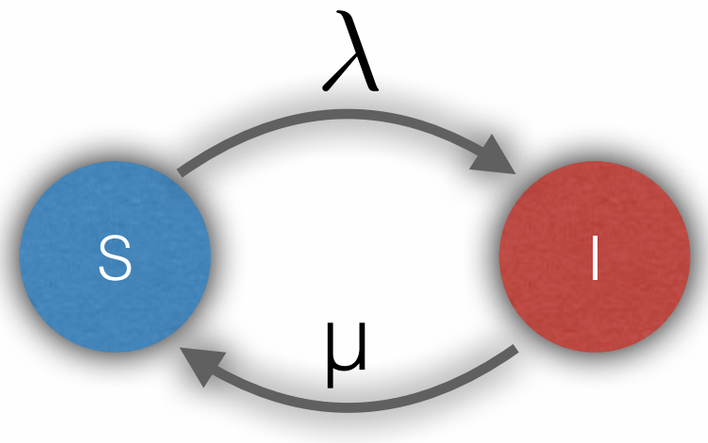


S - Susceptible (Healty) **I** - Infected (and infectious) **R** - Recovered (immune/dead)

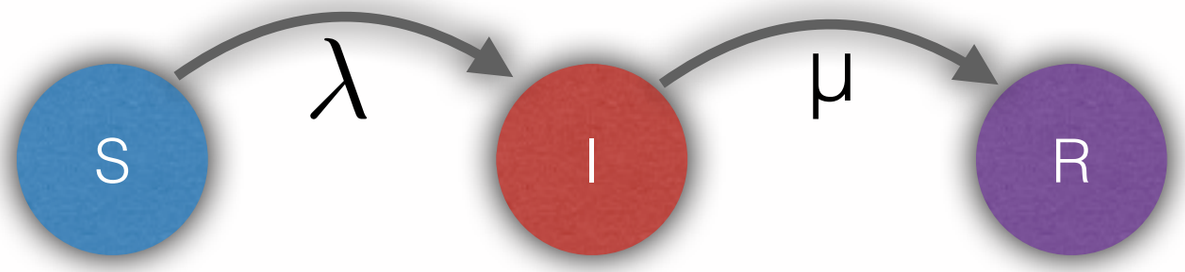
(From Petter Holme's blog)

Some examples

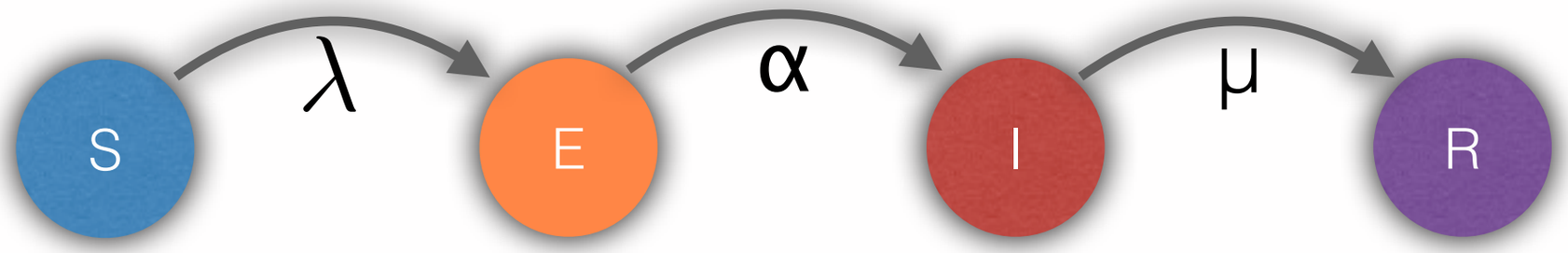
SIS



SIR

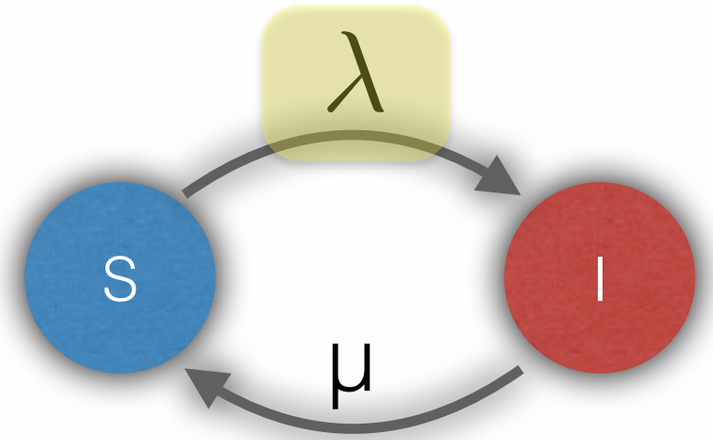


SEIR

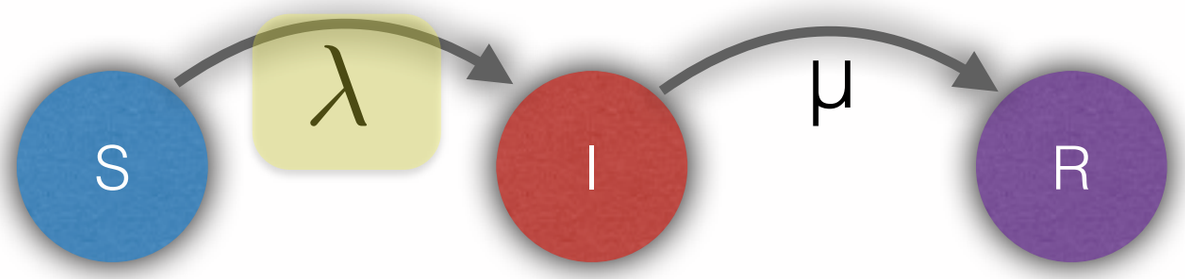


Some examples

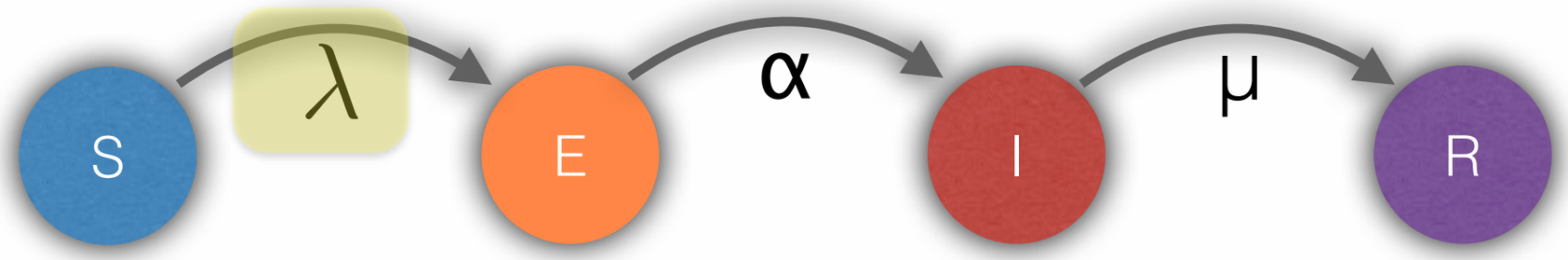
SIS



SIR



SEIR



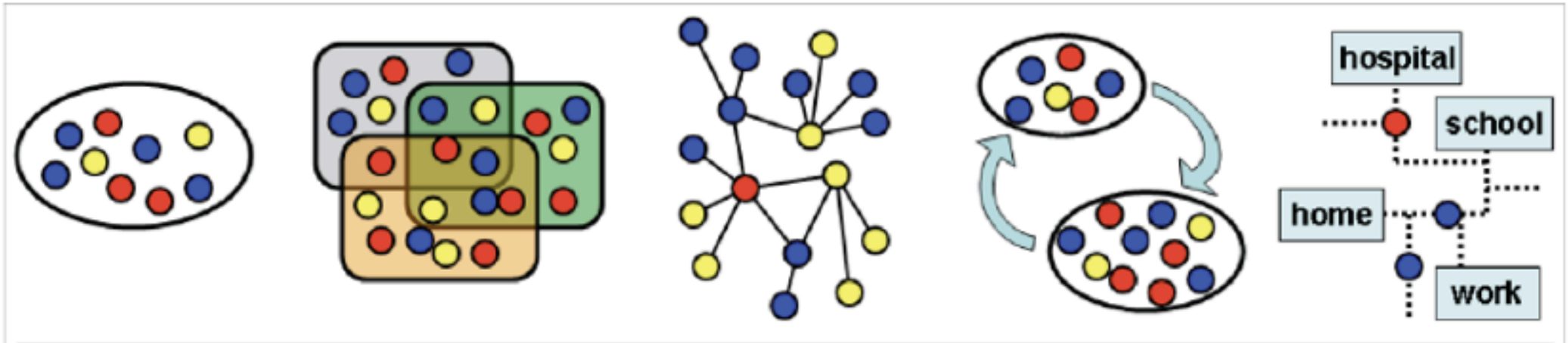
QUESTION: What is the minimum value of λ for the epidemic outbreak to take place?

Part I

Simple Models

Approaches to Epidemic Modeling

From ideal (simple) to real (complex) interactions



Homogeneous mixing	Social structure	Contact network models	Multi-scale models	Agent Based models

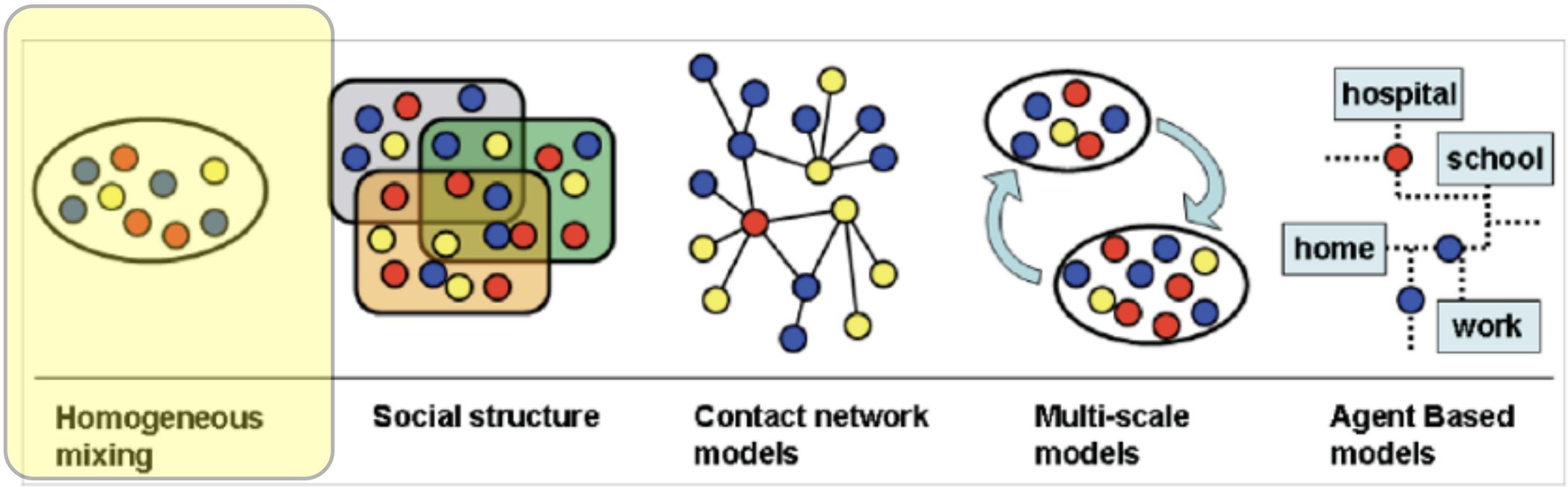
Simple → **Realistic**

Ability to explain (caveats) trends at a population level

Model realism looses in transparency.
Validation is harder.

Approaches to Epidemic Modeling

From ideal (simple) to real (complex) interactions



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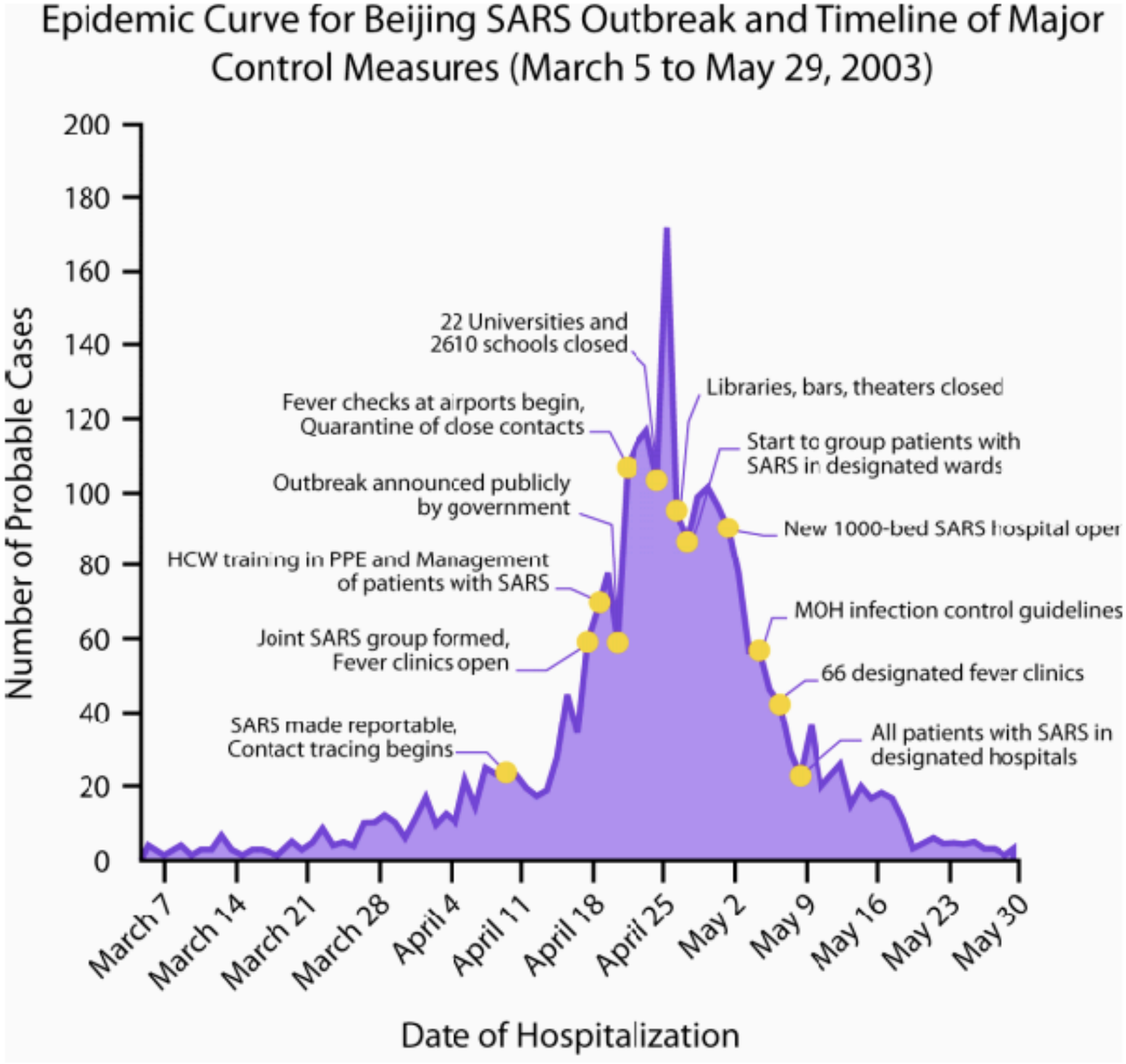
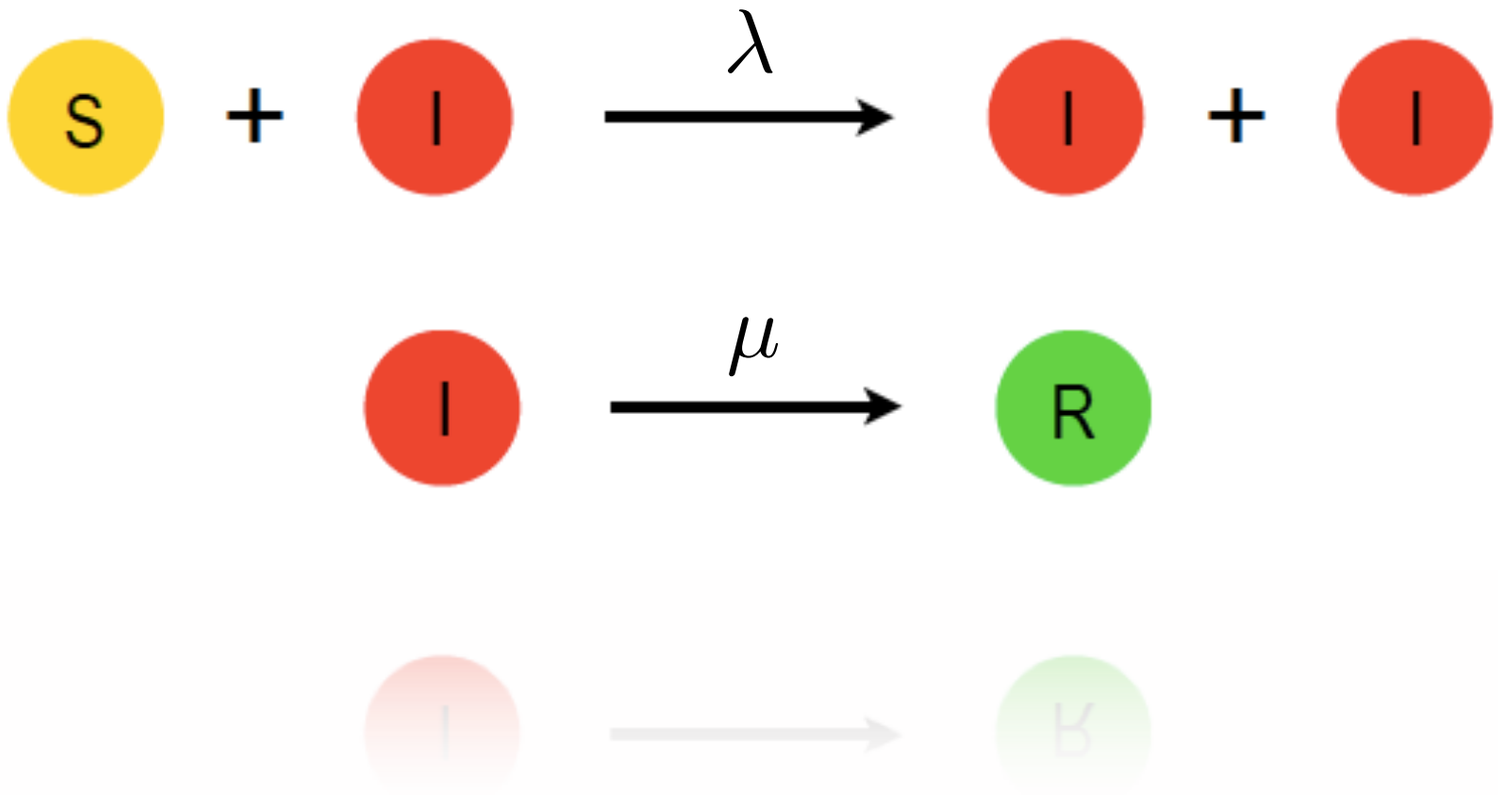


