

Advanced Algorithms and Computational Models (module A)

Spreading phenomena

Giacomo Fiumara
giacomo.fiumara@unime.it

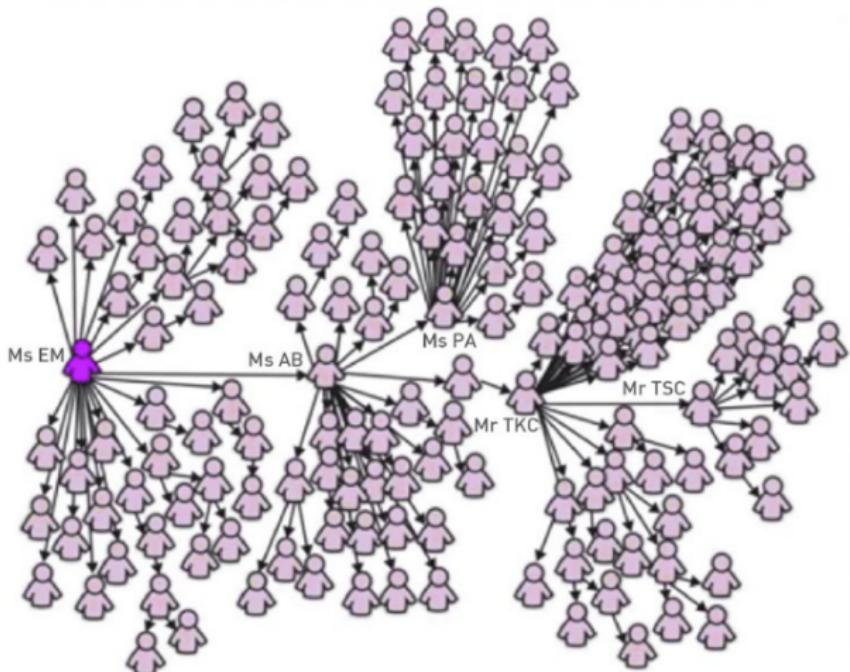
Introduction

- On the night of February 21, 2003, a physician from southern China checked into the Metropole Hotel in Hong Kong. He previously treated patients suffering from a disease that was called **atypical pneumonia**
- Next day, after leaving the hotel, he went to the local hospital, this time as a patient. He died there several days later of atypical pneumonia
- That night sixteen other guests of the Metropole Hotel also contracted the disease that was named **Severe Acute Respiratory Syndrome**, or **SARS**

Introduction

- These guests carried the SARS virus with them to Hanoi, Singapore, and Toronto, sparking outbreaks in each of those cities
- The physician became an example of a **Super Spreader**, an individual who is responsible for a disproportionate number of infections during an epidemic
- A network theorist will recognize Super Spreaders as **Hubs**, nodes with an exceptional number of links in the contact network on which a disease spreads

Introduction



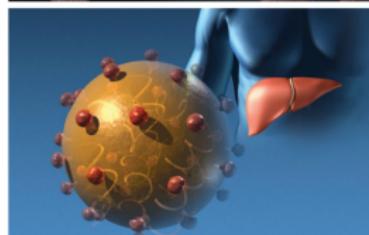
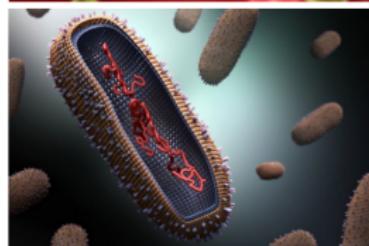
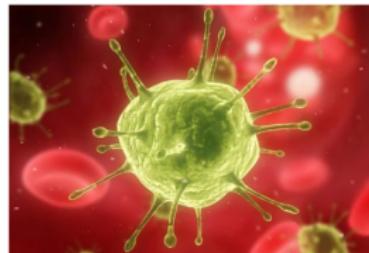
Introduction

Phenomenon	Agent	Network
Venereal Disease	Pathogens	Sexual Network
Rumor Spreading	Information, Memes	Communication Network
Diffusion of Innovations	Ideas, Knowledge	Communication Network
Computer Viruses	Malwares, digital viruses	Internet
Mobile Phone Virus	Mobile Viruses	Social Network
Bedbugs	Parasitic Insects	Hotel, Traveler Network
Malaria	Plasmodium	Mosquito - Human network

Epidemic modeling

The spread of pathogens is modeled starting from two fundamental hypotheses:

