Physics of Life Data Epidemiology

Lect 11: Network epidemiology

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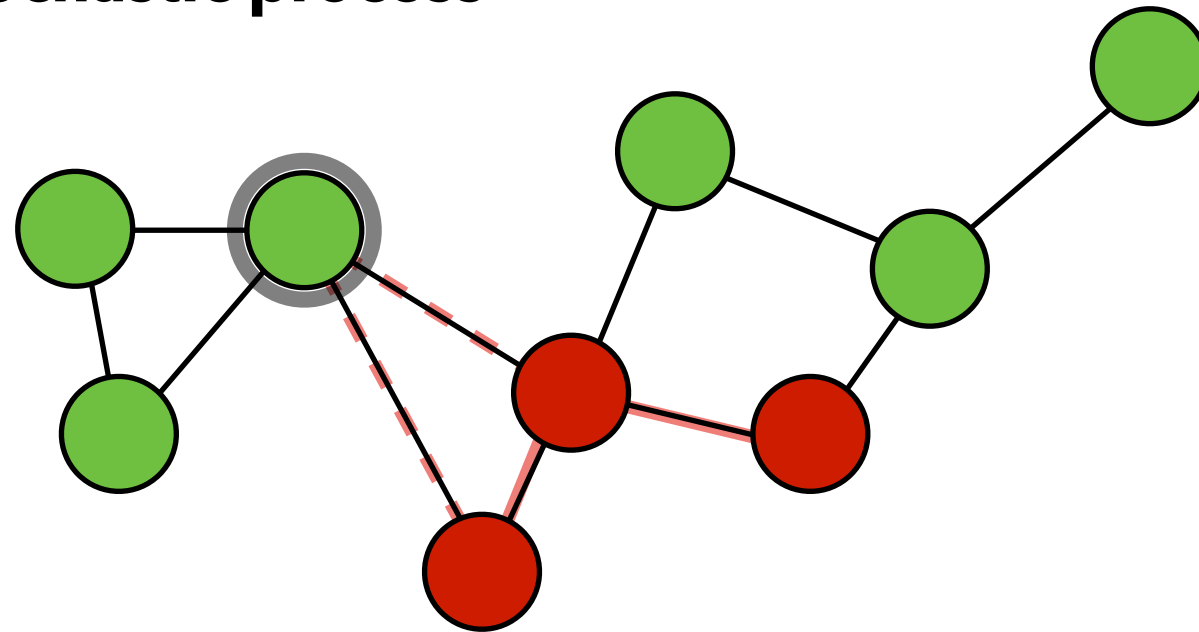mail: chiara.poletto@unipd.it
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modelling epidemic on networks

I can see the network as a static substrate. The infection spreads on the top of the network, as a stochastic process