SIR model

SIR basic processes



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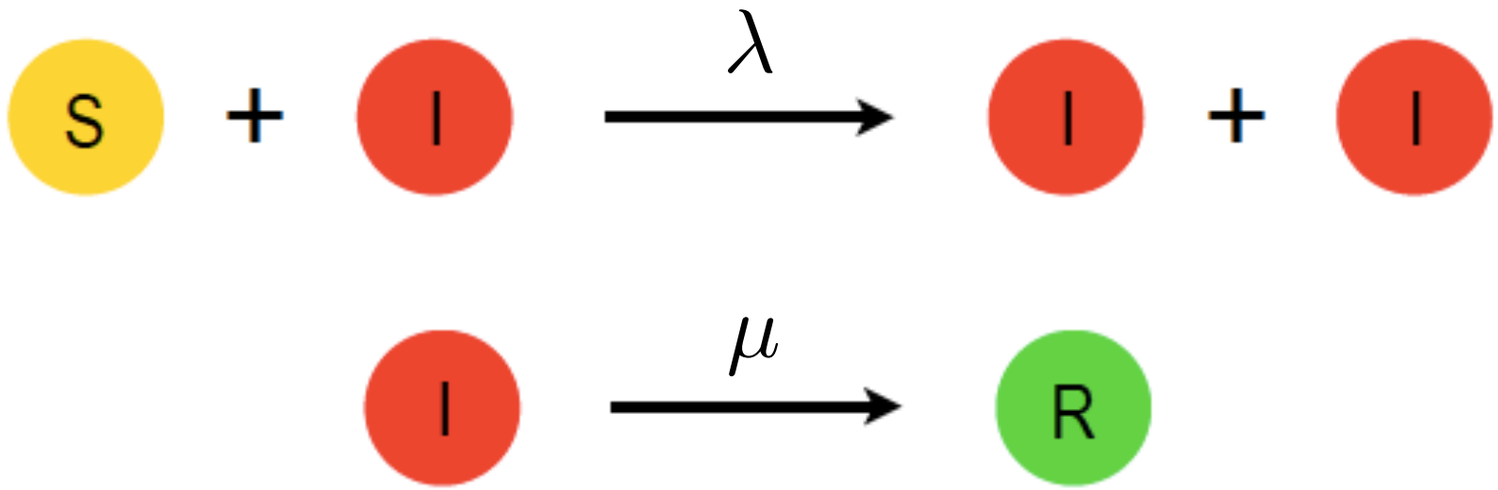
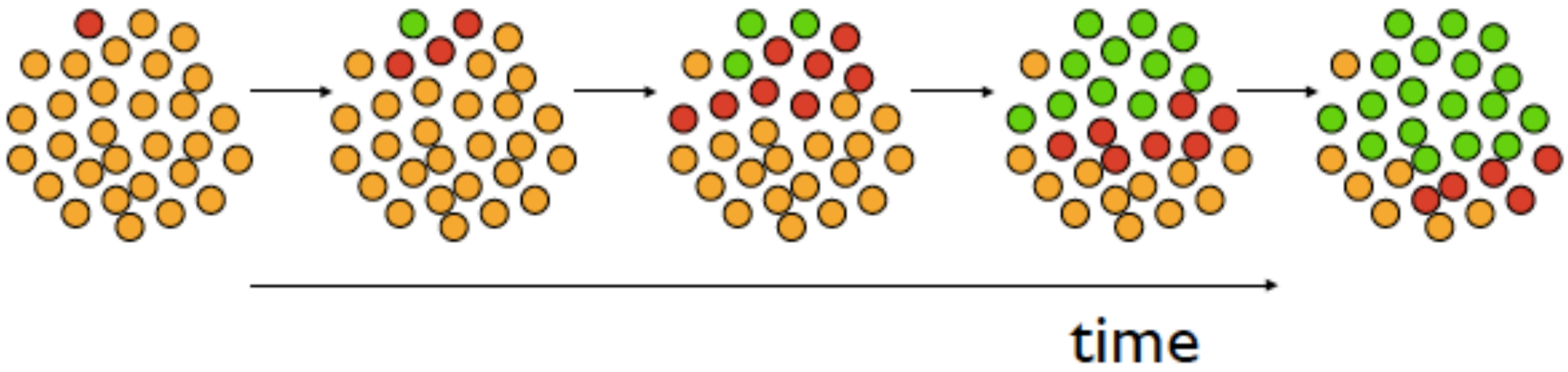
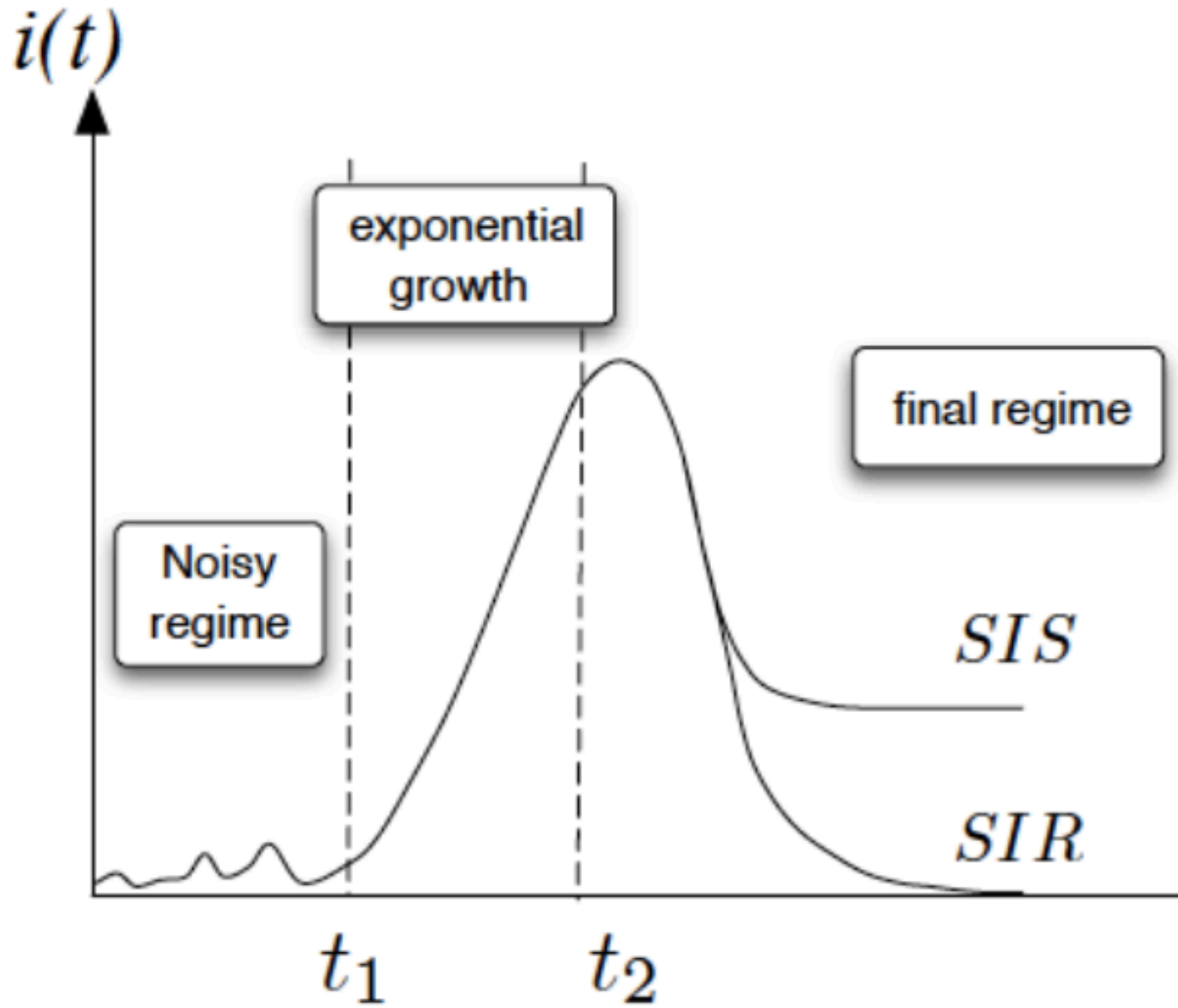


homogeneous mixing



SIS *versus* SIR



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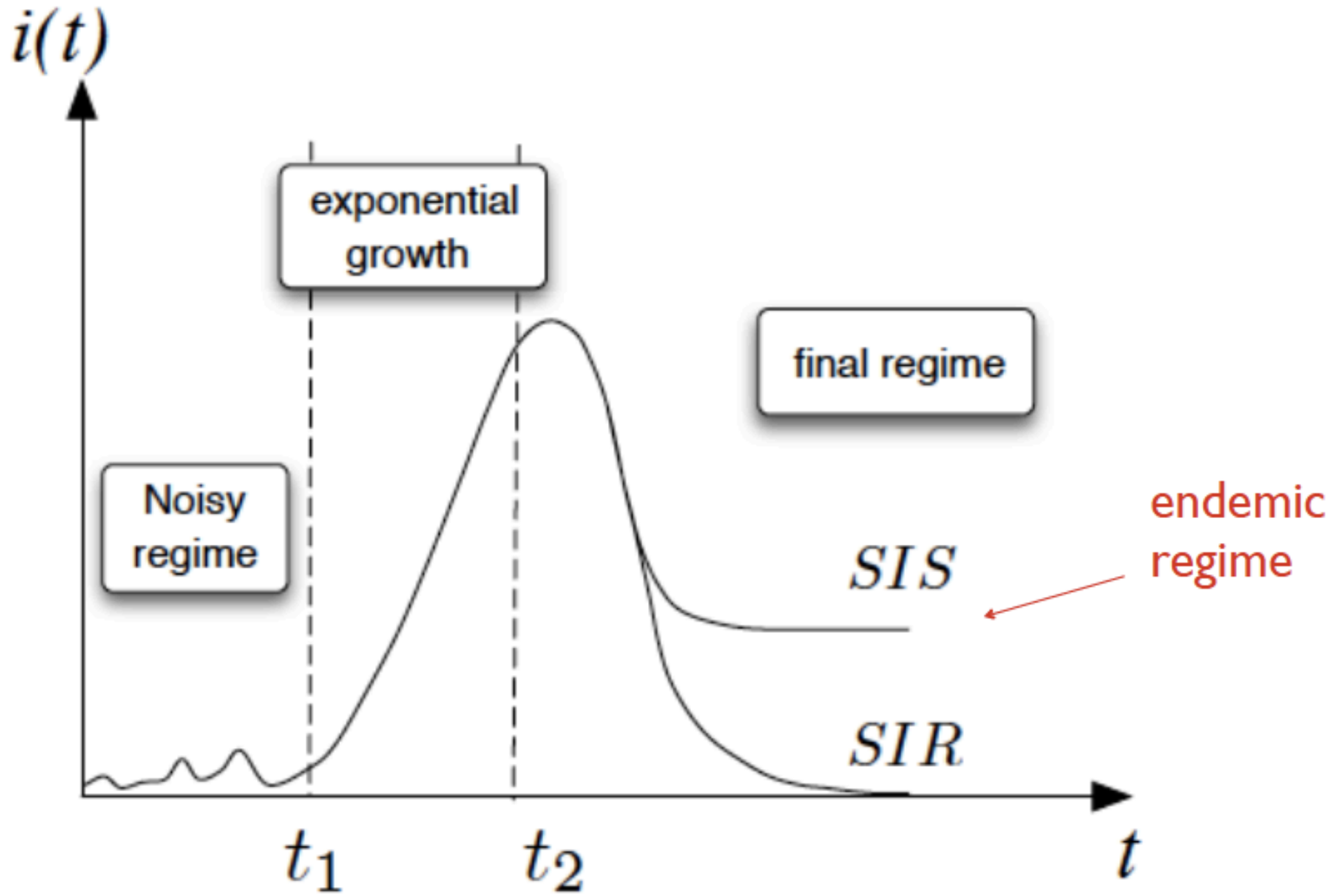

SIR model

$$\frac{dI}{dt} = \lambda \langle k \rangle S \frac{I}{N} - \mu I$$

SIR model

new infections loss of infectiousness

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average #contacts

$$\beta = \lambda \langle k \rangle$$ per-contact transmissibility

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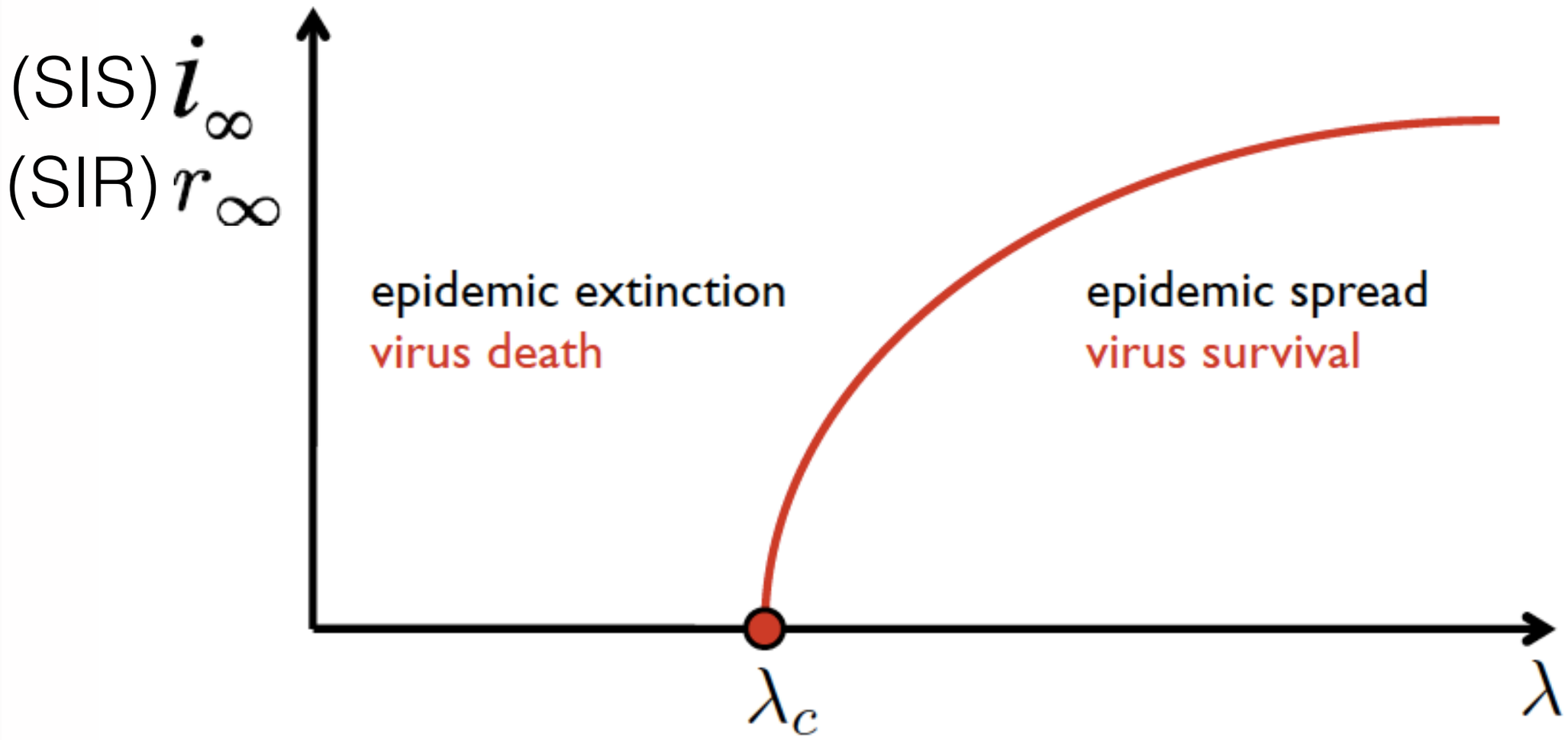
$$\frac{di}{dt} > 0 \Leftrightarrow \lambda > \lambda_c = \mu / \langle k \rangle$$ epidemic threshold

epidemic threshold



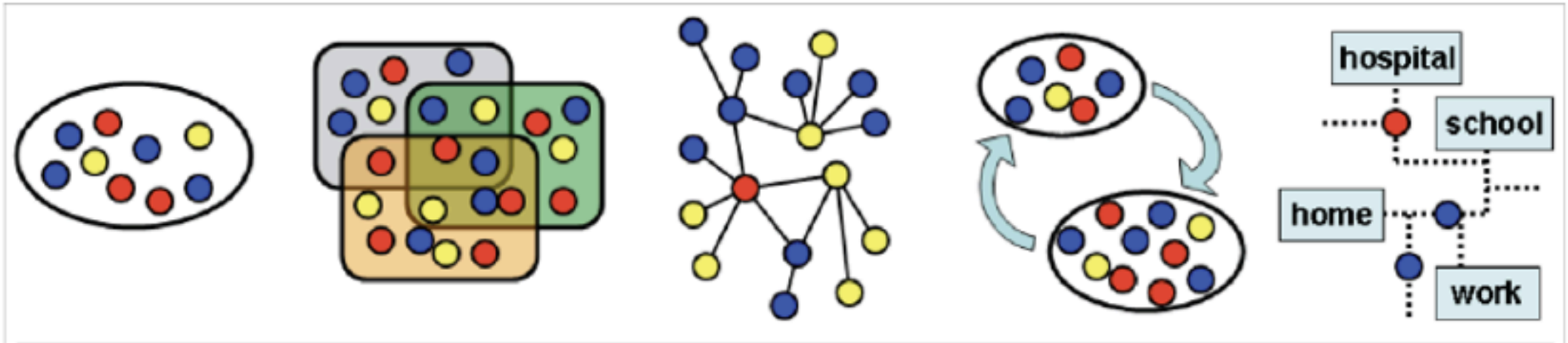
- very general result (SI, SIS, SEIR, ...)
- related to the reproductive number