- **Compartmentalization:** each individual is classified depending on the stage of the disease affecting her
- **Homogeneous mixing:** each individual has the same chance of coming into contact with an infected individual



Epidemic modeling

Compartmentalization

- **Susceptible (S)**: Healthy individuals who have not yet contacted the pathogens
- **Infectious (I)**: Contagious individuals who have contacted the pathogen and hence can infect others
- **Recovered (R)**: Individuals who have been infected before, but have recovered from the disease, hence are not infectious
- **Immune** individuals who cannot be infected (additional state)
- **Latent** individuals, who have been exposed to the disease, but are not yet contagious

Epidemic modeling

Susceptible-Infected (SI) Model

- N Number of individuals (nodes of the network)
- $S(t)$ Number of susceptible (healthy) individuals at time t , $S(0) = N$
- $I(t)$ number of individuals that have been already infected at time t , $I(0) = 0$
- $\langle k \rangle$ Number of contacts of an individual
- β Likelihood that the disease will be transmitted from an infected to a susceptible individual in a unit time
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Epidemic modeling

Susceptible-Infected (SI) Model

- The probability that the infected person encounters a susceptible individual is $S(t)/N$
- Therefore the infected person comes into contact with $\langle k \rangle S(t)$ susceptible individuals in a unit time
- Since $I(t)$ infected individuals are transmitting the pathology, each at rate β , the average number of new infections $dI(t)$ during a frame dt is

$$\beta \langle k \rangle \frac{S(t)I(t)}{N} dt$$

- Therefore:

$$\frac{dI(t)}{dt} = \beta \langle k \rangle \frac{S(t)I(t)}{N}$$

Epidemic modeling

Susceptible-Infected (SI) Model

- The fraction of susceptible and infected population can be defined as

$$s(t) = \frac{S(t)}{N} \quad i(t) = \frac{I(t)}{N}$$

- and therefore

$$\frac{dI(t)}{dt} = \beta \langle k \rangle \frac{S(t)I(t)}{N}$$

- can be written as

$$\frac{di}{dt} = \beta \langle k \rangle si = \beta \langle k \rangle i(1 - i)$$

Epidemic modeling

Susceptible-Infected (SI) Model

- The equation

$$\frac{di}{dt} = \beta \langle k \rangle si = \beta \langle k \rangle i(1 - i)$$

- can be solved by writing

$$\frac{di}{i} + \frac{di}{1 - i} = \beta \langle k \rangle dt$$

- Integrating both sides we have

$$\ln i + \ln (1 - i) + C = \beta \langle k \rangle t$$

Epidemic modeling

Susceptible-Infected (SI) Model

- It is possible to determine the value of C under the initial condition

$$i_0 = i(t = 0)$$

- from which we get

$$C = \frac{i_0}{1 - i_0}$$

- and finally

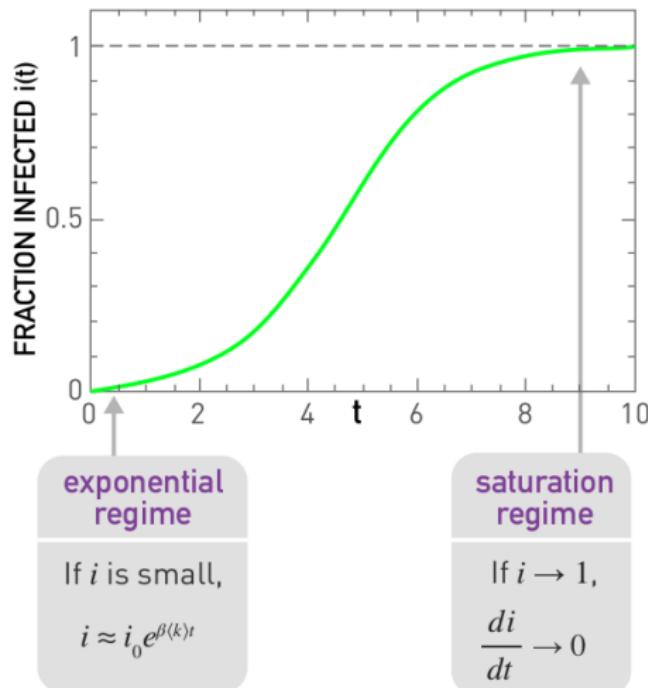
$$i = \frac{i_0 e^{\beta \langle k \rangle t}}{1 - i_0 + i_0 e^{\beta \langle k \rangle t}}$$