Approach similar to compartmental models: the disease natural history can still be described by a list of infectious states (S, E, I, R, ….)
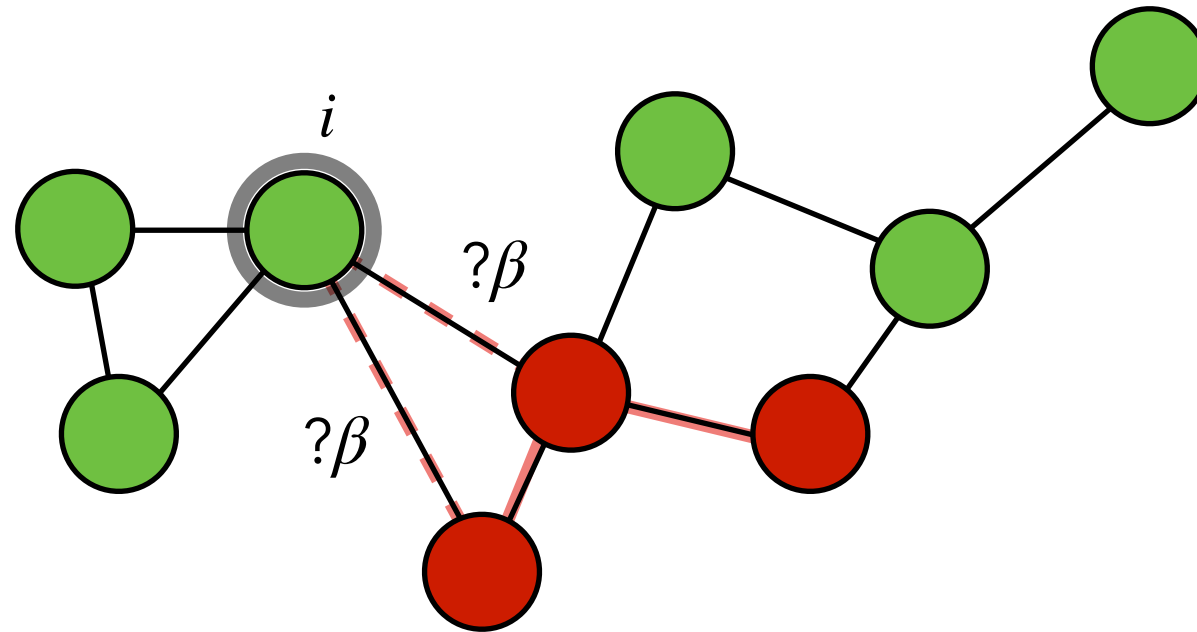
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from population dynamics to an individual based model
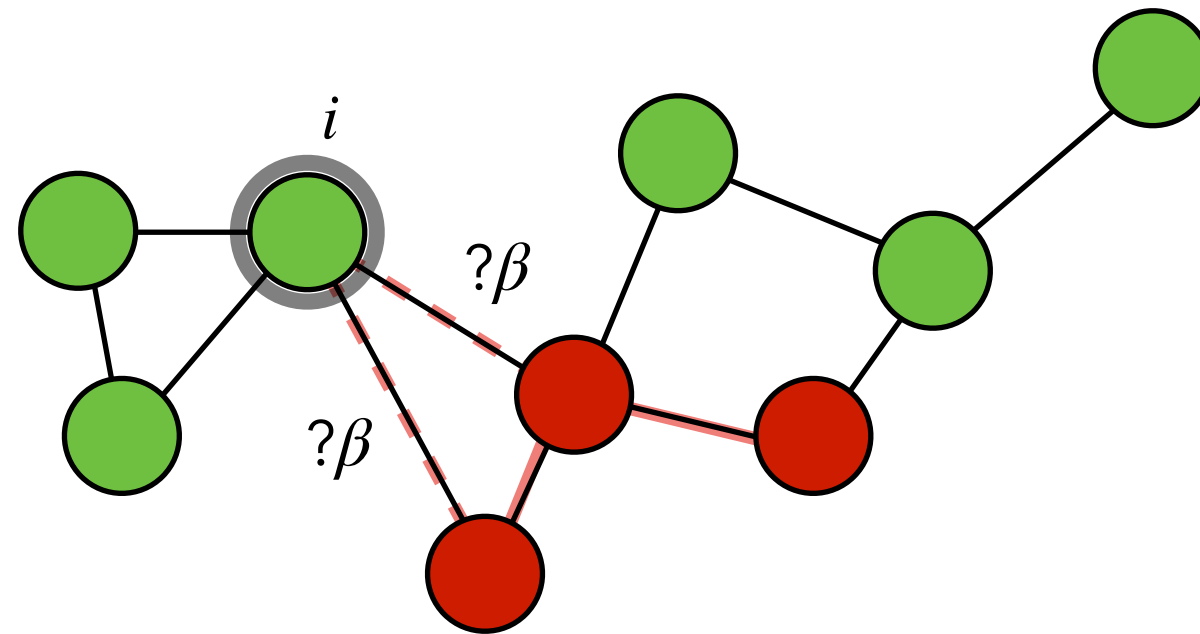
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Epidemics on network are naturally modelled as stochastic processes

modelling epidemic on networks: SIS

- we have 2 states: $\sigma_i(t) = 1$, i.e. infectious, $\sigma_i(t) = 0$, i.e. susceptible

- $\rho(\mathbf{i}, t) \equiv \text{Prob}[\sigma_\mathbf{i}(t) = 1]$

- β is the probability per unit time that the infection is transmitted along a link between a node $j \,|\, \sigma_j(t) = 1$ to a node $i \,|\, \sigma_i(t) = 0$