Part II

Beyond Mean field

Approaches to Epidemic Modeling

From ideal (simple) to real (complex) interactions



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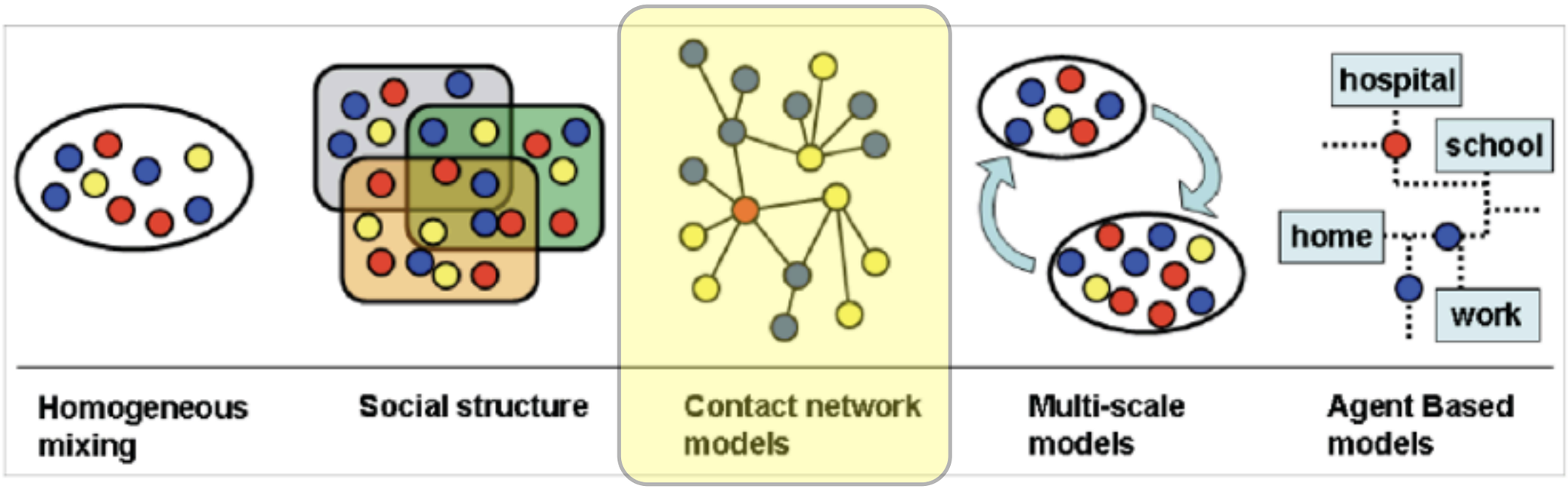

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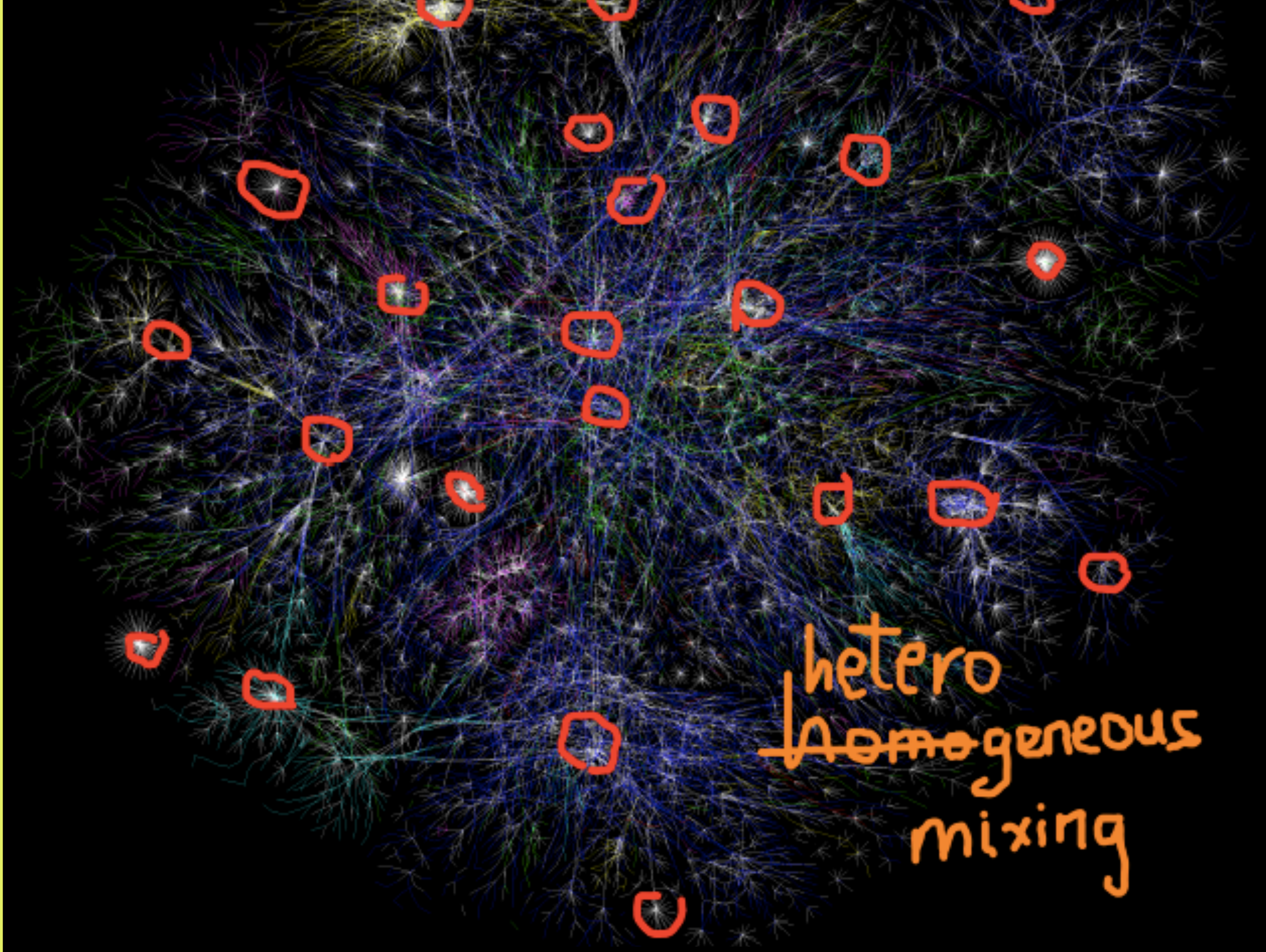
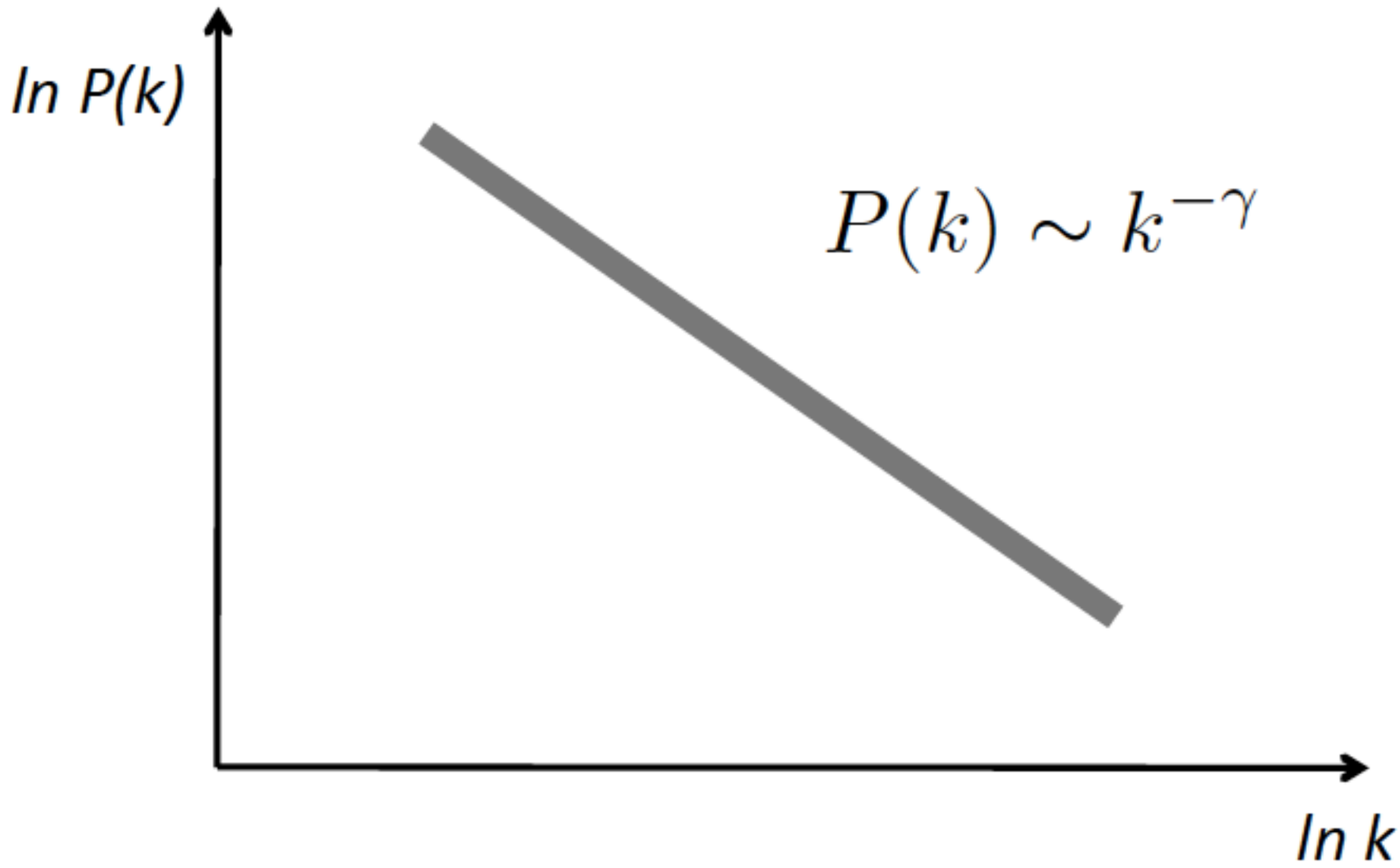
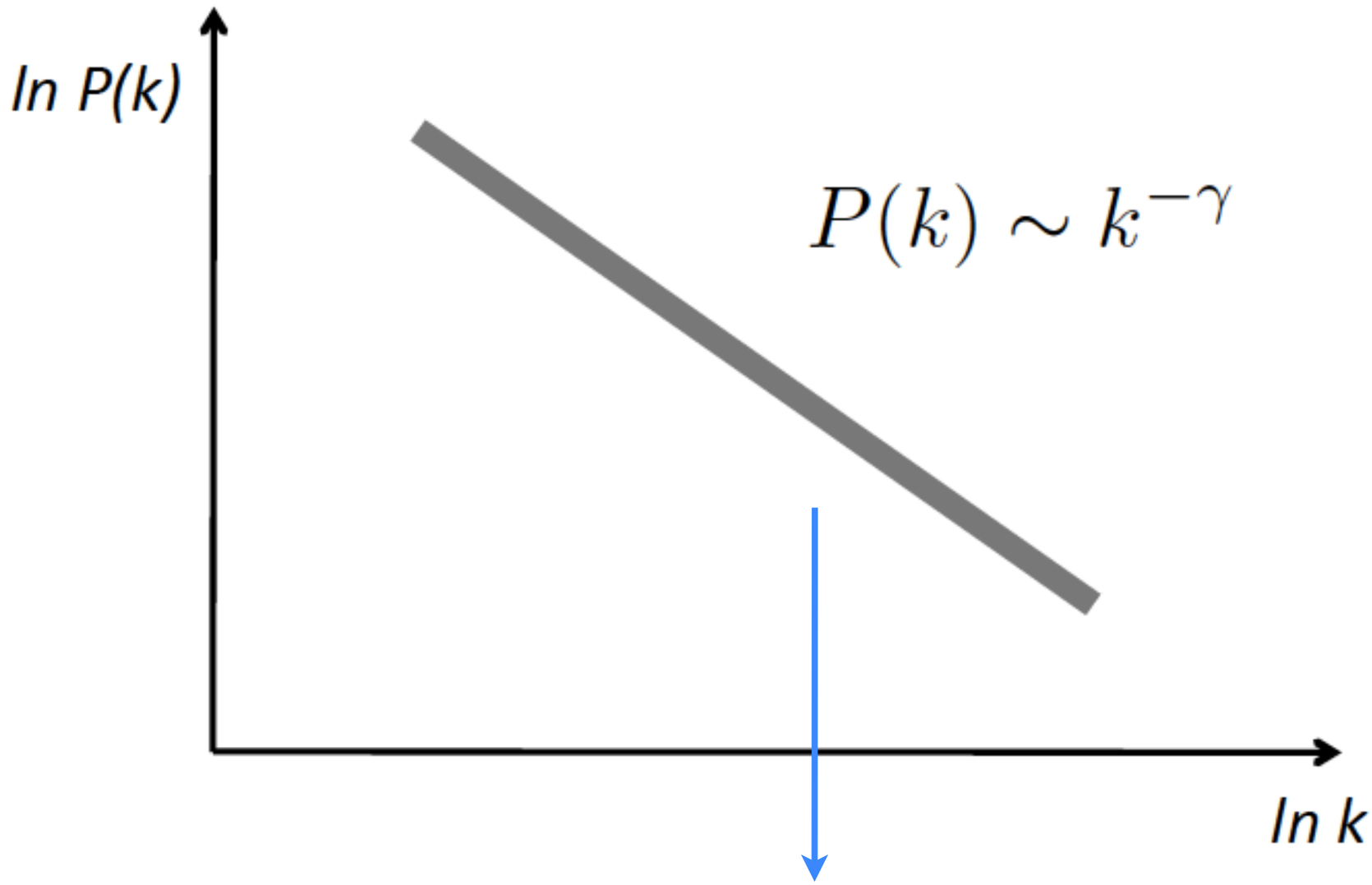

hetero
~~homo~~geneous
mixing

heterogeneous networks

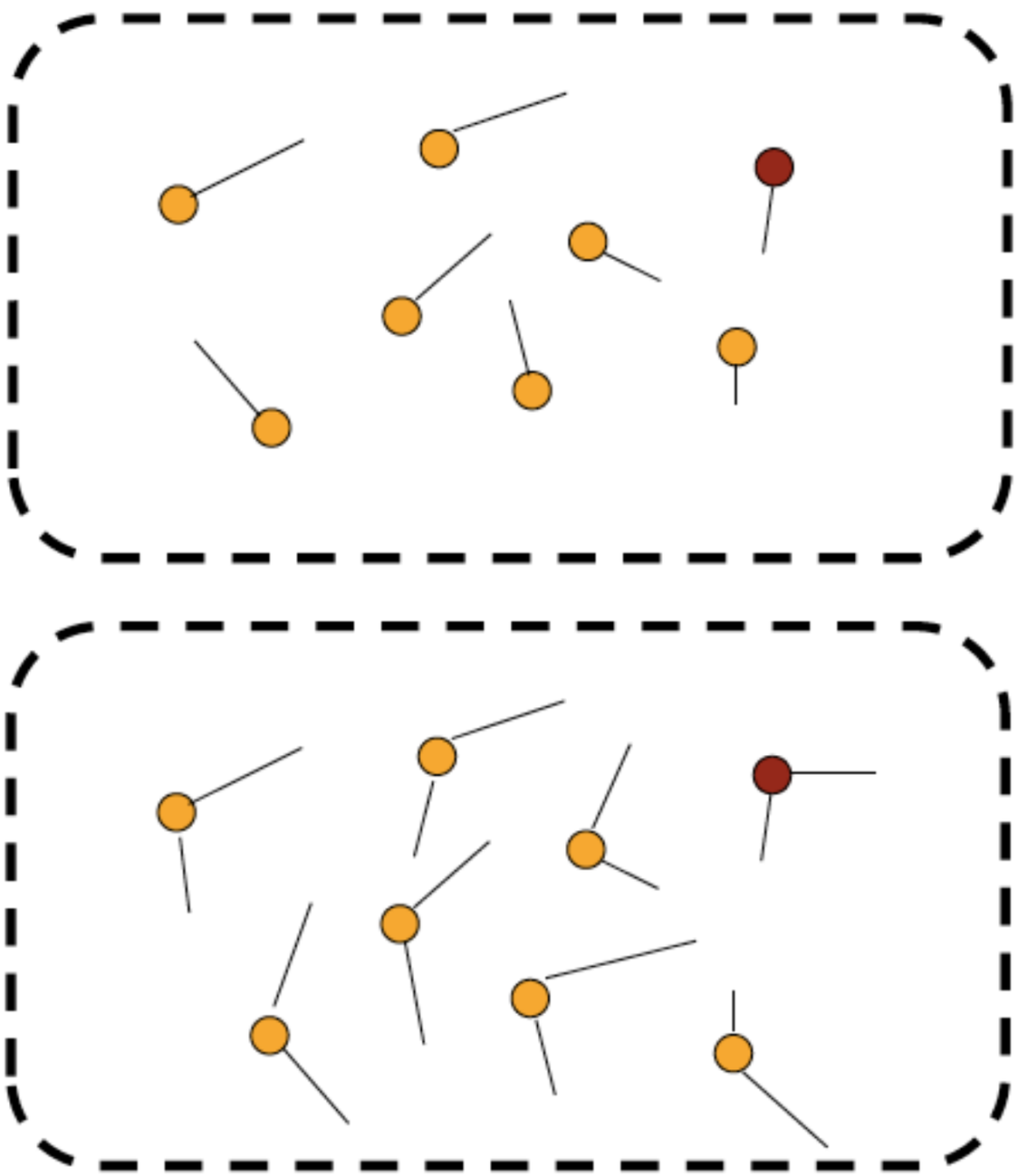


heterogeneous networks



heterogeneous mean field

degree-based representation or HMF



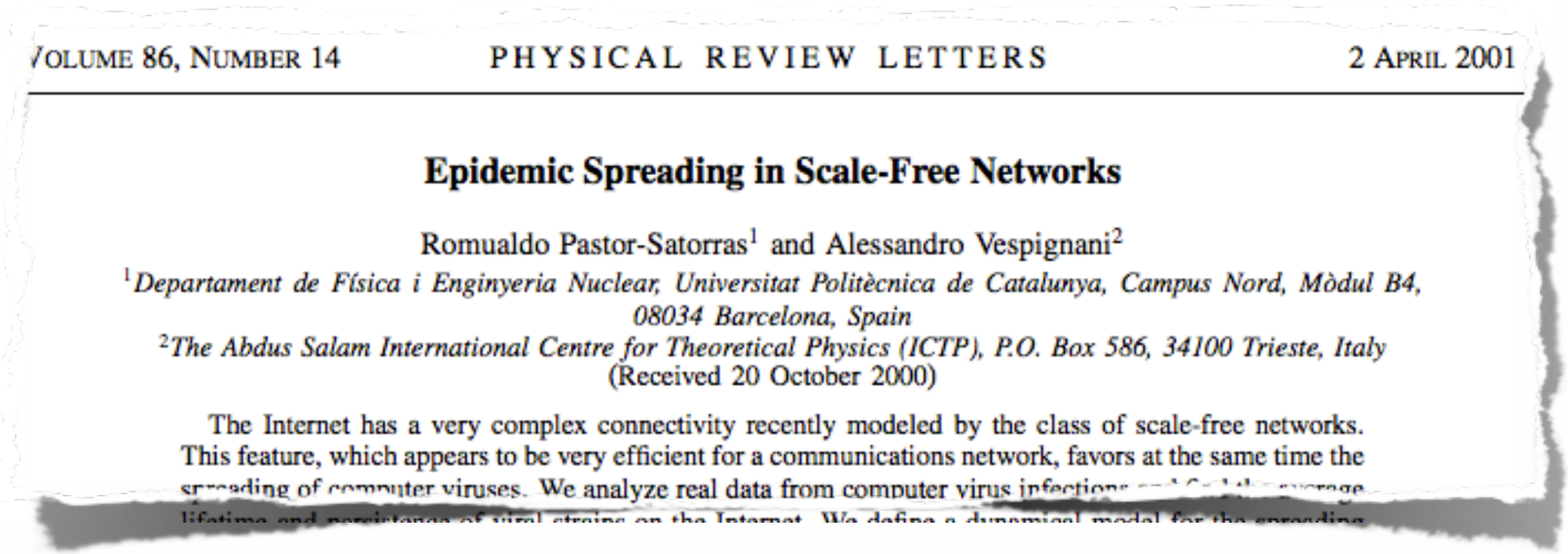
class of individuals with
degree k=1

class of individuals with
degree k=2

etc.