Epidemic modeling

Susceptible-Infected (SI) Model

$$i = \frac{i_0 e^{\beta \langle k \rangle t}}{1 - i_0 + i_0 e^{\beta \langle k \rangle t}}$$

- At the beginning the infected individuals encounter only susceptible individuals, hence the pathogen can easily spread
- The exponent is proportional to β and $\langle k \rangle$
- With time, an infected individual encounters fewer and fewer susceptible individuals



Epidemic modeling

Susceptible-Infected-Susceptible (SIS) Model

- Most pathogens are defeated by the immune system or by treatment
- This fact can be modeled by allowing infected individuals to recover, ceasing to spread the disease
- This feature is reproduced by the SIS model, which has the same two states of the SI model
- The difference is that now infected individuals recover at a fixed rate μ becoming susceptible again

Epidemic modeling

Susceptible-Infected-Susceptible (SIS) Model

- The equation describing the dynamics of this model is an extension of the equation describing the Si model

$$\frac{di}{dt} = \beta \langle k \rangle i(1 - i) - \mu i$$

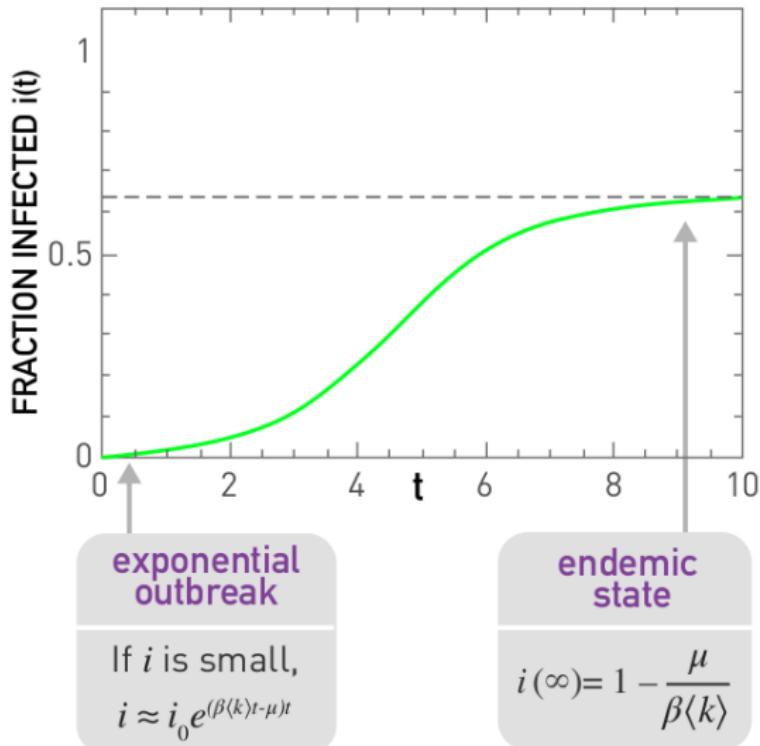
- where μ is the *recovery rate*
- The solution is

$$i = \left(1 - \frac{\mu}{\beta \langle k \rangle}\right) \frac{Ce^{(\beta \langle k \rangle - \mu)t}}{1 + Ce^{(\beta \langle k \rangle - \mu)t}}$$

- This solution predicts two possible outcomes

Epidemic modeling

Susceptible-Infected-Susceptible (SIS) Model



Epidemic modeling

Susceptible-Infected-Susceptible (SIS) Model

Endemic state ($\mu < \beta\langle k \rangle$)

- For low recovery rate i follows a logistic curve similar to the one observed for the SI model
- Not everyone is infected, but i reaches a constant $i(\infty) < 1$ value
- This means that at any moment only a finite fraction of the population is infected
- The number of newly infected individuals equals the number of individuals who recover from the disease
- By setting $di/dt = 0$ the asymptotic value of i can be obtained

$$i(\infty) = 1 - \frac{\mu}{\beta\langle k \rangle}$$

Epidemic modeling

Susceptible-Infected-Susceptible (SIS) Model

Disease-free state ($\mu > \beta\langle k \rangle$)

- For a sufficiently high recovery rate the exponent of the solution is negative
- Therefore i decreases exponentially with time, indicating that an initial infection will die out exponentially
- This happens because the number of individuals cured per unit of time exceeds the number of newly infected individuals
- With time the pathogen disappears from the population