- μ is the probability per unit time that an infected node recovers
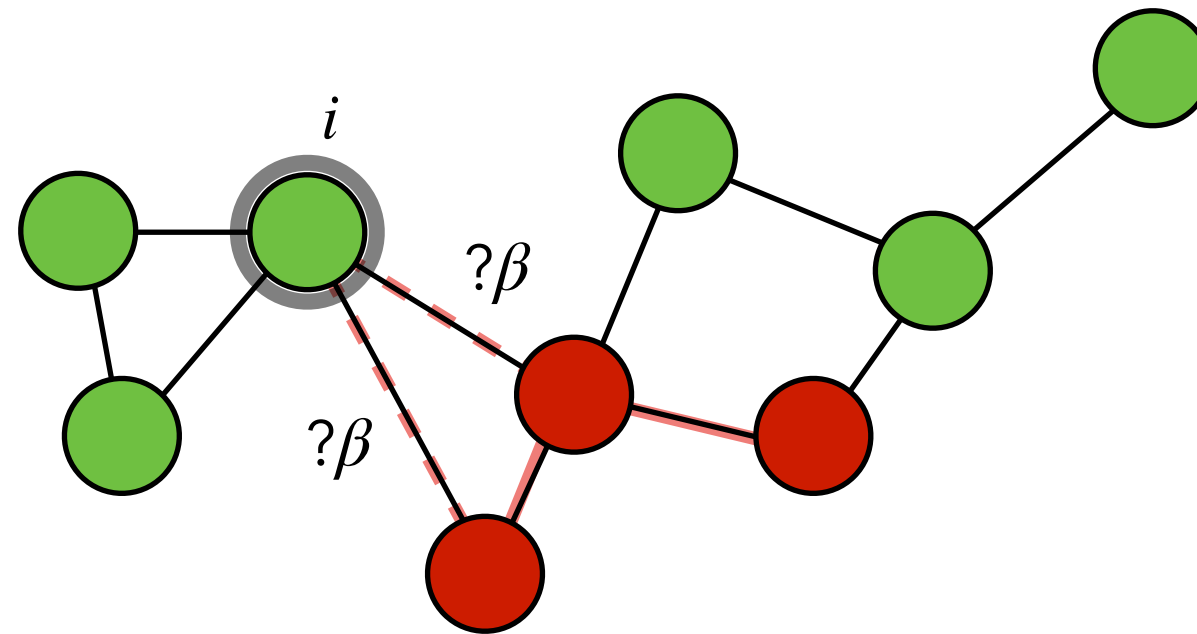
modelling epidemic on networks

Probability that a susceptible node, i, becomes infected:

$1 - (1 - \beta)^{\nu_I(t)}$, where $\nu_I(t)$ is the number of neighbouring nodes in the infectious state

$1 - (1 - \beta)^{\nu_I(t)} \simeq \beta \nu_I(t)$ if $\beta \to 0$

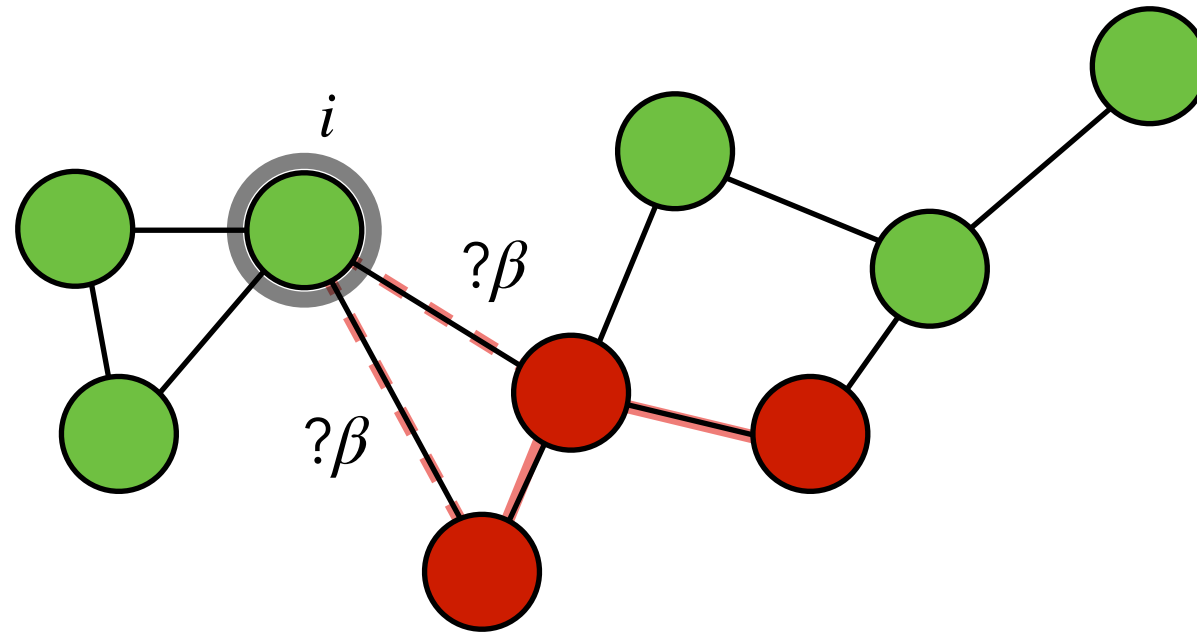# Equation of the SIS dynamics on a network