Contagion Processes & Networks

Probably the most prolific area of Network Science:
more than 5000 papers since 2001



VOLUME 86, NUMBER 14 PHYSICAL REVIEW LETTERS 2 APRIL 2001

Epidemic Spreading in Scale-Free Networks

Romualdo Pastor-Satorras[1] and Alessandro Vespignani[2]
[1]*Departament de Física i Enginyeria Nuclear, Universitat Politècnica de Catalunya, Campus Nord, Mòdul B4, 08034 Barcelona, Spain*
[2]*The Abdus Salam International Centre for Theoretical Physics (ICTP), P.O. Box 586, 34100 Trieste, Italy*
(Received 20 October 2000)

The Internet has a very complex connectivity recently modeled by the class of scale-free networks. This feature, which appears to be very efficient for a communications network, favors at the same time the spreading of computer viruses. We analyze real data from computer virus infections and find the average lifetime and persistence of viral strains on the Internet. We define a dynamical model for the spreading

more than 3300 citations in Google scholar

SIS on heterogeneous networks

In heterogeneous networks the approximation $k \sim \langle k \rangle$ doesn't hold

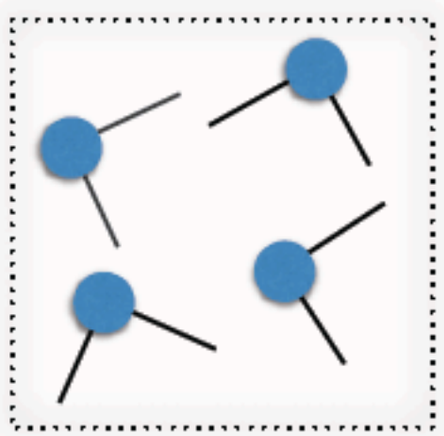
Solution:
Degree Block approximation

~~All the nodes are statistically equivalent~~
All the nodes with the same degree are statistically equivalent

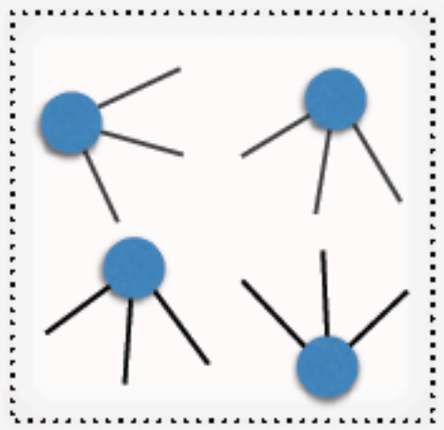
$$i_k = \frac{I_k}{N_k} \qquad s_k = \frac{S_k}{N_k}$$

$$i = \sum_k P(k) i_k \qquad s = \sum_k P(k) s_k$$

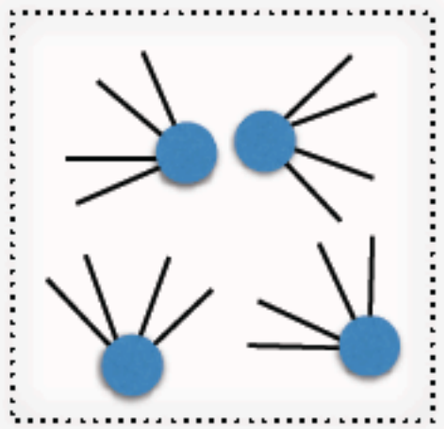
k = 2



k = 3



k = 4



SIS on heterogeneous networks

formulation

$$\frac{di_k(t)}{dt} = \lambda k[1 - i_k]\Theta_k(t) - \mu i_k(t)$$

Density of infected neighbors for a node of degree k

$\Theta_k(t)$ probability that a given link of a node of degree k points to an infected node

$$\Theta_4(t) = \frac{1}{4}$$

in homogeneous networks $\Theta_k(t) = i_k(t)$

SIS on heterogeneous networks

the form of $\Theta_k(t)$

if we assume no degree correlations

Probability of a node of degree k to be connected with a node with degree k'

$$P(k'|k) = \frac{k'P(k')}{\sum_{k'} k'P(k')} = \frac{k'P(k')}{\langle k \rangle}$$

$P(k'|k)$ doesn't depend on *k*

thus

$$\Theta_k(t) = \Theta(t) = \frac{\sum_{k'} k'P(k')i_{k'}(t)}{\langle k \rangle}$$

SIS on heterogeneous networks

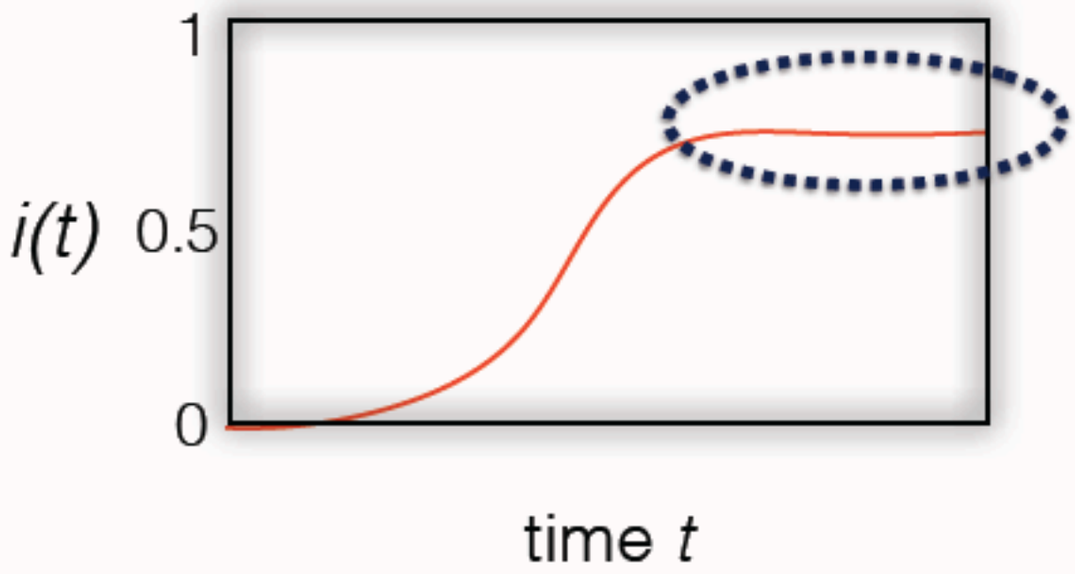
Epidemic threshold: outline of the solution

- consider the stationary state
- write i_k as function of Θ
- Substitute i_k in the expression of Θ and get a self-consistent equation
- Solve it with the graphical method

SIS on heterogeneous networks

the stationary state

$$i_k(t) = i_k \quad \Theta(t) = \Theta \qquad \frac{di_k(t)}{dt} = 0$$



$$\frac{di_k(t)}{dt} = \lambda k[1 - i_k]\Theta_k(t) - \mu i_k(t) \quad \Rightarrow \quad 0 = \lambda\,(1 - i_k)k\Theta - \mu i_k$$

$$i_k = \frac{k\lambda\Theta}{\mu + k\lambda\Theta}$$

SIS on heterogeneous networks

Substitute i_k and get a self-consistent eq

$$i_k = \frac{k\lambda\Theta}{\mu + k\lambda\Theta}$$

if we assume no degree correlations

$$\Theta_k(t) = \Theta(t) = \frac{\sum_{k'} k' P(k') i_{k'}(t)}{\langle k \rangle}$$

self-consistent expression

$$\Theta = \frac{1}{\langle k \rangle} \sum_k k P(k) \frac{k\lambda\Theta}{\mu + k\lambda\Theta}$$

always has the trivial solution ($\Theta = 0$).
We are interested in the no-trivial ones (endemic state)

SIS on heterogeneous networks

idea

plot the two sides of the eq. separately
and look for their intersection

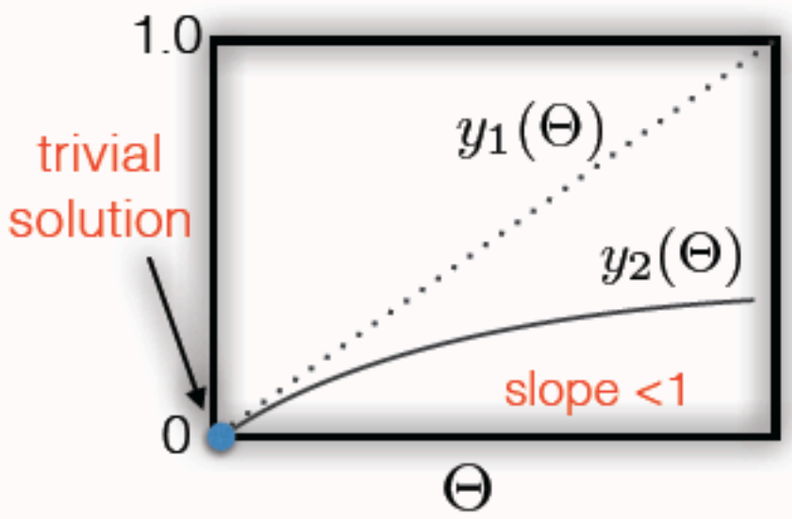
$$\Theta = \frac{1}{\langle k \rangle} \sum_k k P(k) \frac{k\lambda\Theta}{\mu + k\lambda\Theta}$$

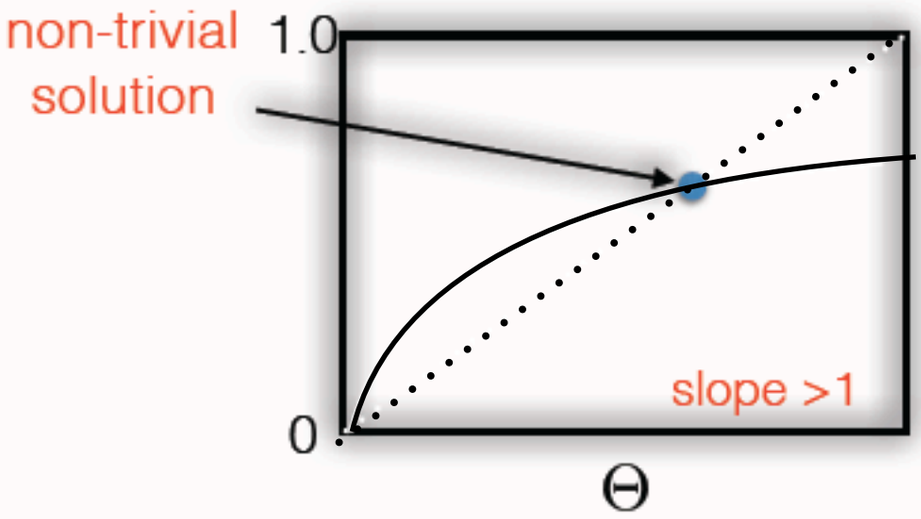
linear with slope 1

$$y_1(\Theta) = \Theta$$

monotonically increasing between $\Theta=0$ and $\Theta=1$

$$y_2(\Theta) = \frac{1}{\langle k \rangle} \sum_k k P(k) \frac{k\lambda\Theta}{\mu + k\lambda\Theta}$$

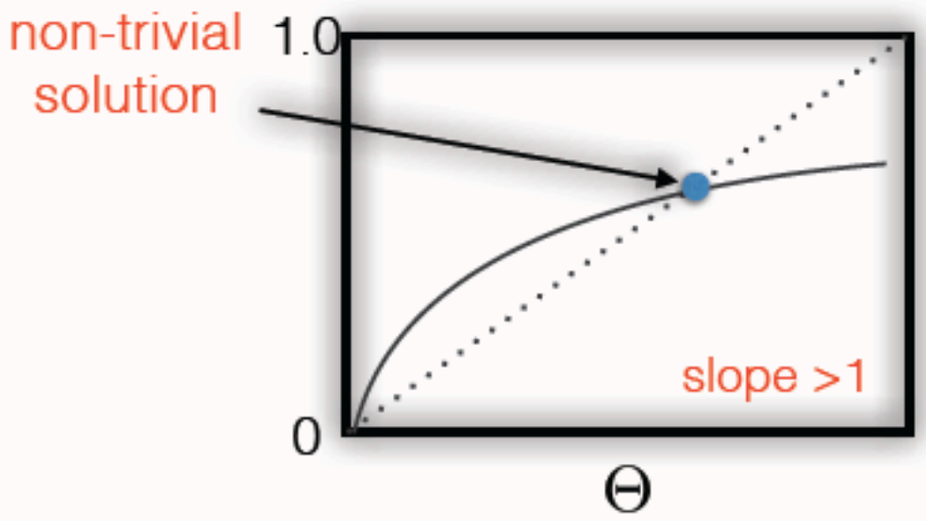




SIS on heterogeneous networks

condition:

smallest ($\Theta=0$) non-trivial solution



epidemic threshold:

$$\frac{dy_1(\Theta)}{d\Theta} = 1 \qquad \left(\frac{dy_2(\Theta)}{d\Theta}\right)_{\Theta=0} \qquad \frac{d}{d\Theta}\left(\frac{1}{\langle k\rangle}\sum_k kP(k)\frac{k\lambda\Theta}{\mu+k\lambda\Theta}\right)_{\Theta=0}$$

after some math

$$\frac{1}{\langle k\rangle}\sum_k kP(k)\,k\lambda\left(\frac{\mu+k\lambda\Theta-k\lambda\Theta}{(\mu+k\lambda\Theta)^2}\right)_{\Theta=0} = \frac{1}{\langle k\rangle}\sum_k kP(k)\,k\lambda\frac{\mu}{\mu^2}$$

SIS on heterogeneous networks

simplifying:

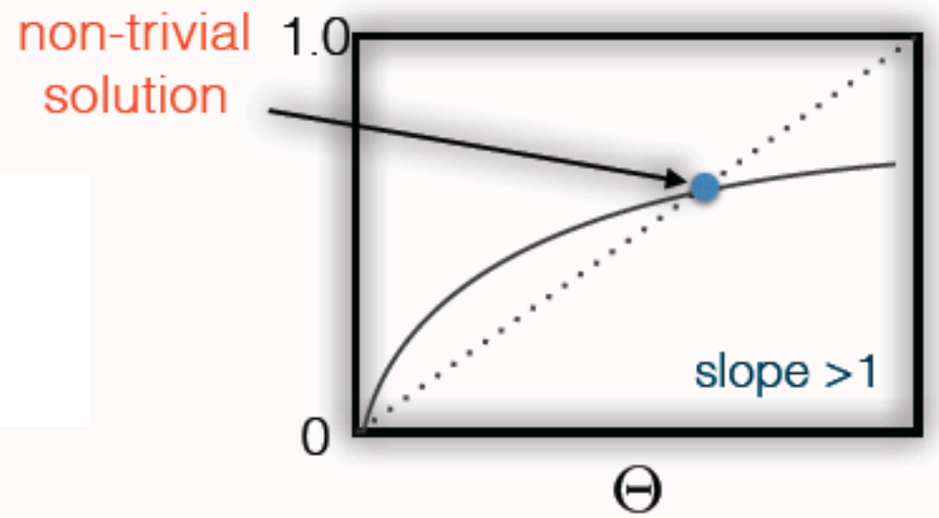
$$\frac{1}{\langle k\rangle}\sum_k kP(k)\,k\lambda\frac{\mu}{\mu^2}=\frac{\lambda}{\mu}\frac{1}{\langle k\rangle}\langle k^2\rangle$$

epidemic threshold:

at the critical point the two derivatives are equal

$$\frac{\lambda}{\mu}\frac{\langle k^2\rangle}{\langle k\rangle}=1$$

$$\lambda_c=\frac{\mu\langle k\rangle}{\langle k^2\rangle}\neq\frac{\mu}{\langle k\rangle}$$

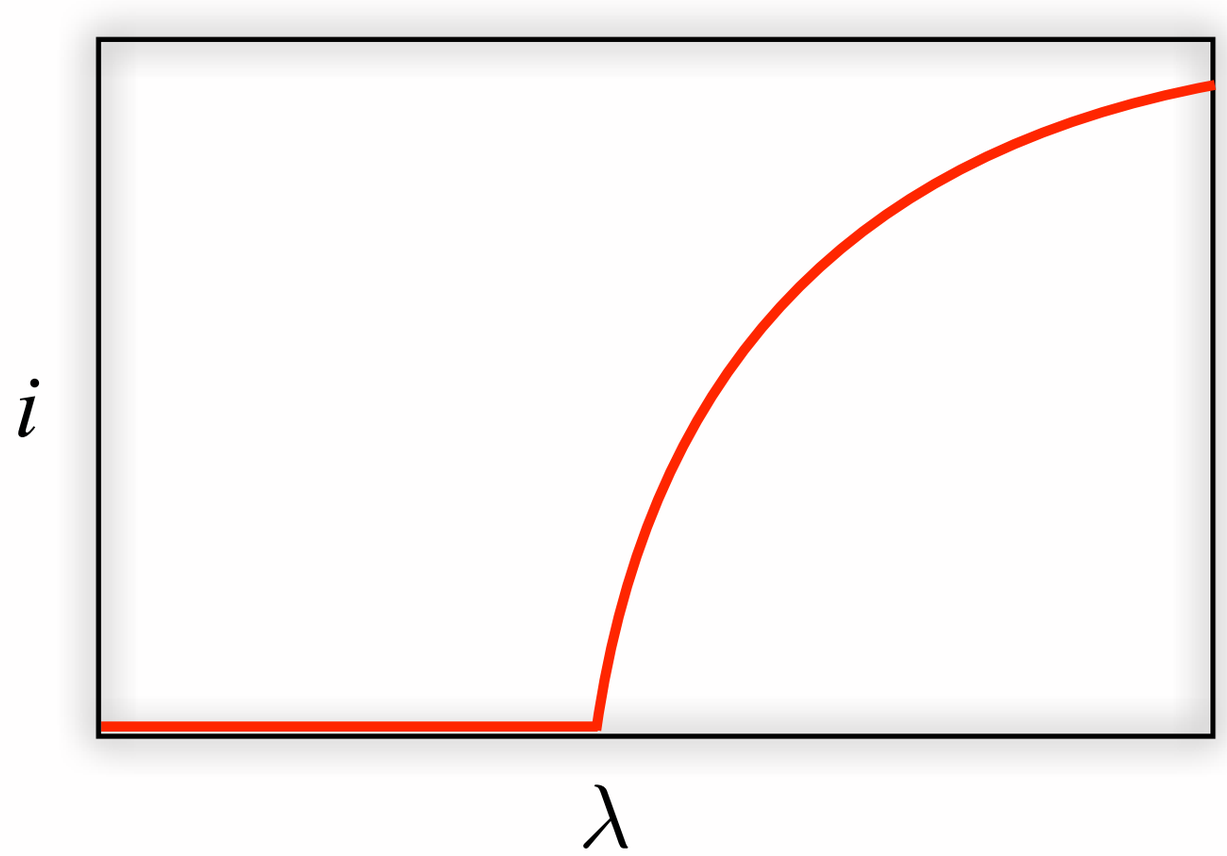


Epidemics on general Networks

$$\lambda_c \sim \frac{\langle k \rangle}{\langle k^2 \rangle}$$

- in **Homogenous** networks:

$$\langle k^2 \rangle = \langle k \rangle^2 \longrightarrow \lambda_c \sim \frac{1}{\langle k \rangle}$$