Epidemic modeling

Susceptible-Infected-Susceptible (SIS) Model

- The ratio

$$R_0 = \frac{\beta \langle k \rangle}{\mu}$$

- is called *basic reproductive number*
- It represents the average number of susceptible individuals infected by an infected individual during its infectious period in a fully susceptible population
- R_0 is the number of new infections each infected individual causes under ideal circumstances

Epidemic modeling

Susceptible-Infected-Susceptible (SIS) Model

Disease	Transmission	R_0
Measles	Airborne	12-18
Pertussis	Airborne droplet	12-17
Diphtheria	Saliva	6-7
Smallpox	Social contact	5-7
Polio	Fecal-oral route	5-7
Rubella	Airborne droplet	5-7
Mumps	Airborne droplet	4-7
HIV/AIDS	Sexual contact	2-5
SARS	Airborne droplet	2-5
Influenza	Airborne droplet	2-3

Epidemic modeling

Susceptible-Infected-Recovered (SIR) Model

- For many pathogens, like most strains of influenza, individuals develop immunity after they recover from the infection
- Instead of returning to the susceptible state, they are “removed” from the population
- These immune individuals do not count anymore from the perspective of the pathogen as they cannot be infected, nor can they infect others

Epidemic modeling

Susceptible-Infected-Recovered (SIR) Model

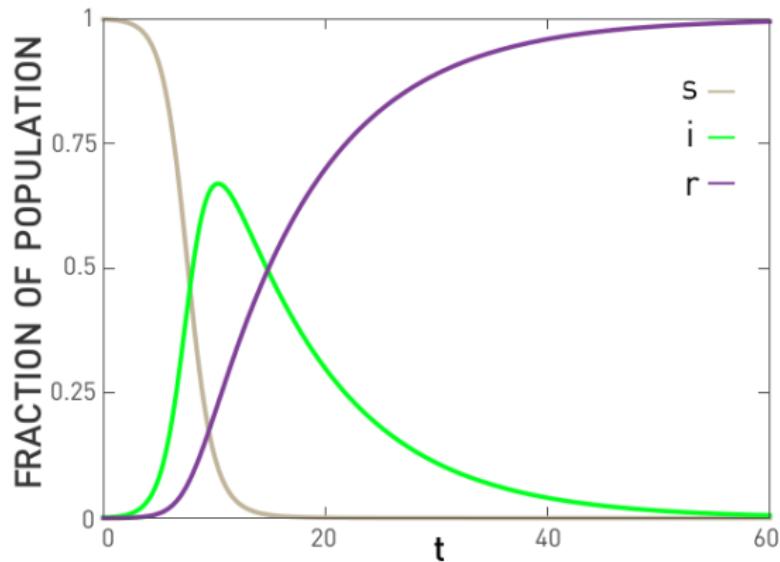
$$\frac{ds}{dt} = -\beta \langle k \rangle i (1 - r - i)$$