Markov chain of the epidemic process

$$\frac{d}{dt}\rho(i,t) = \frac{d}{dt}\text{Prob}[\sigma_{\mathbf{i}}(t) = 1] = -\mu\rho(i,t) + \beta\sum_{j}A_{ij}\text{Prob}[\sigma_i(t) = 0, \sigma_j(t) = 1]$$

$A_{i,j}$: the adjacency matrix

$\text{Prob}[\sigma_i(t) = 0, \sigma_j(t) = 1]$: joint probability distribution for the states of nodes i and j

Equation of the SIS dynamics on a network

Markov chain of the epidemic process

N couples differential equations

$$\frac{d}{dt}\rho(i,t) = \frac{d}{dt}\text{Prob}[\sigma_{\mathbf{i}}(t) = 1] = -\mu\rho(i,t) + \beta\sum_j A_{ij}\text{Prob}[\sigma_i(t) = 0, \sigma_j(t) = 1]$$

$A_{i,j}$: the adjacency matrix

$\text{Prob}[\sigma_i(t) = 0, \sigma_j(t) = 1]$: joint probability distribution for the states of nodes i and j

Extremely difficult to compute

mean field approaches

In physics and probability theory, mean-field theory studies the behavior of high-dimensional stochastic models by studying a simpler model that approximates the original by averaging over degrees of freedom.

The effect of all the other individuals on any given individual is approximated by a single averaged effect, thus reducing a many-body problem to a one-body problem.

The mean field approximation can be defined at different level
the population dynamics SIR model is a mean-field approximation of the individual based model

Substitute $\text{Prob}[\sigma_i(t) = 0, \sigma_j(t) = 1]$ with an average probability

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$\text{Prob}[\sigma_i(t) = 0, \sigma_j(t) = 1] = \text{Prob}[\sigma_i(t) = 0 \mid \sigma_j(t) = 1]\text{Prob}[\sigma_j(t) = 1]$

mean field approximation $\text{Prob}[\sigma_i(t) = 0 \mid \sigma_j(t) = 1] \simeq \text{Prob}[\sigma_i(t) = 0]$

I assume the status of i and j are independent

mean field approaches

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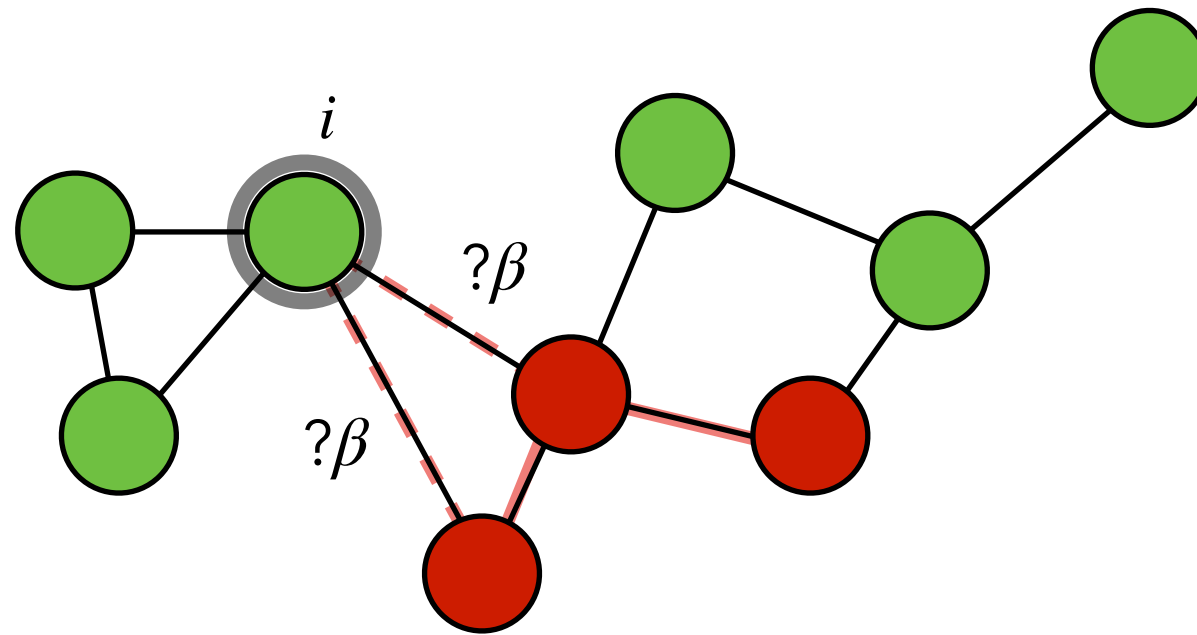
I assume the status of i and j are independent