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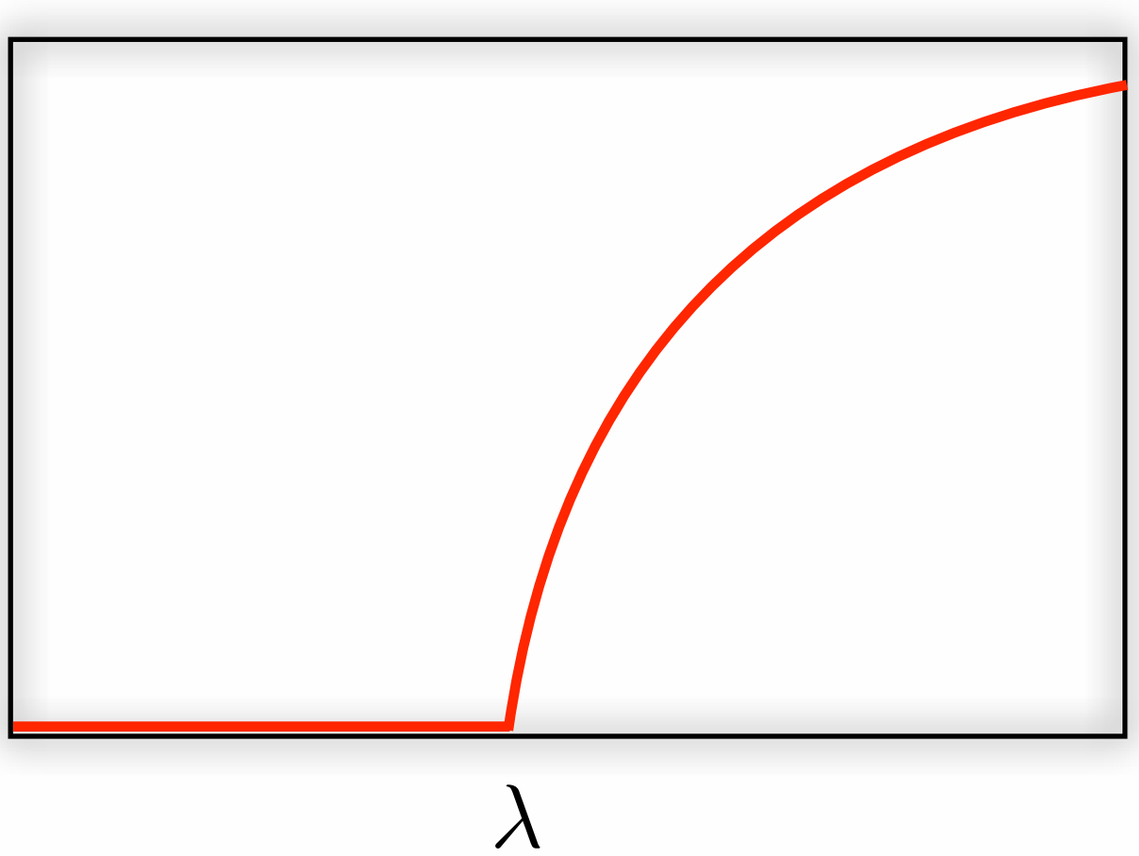
- in **Scale-Free** networks $P(k) \sim k^{-\gamma}$

if $2 < \gamma < 3$ then $\langle k^2 \rangle \to \infty$

$$\lambda_c \to 0$$



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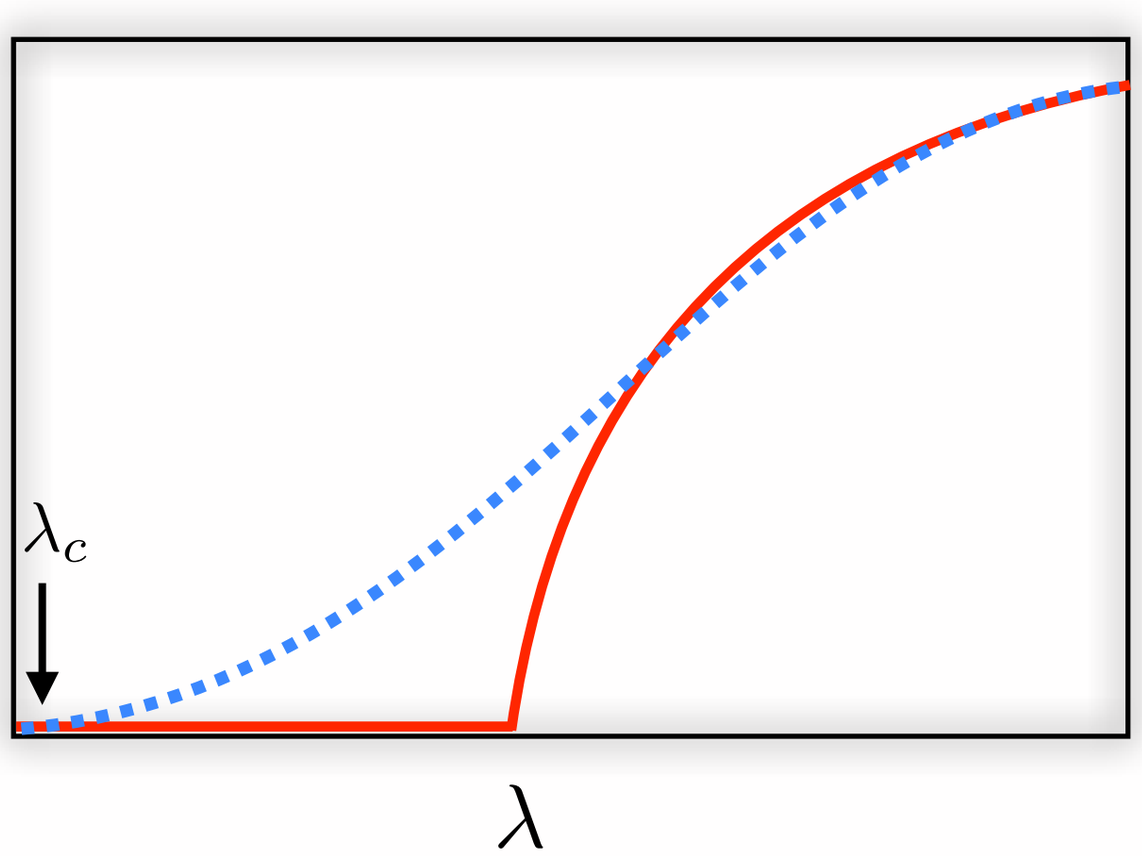

Alternative Analysis

Microscopic Markov Chain Approach

SIS model

$p_i(t)$: Probability that agent (node) i is infected at time t

SIS model

$p_i(t)$: Probability that agent (node) i is infected at time t

Prob. it remains inf. if inf.

$$p_i(t+1) = p_i(t)(1-\mu) + (1-p_i(t))\,q_i(t)$$

Prob. it gets infected if healthy

SIS model

$p_i(t)$: Probability that agent (node) i is infected at time t

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$$p_i(t+1) = p_i(t)(1-\mu) + (1-p_i(t))\,q_i(t)$$

Prob. it gets infected if healthy

$$q_i(t) = 1 - \prod_{j=1}^{N} [1 - \lambda A_{ij} p_j(t)]$$

SIS model

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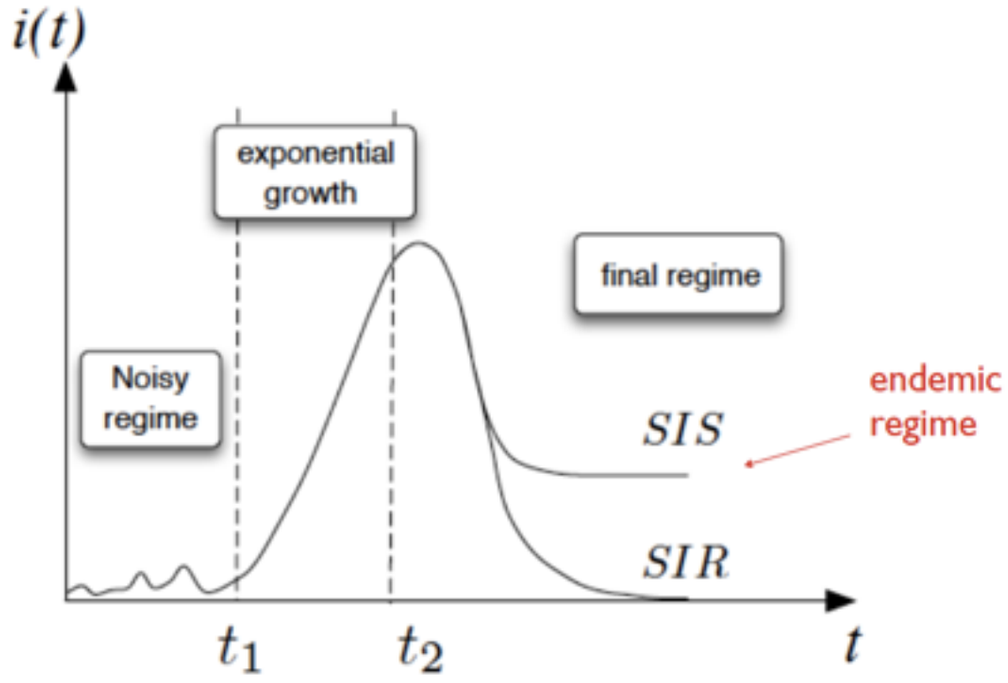
$$q_i(t) = 1 - \prod_{j=1}^{N} [1 - \lambda A_{ij} p_j(t)]$$

$$< I > (t) = \sum_{i=1}^{N} p_i(t)$$

SIS model

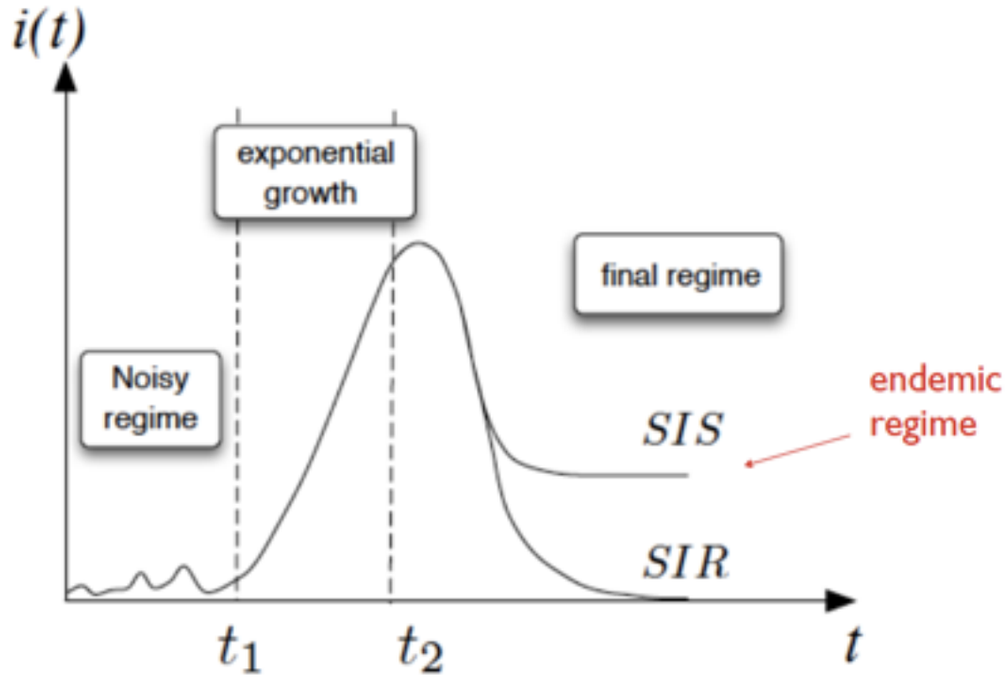
$$\lim_{t\to\infty} p_i(t) \to p_i^*$$



SIS model

$$\lim_{t\to\infty} p_i(t) \to p_i^*$$

$$p_i(t+1) = p_i(t) = p_i^*$$



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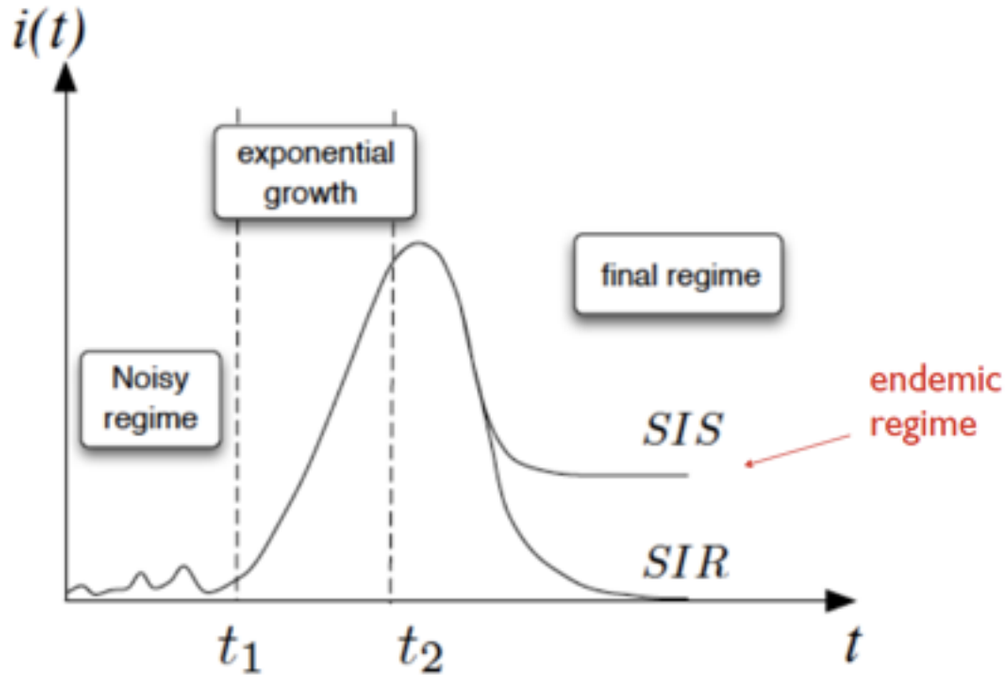

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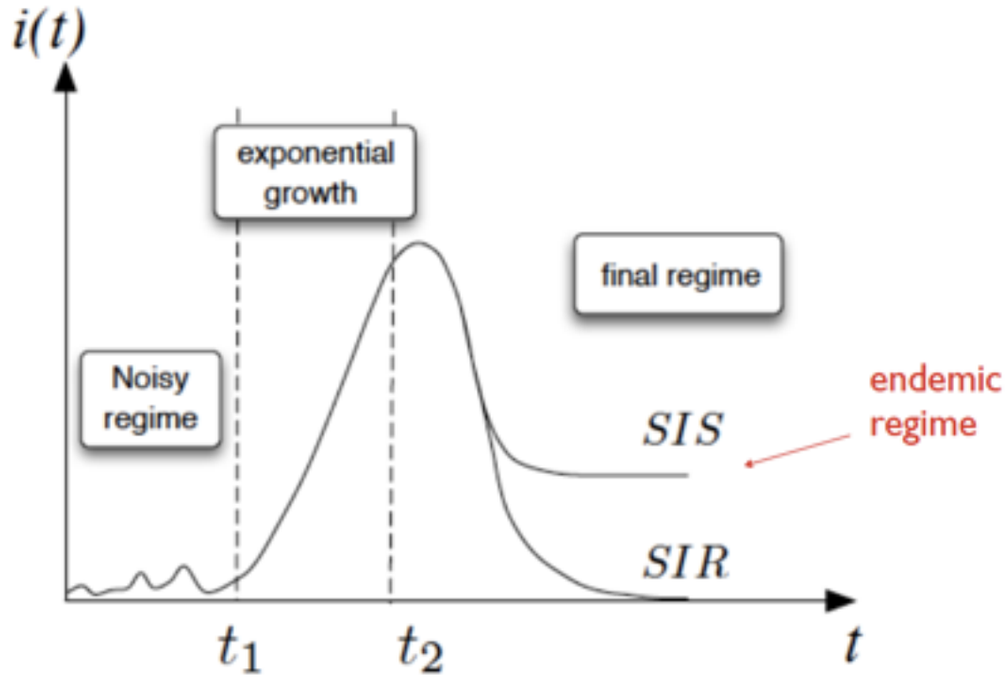
SIS model

$$\lim_{t\to\infty} p_i(t) \to p_i^*$$



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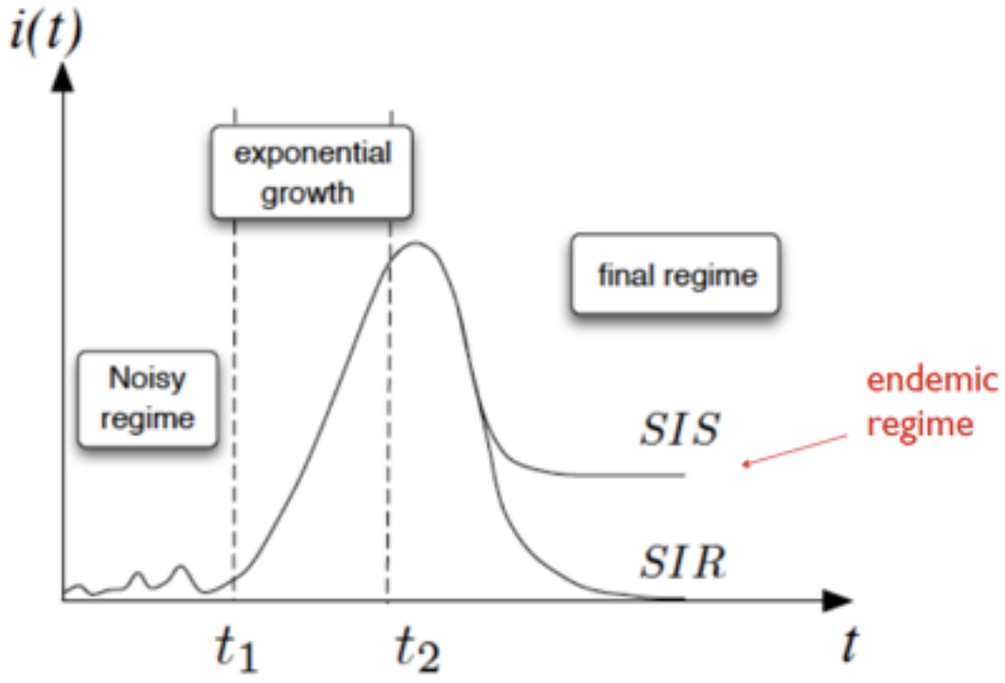
$$q_i^* = 1 - \prod_{j=1}^{N} \left[1 - \lambda A_{ij} p_j^*\right]$$