$$\frac{di}{dt} = -\mu i + \beta \langle k \rangle i (1 - r - i)$$

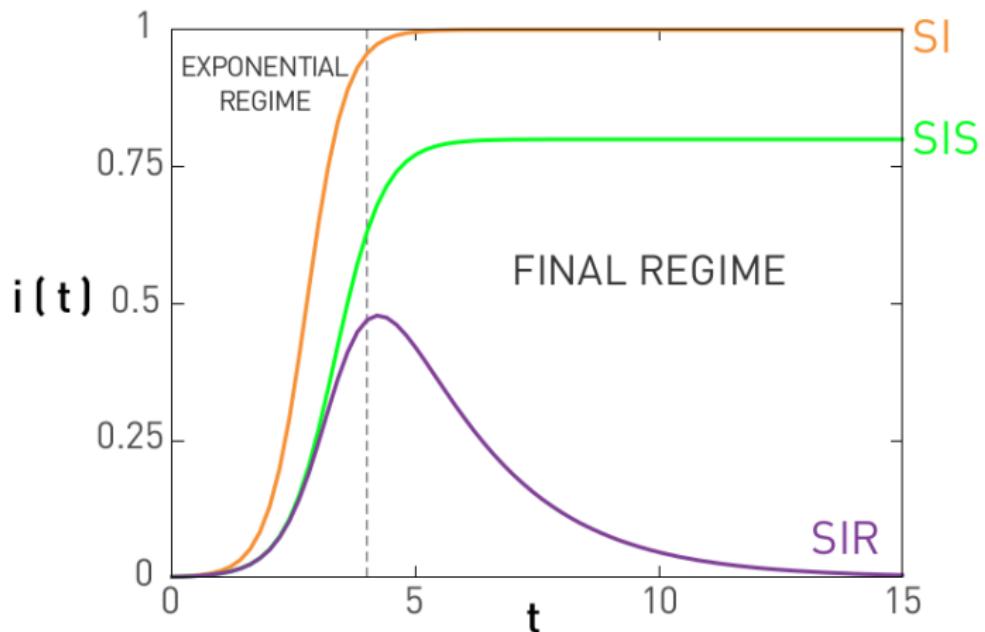
$$\frac{dr}{dt} = \mu i$$

Epidemic modeling

Susceptible-Infected-Recovered (SIR) Model



Epidemic modeling



Network Epidemics

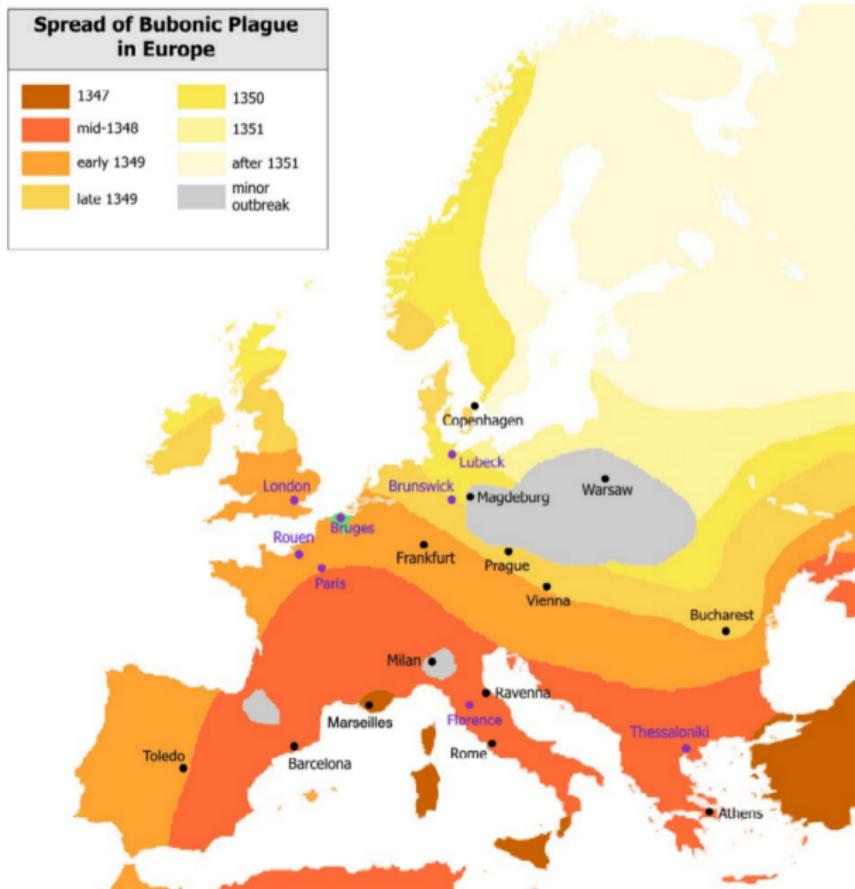
The homogeneous epidemic models:

- Do not incorporate the structure of the contact network that facilitates the spread of a pathogen
- Assume that any individual can come into contact with any other individual
- Assume that all individuals have comparable number of contacts, $\langle k \rangle$

These assumptions are false

- Individuals can transmit a pathogen only to those they come into contact with (pathogens spread on a complex contact network)
- These contact networks are often scale-free, hence $\langle k \rangle$ is not sufficient to characterize their topology

Epidemic modeling



Network Epidemics

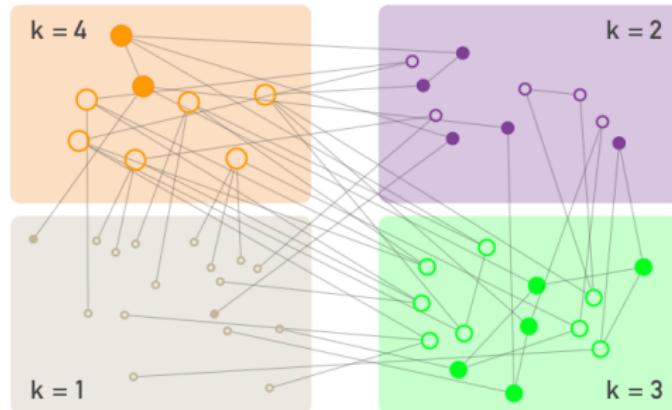
Susceptible-Infected (SI) model on a network