$$\frac{d}{dt}\text{Prob}[\sigma_i(t) = 1] = -\mu\rho(i,t) + \beta \sum_j A_{ij}\text{Prob}[\sigma_i(t) = 0, \sigma_j(t) = 1] \Rightarrow$$

$$\frac{d}{dt}\text{Prob}[\sigma_i(t) = 1] = -\mu\rho(i,t) + \beta \sum_j A_{ij}\text{Prob}[\sigma_i(t) = 0]\text{Prob}[\sigma_j(t) = 1]$$

$$\frac{d}{dt}\text{Prob}[\sigma_i(t) = 1] = -\mu\rho(i,t) + \beta\,\text{Prob}[\sigma_i(t) = 0] \sum_j A_{ij}\text{Prob}[\sigma_j(t) = 1]$$

individual-based mean-field approach

individual-based mean-field approach

it accounts for the whole structure of the network A_{ij}

$\rho_i(t) \equiv \text{Prob}[\sigma_i(t) = 1]$

$$\frac{d}{dt}\rho_i(t) = -\mu\rho_i(t) + \beta\left(1 - \rho_i(t)\right)\sum_j A_{ij}\rho_j(t)$$

$q_i(t) \equiv \beta\sum_j A_{ij}\rho_i(t)$ probability i gets infected at time t

$$\frac{d}{dt}\rho_i(t) = -\mu\rho_i(t) + \left(1 - \rho_i(t)\right)q_i(t)$$

[Wang et al. SRDS 2003, Gómez et al. EPL 2010]

numerical simulations

The system can be solved numerically by iteration

$$\rho_i(t+1) = \rho_i(t)(1-\mu) + (1-\rho_i(t))q_i(t)$$

- Faster than numerical simulations
- No need of averages
- Reproduces individual nodes probabilities
- we can numerically compute e.g. the epidemic size

[Wang et al. SRDS 2003, Gómez et al. EPL 2010]

analytical considerations: epidemic threshold

$$\frac{d}{dt}\rho_i(t) = -\mu\rho_i(t) + \left(1 - \rho_i(t)\right) q_i(t)$$

this is an SIS process (with transmission and recovery): we can expect that an active steady state is possible if β and μ satisfy certain conditions

epidemic threshold = minimum transmissibility β_c, t.c. $\beta > \beta_c$ we have an active steady state

steady state: $\lim\limits_{t\to\infty} \rho_i(t) = \rho_i^*$

$$\mu\rho_i^* = (1 - \rho_i^*)q_i^*$$

[Wang et al. SRDS 2003, Gómez et al. EPL 2010]

analytical considerations: epidemic threshold

Assuming being close to the epidemic threshold means that ρ_i^* can be assumed to be small $\rho_i^* = \epsilon_i^* \ll 1$

This implies

$$q_i^* = 1 - \prod_{j=1}^{N} [1 - \beta A_{ij}\epsilon_j^*] \simeq \beta \sum_{j=1}^{N} A_{ij}\epsilon_j^*$$

$$\mu\epsilon_i^* = \beta(1 - \epsilon_i^*) \sum_{j=1}^{N} A_{ij}\epsilon_j^*$$

$$\mu\epsilon_i^* = \beta \sum_{j=1}^{N} A_{ij}\epsilon_j^* - \beta\epsilon_i^* \sum_{j=1}^{N} A_{ij}\epsilon_j^* \quad \text{(neglecting second order terms)}$$