SIS model



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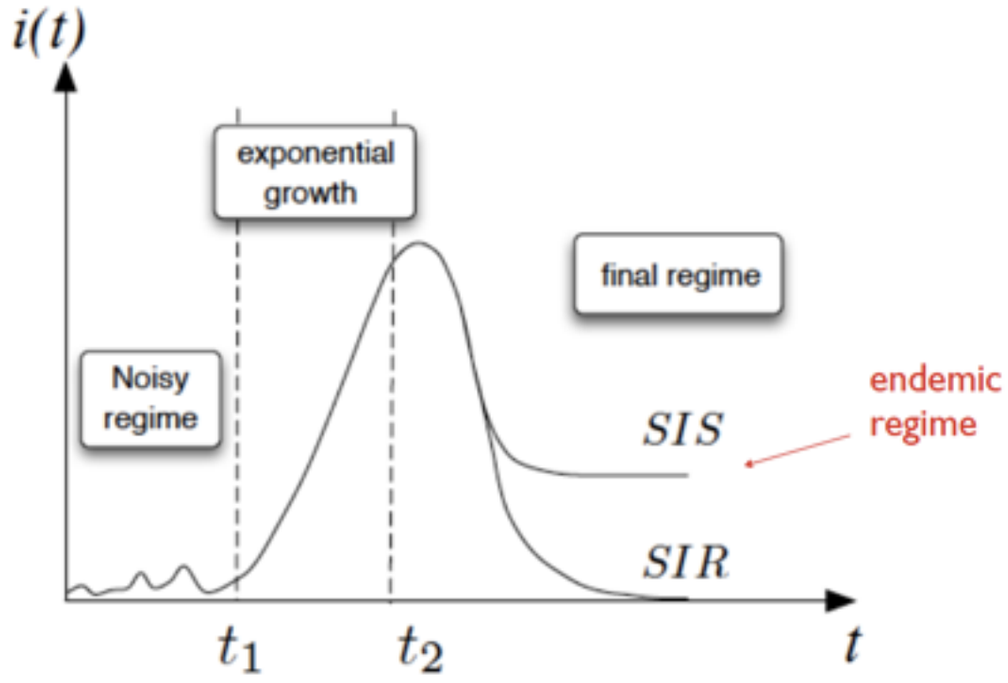
Epidemic Onset $\longrightarrow$ $p_i^\star = \epsilon_i^\star \ll 1$

SIS model

$$\lim_{t\to\infty} p_i(t) \to p_i^*$$



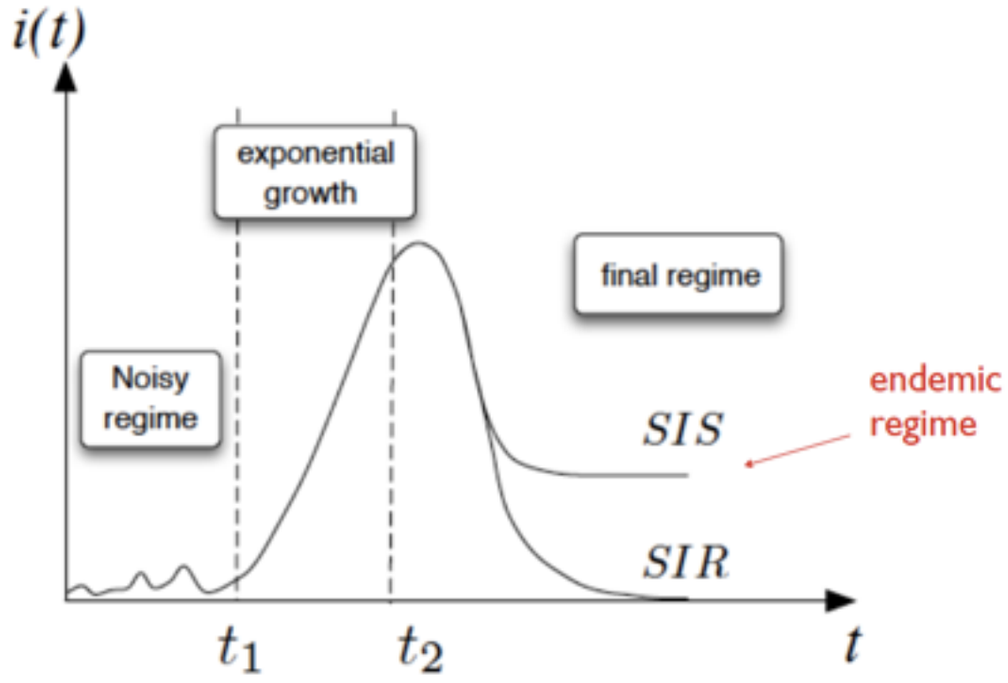
$$p_i(t+1) = p_i(t) = p_i^* \longrightarrow \mu p_i^* = (1-p_i^*)q_i^*$$

$$q_i^* = 1 - \prod_{j=1}^{N} \left[1 - \lambda A_{ij} p_j^*\right] \simeq \lambda \sum_{j=1}^{N} A_{ij}\epsilon_j^\star$$

Epidemic Onset $\longrightarrow$ $p_i^\star = \epsilon_i^\star \ll 1$

SIS model

$$\mu p_i^\star = (1 - p_i^*) q_i^*$$



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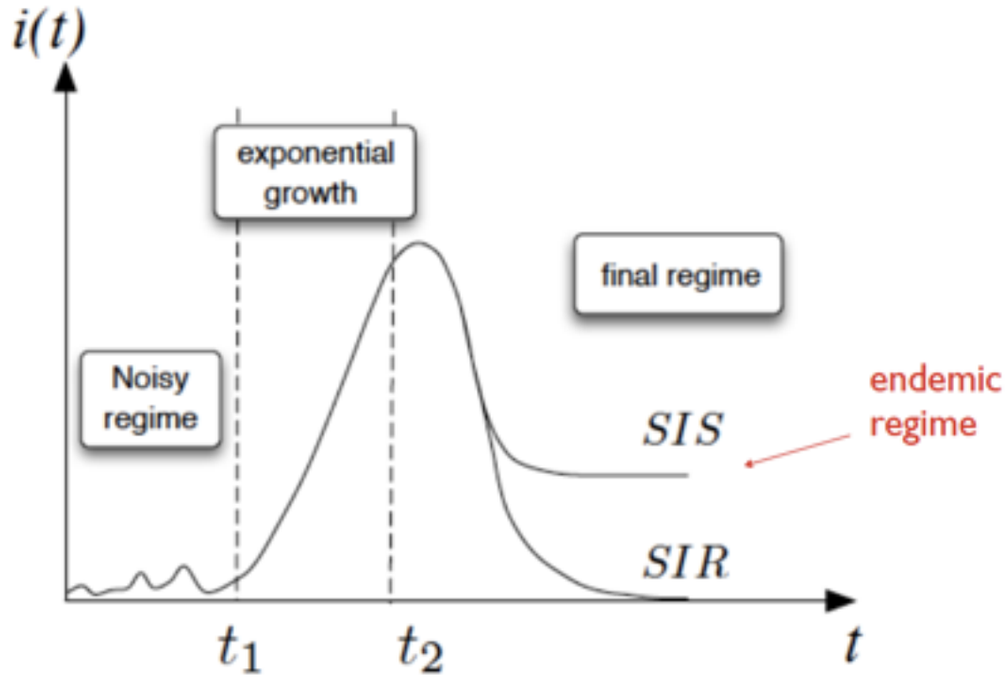

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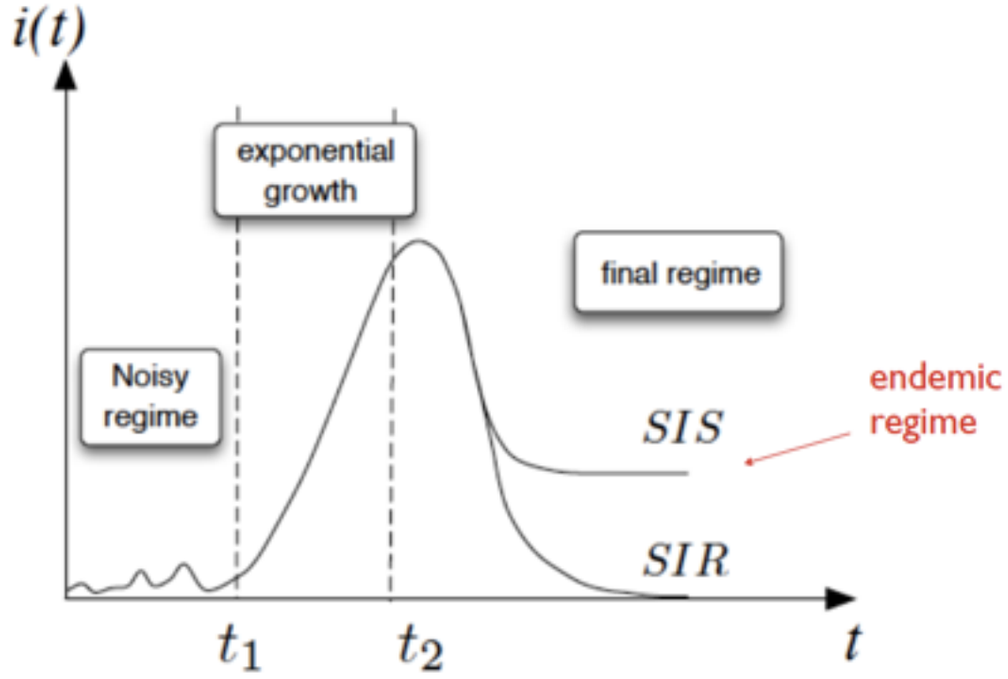
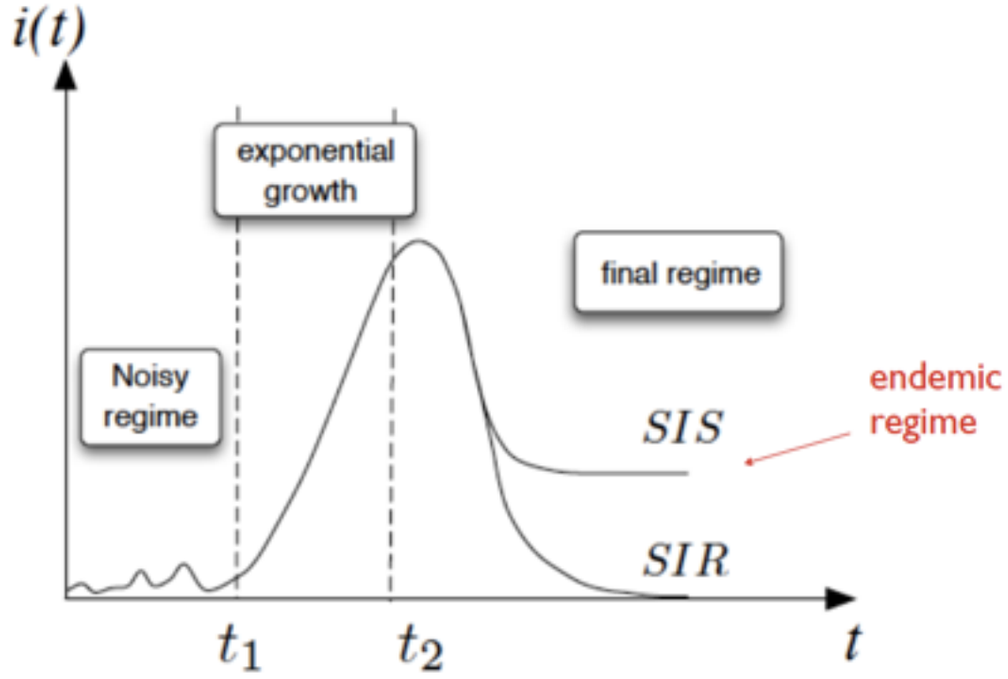


$$p_i^\star = \epsilon_i^\star \ll 1 \longrightarrow \mu \epsilon_i^\star = (1 - \epsilon_i^\star) \lambda \sum_{j=1}^{N} A_{ij} \epsilon_j^*$$

SIS model

$$\mu p_i^\star = (1 - p_i^*) q_i^*$$

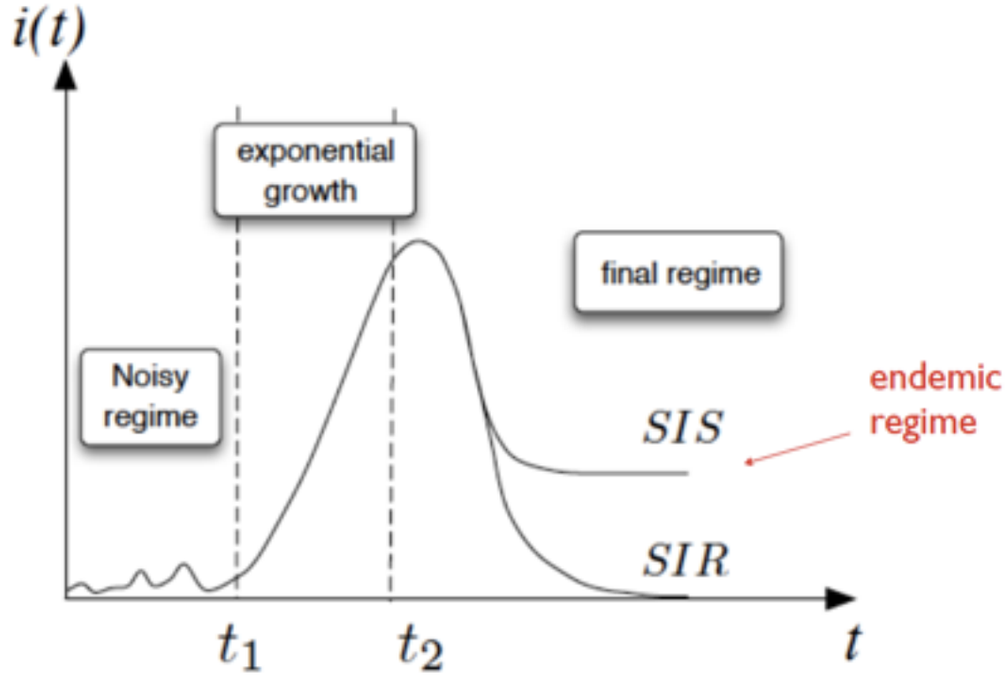


$$p_i^\star = \epsilon_i^\star \ll 1 \longrightarrow \mu\epsilon_i^\star = (1 - \epsilon_i^\star)\lambda \sum_{j=1}^{N} A_{ij}\epsilon_j^*$$

$$\mu\epsilon_i^\star = \lambda \sum_{j=1}^{N} A_{ij}\epsilon_j^* - \lambda \sum_{j=1}^{N} A_{ij}\epsilon_i^\star\epsilon_j^*$$

SIS model

$$\mu p_i^\star = (1 - p_i^*) q_i^*$$



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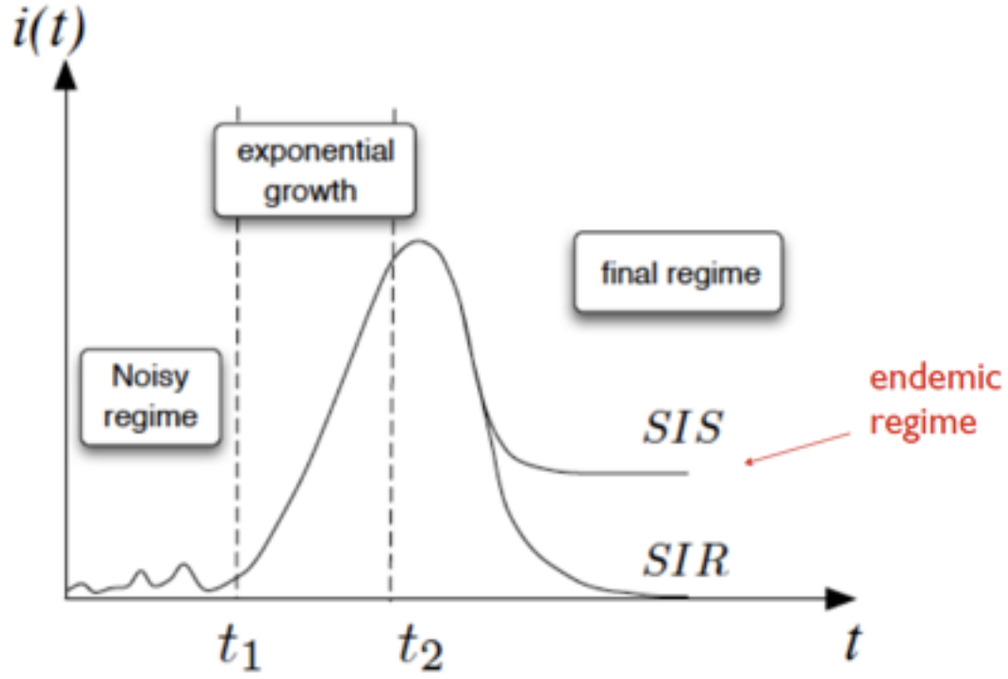

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$$\mu\epsilon_i^\star = \lambda \sum_{j=1}^{N} A_{ij}\epsilon_j^*$$

$\frac{\mu}{\lambda}$ should be an eigenvalue of the Adjacency matrix

SIS model

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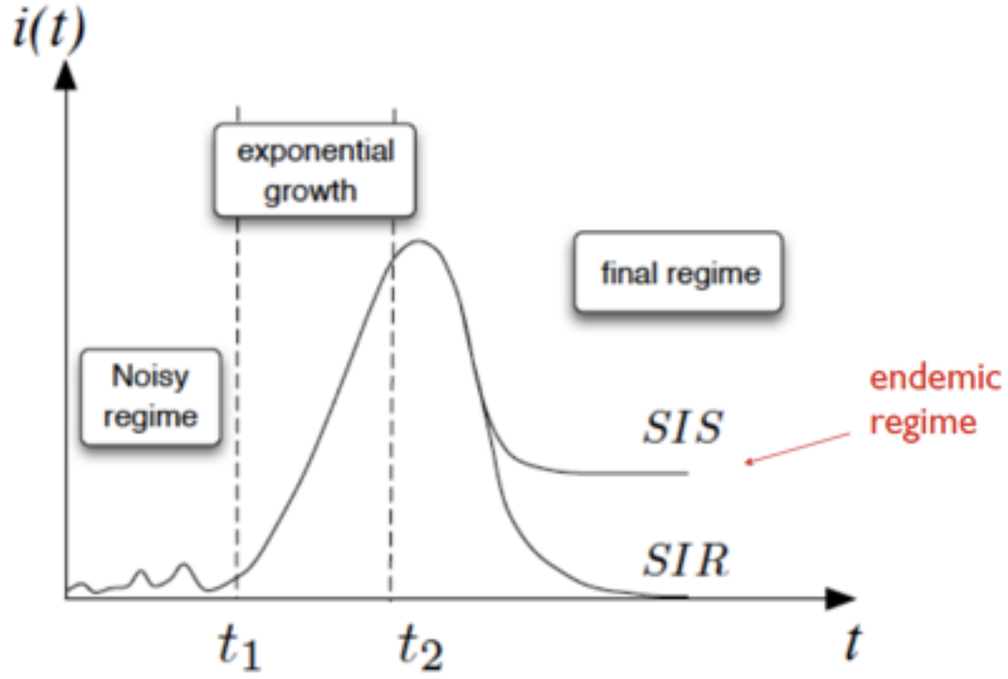