- If a pathogen spreads on a network, individuals with more links are more likely to be in contact with an infected individual
- Therefore the degree of each node must be considered
- This is achieved by the **degree block approximation**, that distinguishes nodes based on their degree and assumes that nodes with the same degree are statistically equivalent
- The fraction of nodes with degree k infected among all N_k degree- k nodes in the network is

$$i_k = \frac{I_k}{N_k}$$

Epidemic modeling

Susceptible-Infected (SI) model on a network



Network Epidemics

Susceptible-Infected (SI) model on a network

- The total fraction of infected nodes is the sum of all infected degree- k nodes

$$i = \sum_k p_k i_k$$

- It is now possible to write the SI model for each degree k separately

$$\frac{di_k}{dt} = \beta (1 - i_k) k \Theta_k$$

- The density function Θ_k represents the fraction of infected neighbors of a susceptible node having degree k
- This equation represents a system of k_{max} coupled equations, one for each degree present in the network

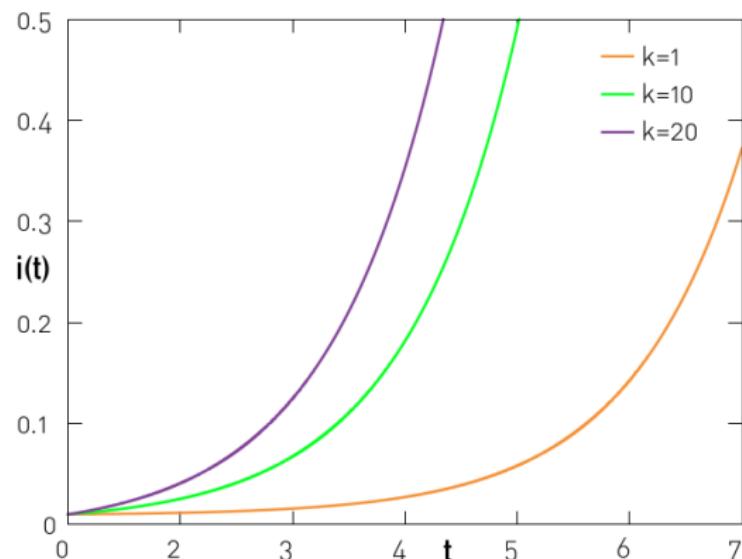
Network Epidemics

Susceptible-Infected (SI) model on a network

- It is interesting to study the early time behavior of i_k , because of theoretical and practical considerations
- Developing vaccines, cures and other medical interventions may take months to years
- In this meantime, the only way to alter the course of an epidemic is to use quarantine, travel restrictions and transmission-slowing measures to halt its spread
- The right decision needs an accurate estimate of the number of individuals infected in the early stages of the epidemic

Network Epidemics

Susceptible-Infected (SI) model on a network



Network Epidemics

Susceptible-Infected (SI) model on a network

$$\frac{di_k}{dt} = \beta (1 - i_k) k \Theta_k$$

- At the beginning of the epidemic i_k is small and the higher order term can be neglected. Therefore a good approximation is

$$\frac{di_k}{dt} \approx \beta k \Theta_k$$

- For a network lacking degree correlations the Θ_k function is independent of k , so that we have

$$\frac{di_k}{dt} \approx \beta k i_0 \frac{\langle k \rangle - 1}{\langle k \rangle} e^{t/\tau^{SI}}$$

- where

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

Network Epidemics

Susceptible-Infected (SI) model on a network

τ^{SI} has been derived for different networks:

- Random network

$$\tau_{ER}^{SI} = \frac{1}{\beta k}$$

- Scale-free network with $\gamma \geq 3$: $\langle k \rangle$ and $\langle k \rangle^2$ are finite. In this case, τ^{SI} is finite and the spreading dynamics is similar to the behavior predicted for a random network
- Scale-free network with $\gamma \leq 3$: in this case $\langle k \rangle^2 \rightarrow \infty$ in the limit $N \rightarrow \infty$. In other words, the spread of a pathogen on a scale-free network is instantaneous