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

[Wang et al. SRDS 2003, Gómez et al. EPL 2010]

analytical considerations: epidemic threshold

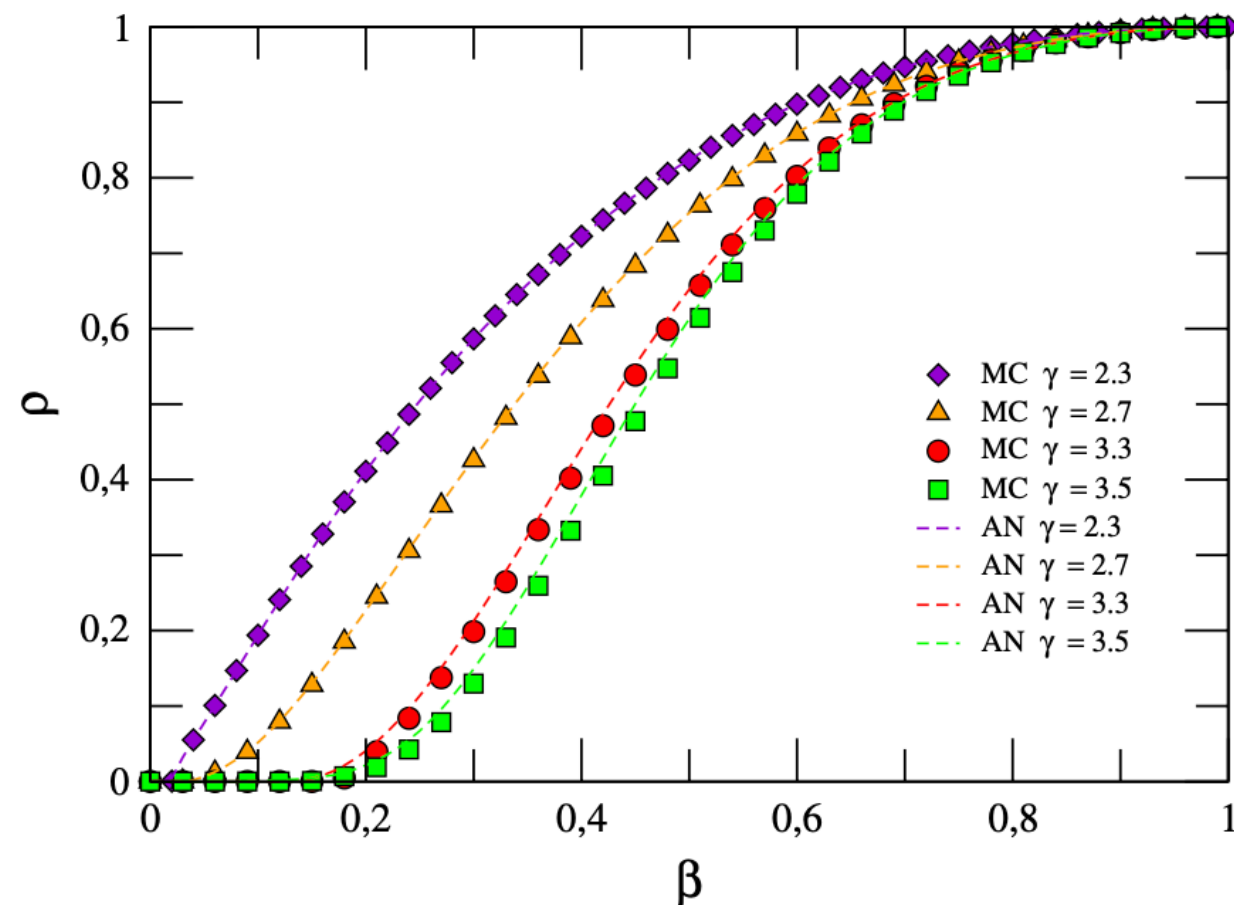$$\frac{\mu}{\beta}\epsilon_i^* = \sum_{j=1}^{N} A_{ij}\epsilon_j^*$$

Linear system that has solution only if $\dfrac{\mu}{\beta}$ is an eigenvalue of the adjacency matrix A_{ij}

epidemic threshold = minimum transmissibility β_c, t.c. $\beta > \beta_c$ we have the epidemic

$$\Rightarrow \beta_c = \frac{\mu}{\Lambda(A_{ij})}, \text{ with } \Lambda(A_{ij}) = \text{spectral radius of } A_{ij} \text{ (largest eigenvalue)}$$

[Wang et al. SRDS 2003, Gómez et al. EPL 2010]

analytical considerations: epidemic threshold

Comparison between stochastic simulations
and Markov chain integration for a random
power law network $p(k) \sim k^{-\gamma}$

limit of the approximation:

the approximation may be not so

good for network with certain

structural properties:

- networks with high clustering
- presence of communities
- assortative/dis-assortative

[S. Gómez, et al. EPL, 89 3 38009 (2010)]