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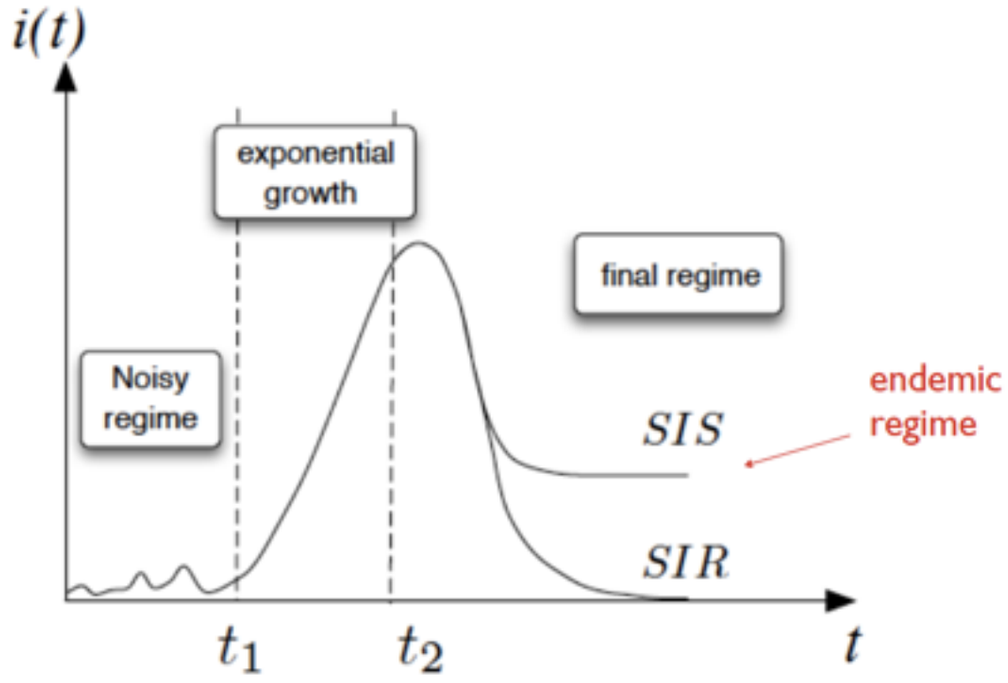
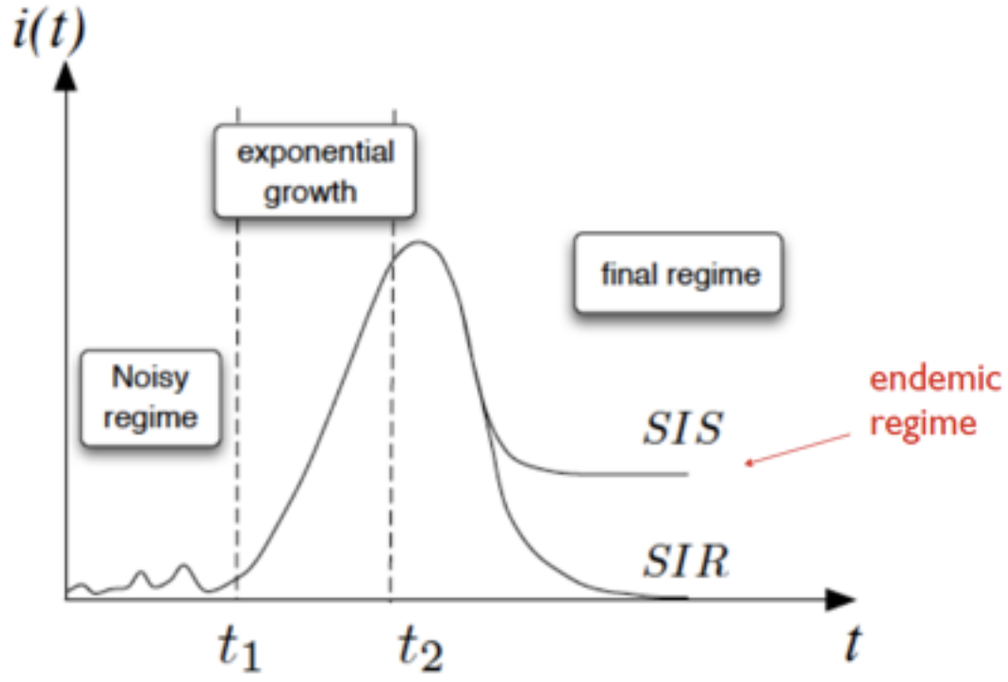
$\frac{\mu}{\lambda}$ should be an eigenvalue of the Adjacency matrix

$$\lambda_c = \frac{\mu}{\Lambda_{max}(A)}$$

SIS model


i(t)
exponential growth
final regime
Noisy regime
endemic regime
SIS
SIR
t_1
t_2
t

SIS model



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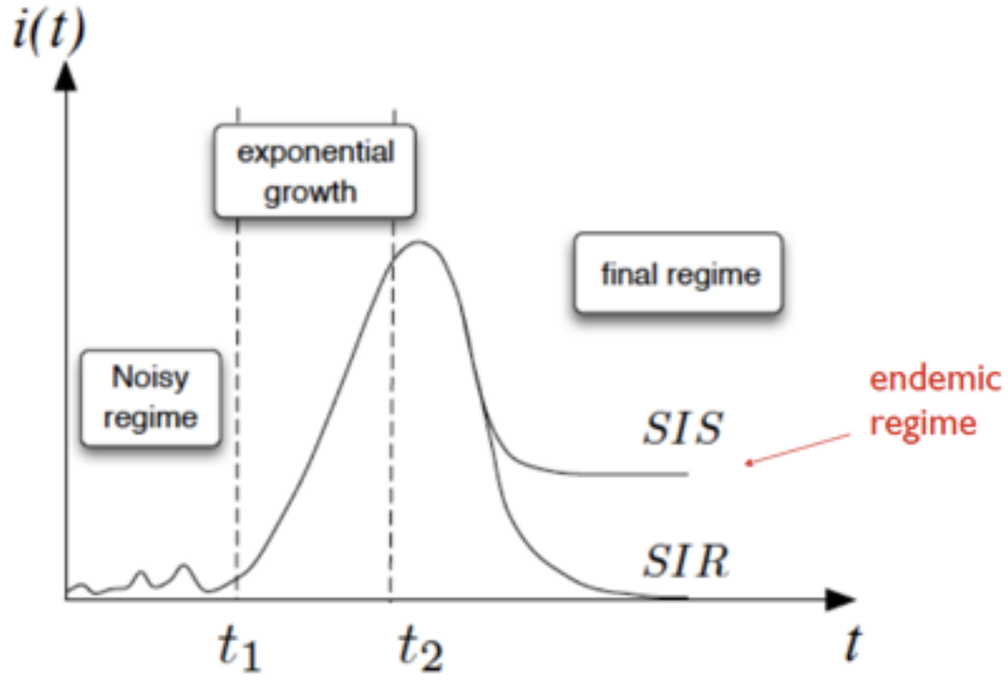
SIS model

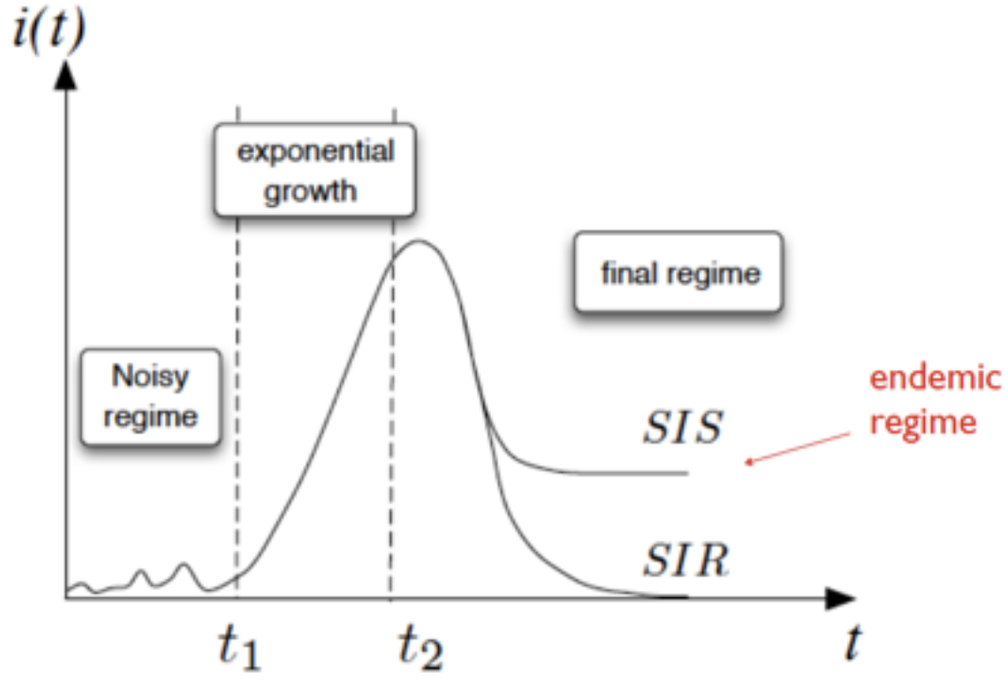


$$\lambda_c = \frac{\mu}{\Lambda_{max}(A)}$$

$$\Lambda_{max}(A) \sim \frac{\langle k^2 \rangle}{\langle k \rangle}$$

Chung F., et al. *Spectra of random graphs with given expected degrees*, PNAS 100, 6313 (2003)

SIS model



$$\lambda_c = \frac{\mu}{\Lambda_{max}(A)}$$

$$\Lambda_{max}(A) \sim \frac{\langle k^2 \rangle}{\langle k \rangle}$$

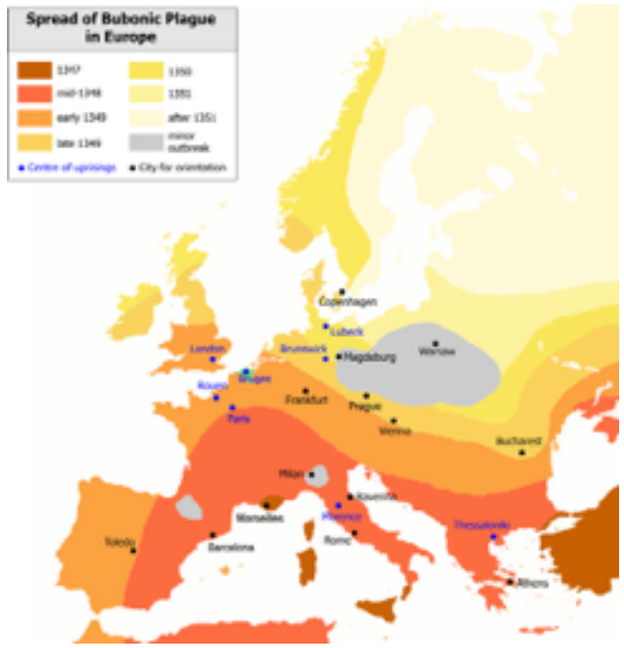
$$\lambda_c \simeq \frac{\mu \langle k \rangle}{\langle k^2 \rangle}$$

Chung F., et al. ***Spectra of random graphs with given expected degrees*****, PNAS 100, 6313 (2003)**

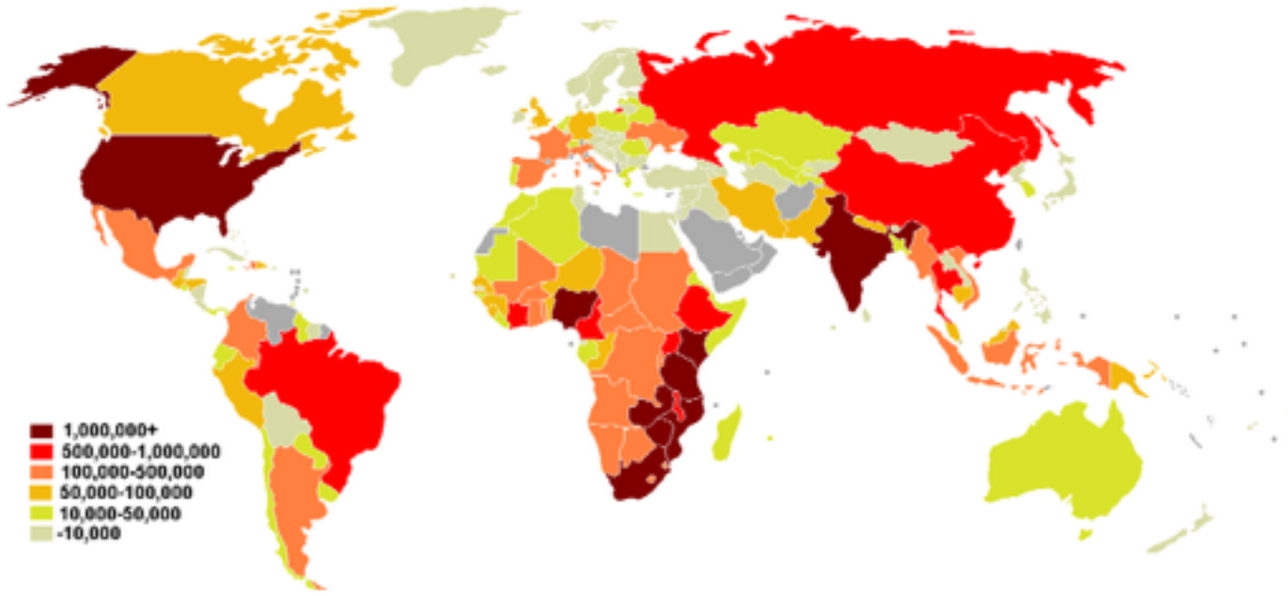
Part III

Metapopulation Models

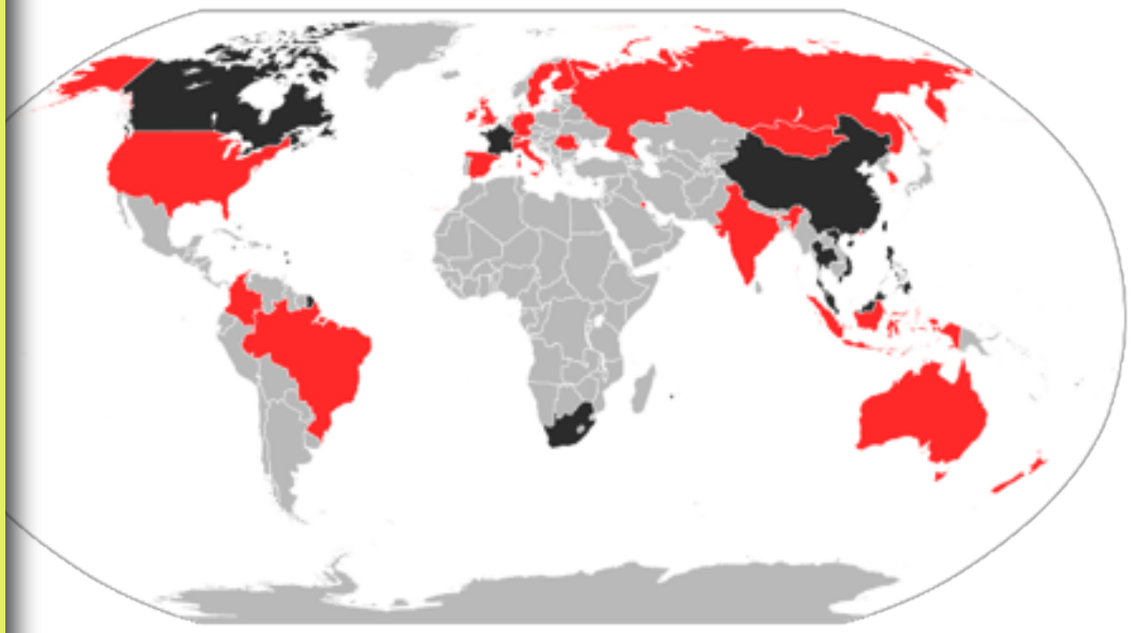
Beyond contact networks: Facing a global challenge



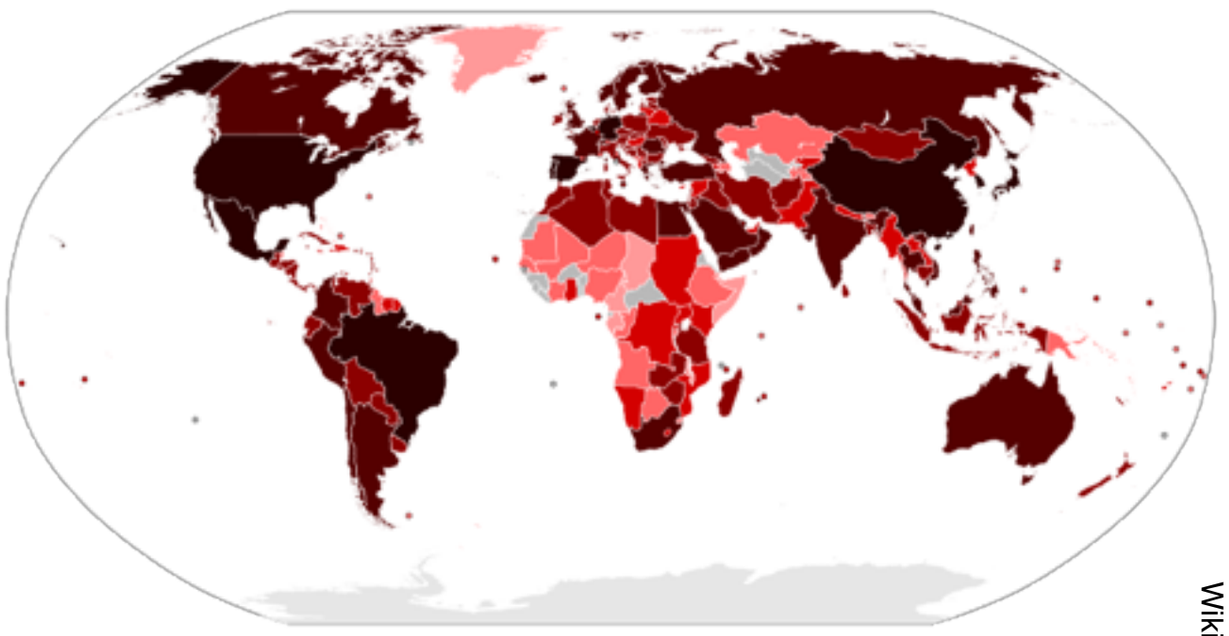
The black death (~ 700 years ago)



HIV (2008)



SARS (2009)

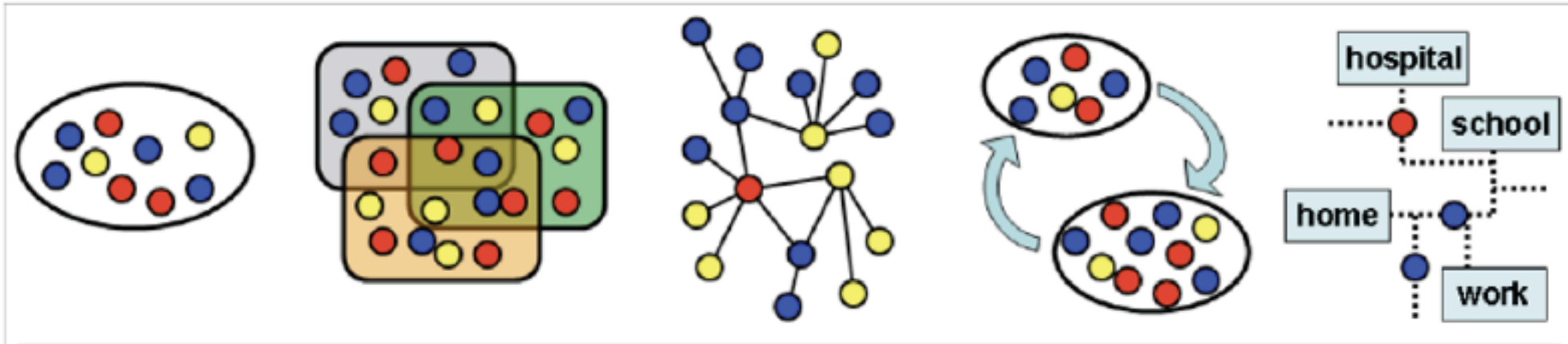


H1N1 (2011)

Wikipedia

... so let's Model!

Approaches to Epidemic Modeling: From Simple to Complex



Homogeneous mixing	Social structure	Contact network models	Multi-scale models	Agent Based models

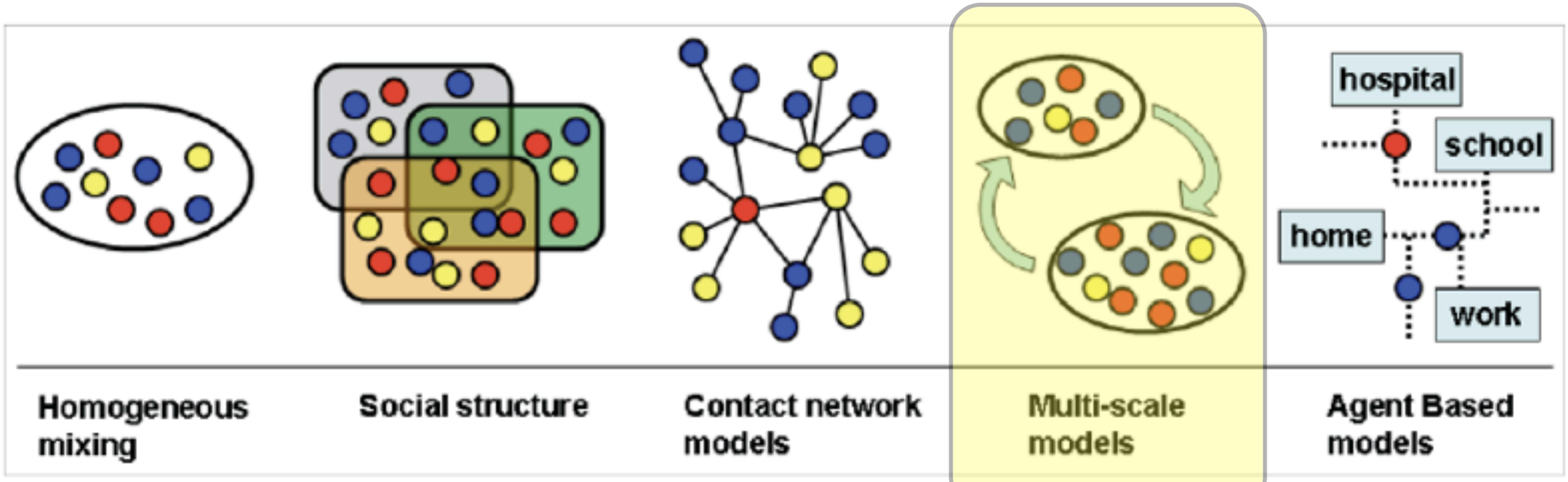
Simple → **Realistic**

Ability to explain (caveats) trends at a population level

Model realism looses in transparency.
Validation is harder.

... so let's Model!

Approaches to Epidemic Modeling: From Simple to Complex



Homogeneous mixing	Social structure	Contact network models	Multi-scale models	Agent Based models

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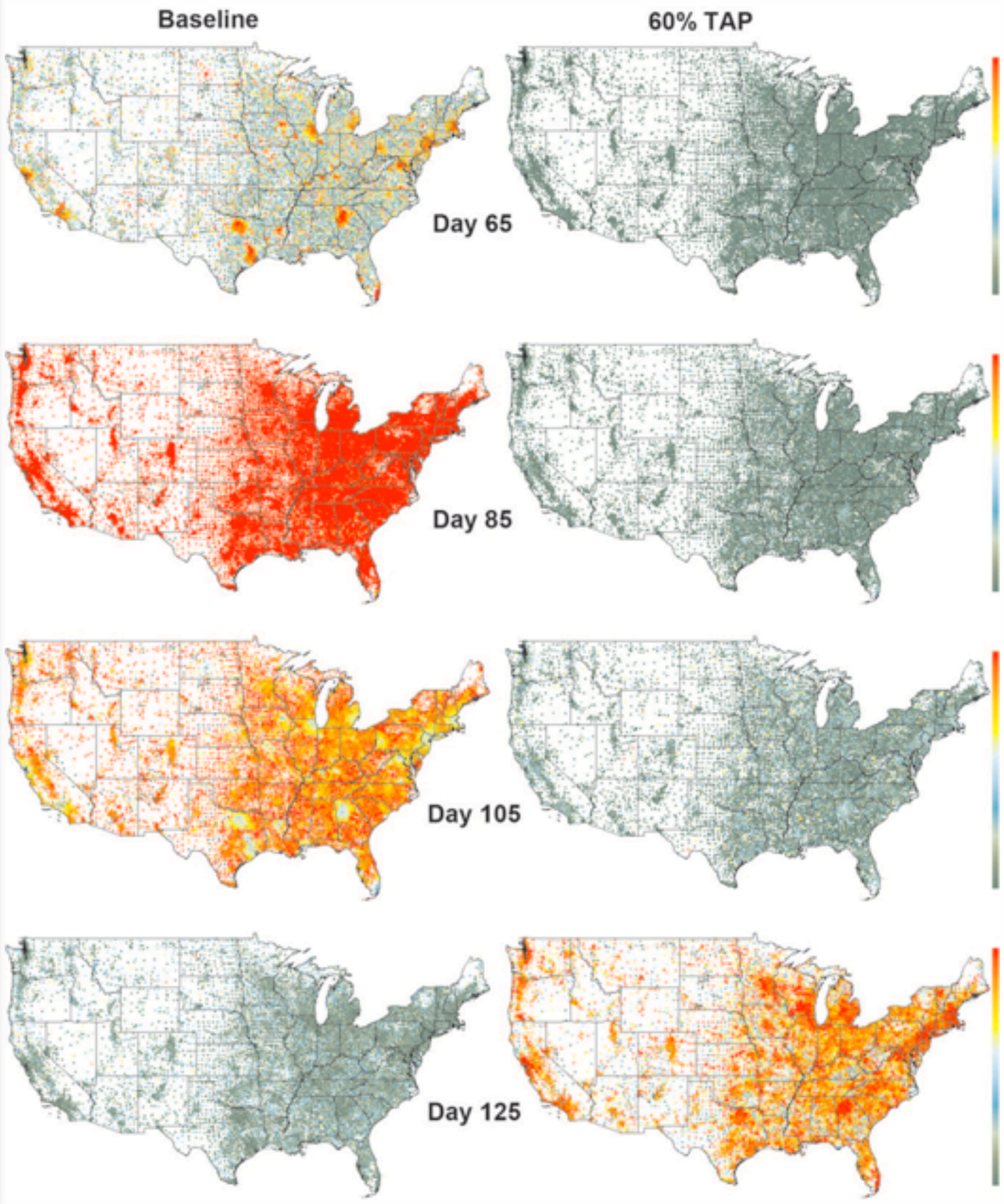
Computational Epidemiology



Goal

Add Spatial Resolution
&
Design Localized
Immunization policies

Mitigation strategies for pandemic influenza in the United States

Timothy C. Germann*†, Kai Kadau*, Ira M. Longini, Jr.‡, and Catherine A. Macken*

PNAS 103, 5935 (2006)

Fig. 1. Two simulated pandemic influenza outbreaks with $R_0 = 1.9$, initiated by the daily entry of a small number of infected individuals through 14 major international airports in the continental U.S. (beginning on day 0). The tract-level prevalence of symptomatic cases at any point in time is indicated on a logarithmic color scale, from 0.03% (green) to 3% (red) of the population. No mitigation strategies are used in the baseline simulation (*Left*), resulting in a 43.5% attack rate. (*Right*) A 60% TAP intervention begins at day 31, or 7 days after the pandemic alert. At day 99, the nationwide supply of 20 million antiviral courses is exhausted, leading to a nationwide pandemic.

Theory

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Journal of Theoretical Biology

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Epidemic modeling in metapopulation systems with heterogeneous coupling pattern: Theory and simulations

Vittoria Colizza[a,*], Alessandro Vespignani[b,c]

PNAS

Multiscale mobility networks and the spatial spreading of infectious diseases

Duygu Balcan[a,b], Vittoria Colizza[c], Bruno Gonçalves[a,b], Hao Hu[d], José J. Ramasco[b], and Alessandro Vespignani[a,b,c,1]

[a]Center for Complex Networks and Systems Research, School of Informatics and Computing, Indiana University, Bloomington, IN 47408; [b]Pervasive Technology Institute, Indiana University, Bloomington, IN 47404; [c]Computational Epidemiology Laboratory, Institute for Scientific Interchange Foundation, 10133 Torino, Italy; and [d]Department of Physics, Indiana University, Bloomington, IN 47406

Edited by H. Eugene Stanley, Boston University, Boston, MA, and approved October 13, 2009 (received for review

Among the realistic ingredients to be considered in the
modeling of infectious diseases, human mobility repre
challenge both on the theoretical side and in view
availability of empirical data. To study the interplay be

ARTICLES

Reaction–diffusion processes and metapopulation models in heterogeneous networks

VITTORIA COLIZZA[1,2*], ROMUALDO PASTOR-SATORRAS[3] AND ALESSANDRO VESPIGNANI[1,2*]

[1]Complex Networks Lagrange Laboratory, Institute for Scientific Interchange (ISI), Torino 10133, Italy
[2]School of Informatics and Department of Physics, Indiana University, Bloomington 47406 Indiana, USA
[3]Departament de Física i Enginyeria Nuclear, Universitat Politècnica de Catalunya, Campus Nord B4, 08034 Barcelona, Spain
*e-mail: vcolizza@indiana.edu, alexv@indiana.edu

Applications

OPEN ACCESS Freely available online

PLoS one

Human Mobility Networks, Travel Restrictions, and the Global Spread of 2009 H1N1 Pandemic

Paolo Bajardi[1,2], Chiara Poletto[1], Jose J. Ramasco[3], Michele Tizzoni[1,4], Vittoria Colizza[5,6,7]*, Alessandro Vespignani[8,9,10]*

1 Computational Epidemiology Laboratory, Institute for Scientific Interchange (ISI), Torino, Italy, **2** Centre de Physique Théorique (CNRS UMR 6207), Marseille, France, **3** Instituto de Física Interdisciplinar y Sistemas Complejos IFISC (CSIC-UIB), Palma de Mallorca, Spain, **4** Scuola di Dottorato, Politecnico di Torino, Torino, Italy, **5** INSERM, U707, Paris, France, **6** UPMC Université Paris 06, Faculté de Médecine Pierre et Marie Curie, UMR S 707, Paris, France, **7** Complex Systems Lagrange Laboratory, Institute for Scientific Interchange (ISI), Torino, Italy, **8** Center for Complex Networks and Systems Research (CNetS), School of Informatics and Computing, Indiana University, Bloomington, Indiana, United States of America, **9** Pervasive Technology Institute, Indiana University, Bloomington, Indiana, United States of America, **10** Institute for Scientific Interchange (ISI), Torino, Italy

Abstract

BMC Medicine

Research article

Seasonal transmission potential and activity peaks of the new influenza A(H1N1): a Monte Carlo likelihood analysis based on human mobility

Duygu Balcan[†1,2], Hao Hu[†1,2,3], Bruno Goncalves[†1,2], Paolo Bajardi[†4,5], Chiara Poletto[†4], Jose J Ramasco[4], Daniela Paolotti[4], Nicola Perra[1,6,7], Michele Tizzoni[4,8], Wouter Van den Broeck[4], Vittoria Colizza[4] and Alessandro Vespignani[*1,2,4]

...ion radical-pair model[28] with an isotropic hyperfine coupling, a, of ... an anisotropy, α of 0.3, and a lifetime of 20 μs (corresponding to the observed lifetime of flavin-tryptophan radical pairs[15]). We solved the stochastic Liouville equation to determine the triplet yield in the presence of a static magnetic field of 46 μT. We then calculated, by direct numerical integration of the stochastic Liouville equation, the change ... triplet yield, $\Delta\Phi_{OMF}$, caused by an additional 1.3 MHz oscillating magnetic field in ... esonance with the splitting due to the 46 μT static field. For comparison, we also ...calculated the triplet yield change, $\Delta\Phi_{static}$, resulting from a decrease of 12 μT in static field, noting that such a change led to disorientation in the magnetic compass orientation responses of robins[29]. The intensity of the oscillating field required for $\Delta\Phi_{OMF}$ to equal $\Delta\Phi_{static}$ is 0.033 μT, that is, less than any of the intensities employed in our experiments.

Received 2 September 2003; accepted 30 March 2004; doi:10.1038/nature02534.

1. Wiltschko, W. & Wiltschko, R. Magnetic compass of European robins. *Science* **176**, 62–64 (1972).
2. Wiltschko, R. & Wiltschko, W. *Magnetic Orientation in Animals* (Springer, Berlin, 1995).
3. Kirschvink, J. & Gould, J. Biogenic magnetite as a basis for magnetic field detection in animals. *BioSystems* **13**, 181–201 (1981).

Modelling disease outbreaks in realistic urban social networks

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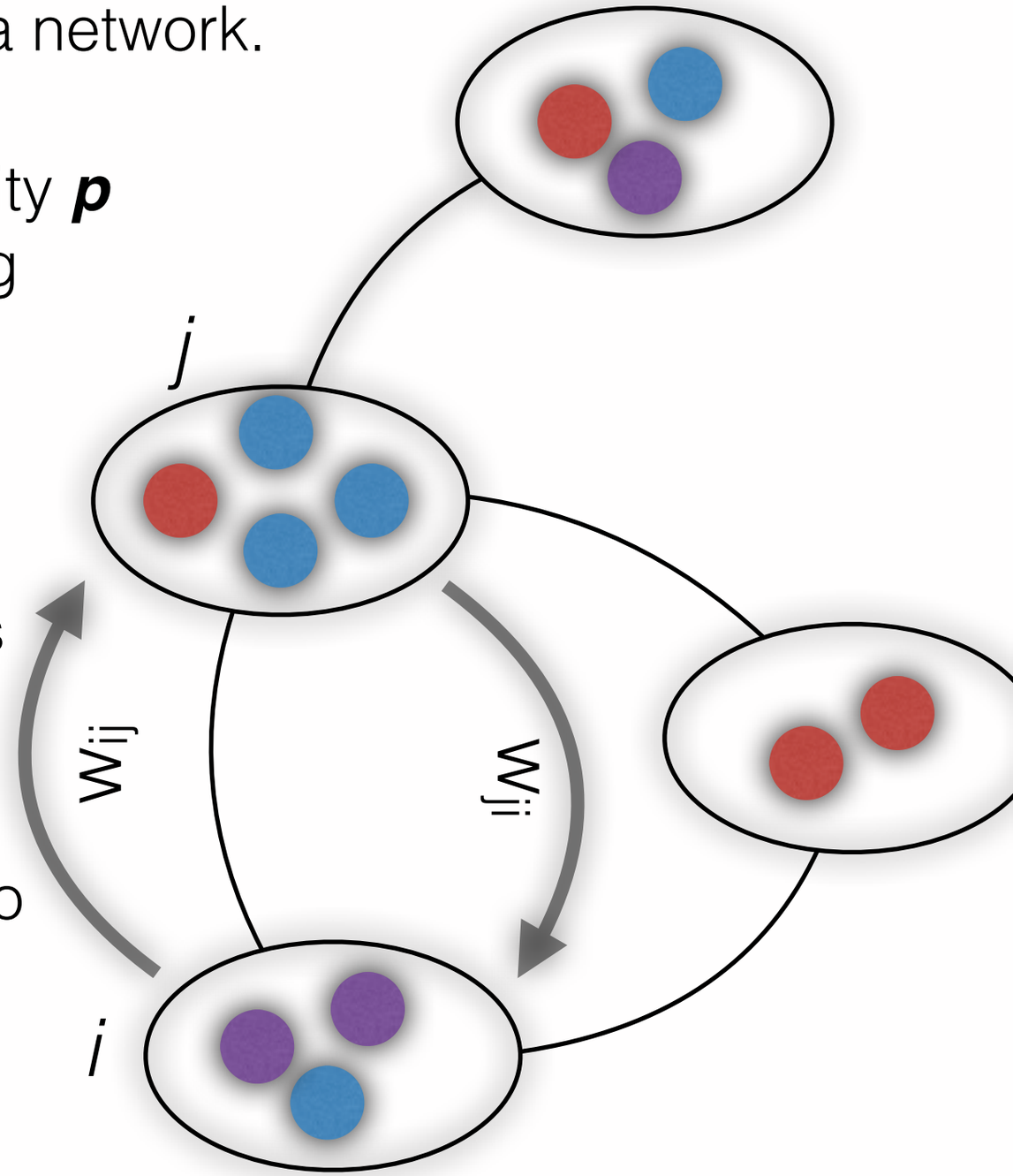
Basic Model

- Different populations connected as a network.
- Each individual moves with probability ***p*** from one population to a neighboring one, according to the empirical observations*.
- Inside each subpopulation, at each time step, epidemic dynamics takes place (λ and μ).
- Then, each individual comes back to its original subpopulation (node).



Lets construct the Markov Equations!