Epidemics

Introduction to Network Science

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Topic 16

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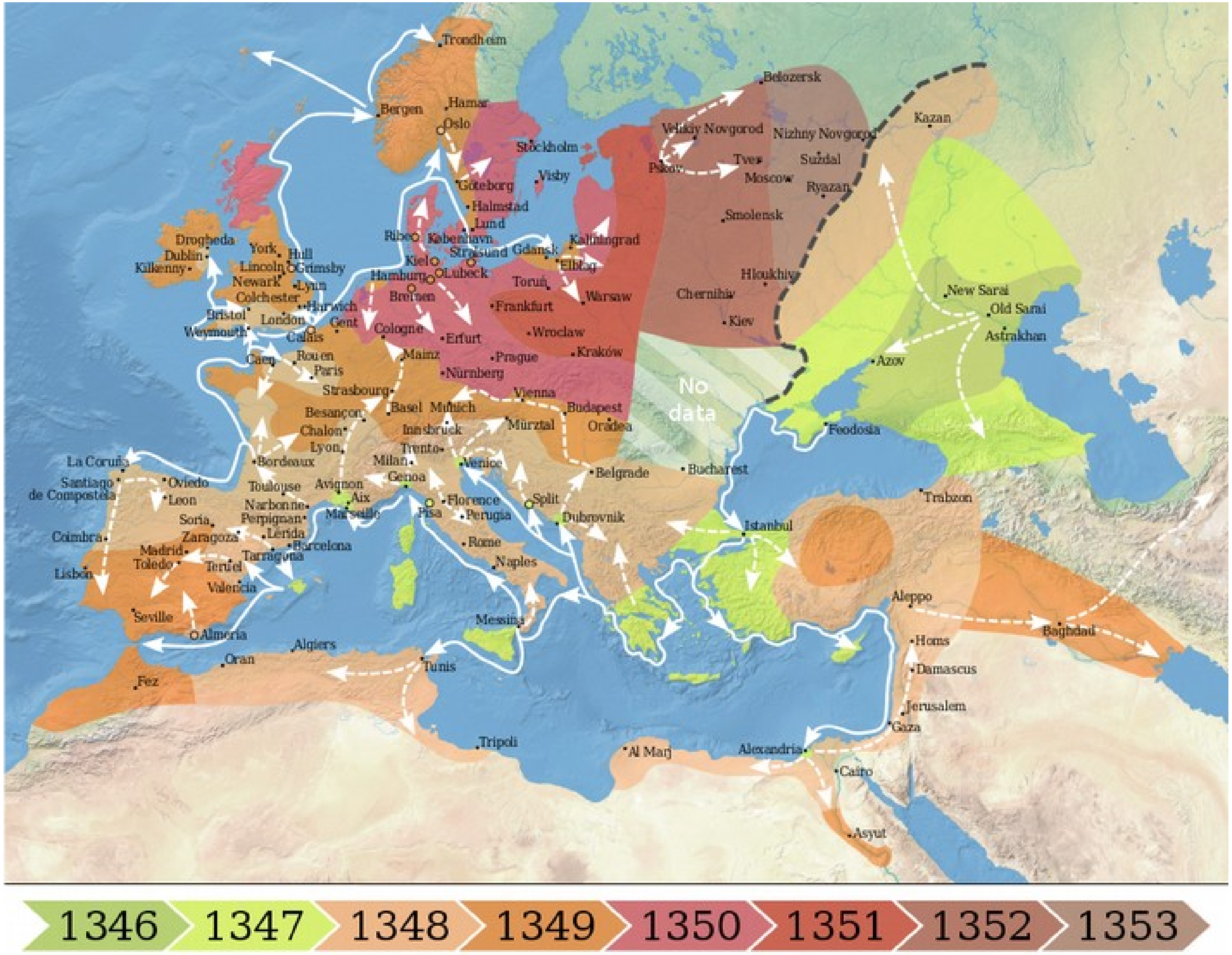
Sources

- Barabási (2016): Network Science Ch. 10
- Easley and Kleinberg (2010): Networks, Crowds, and Markets Ch 21.

Examples: human epidemics

- Influenza, measles, STDs
- The “Black Death”
  [next slide]
- Smallpox and other diseases brought by Europeans to America since early 1500s

https://en.wikipedia.org/wiki/Cocoliztli_Epidemic_of_1545-1548



The "Black Death" (Bubonic plague)

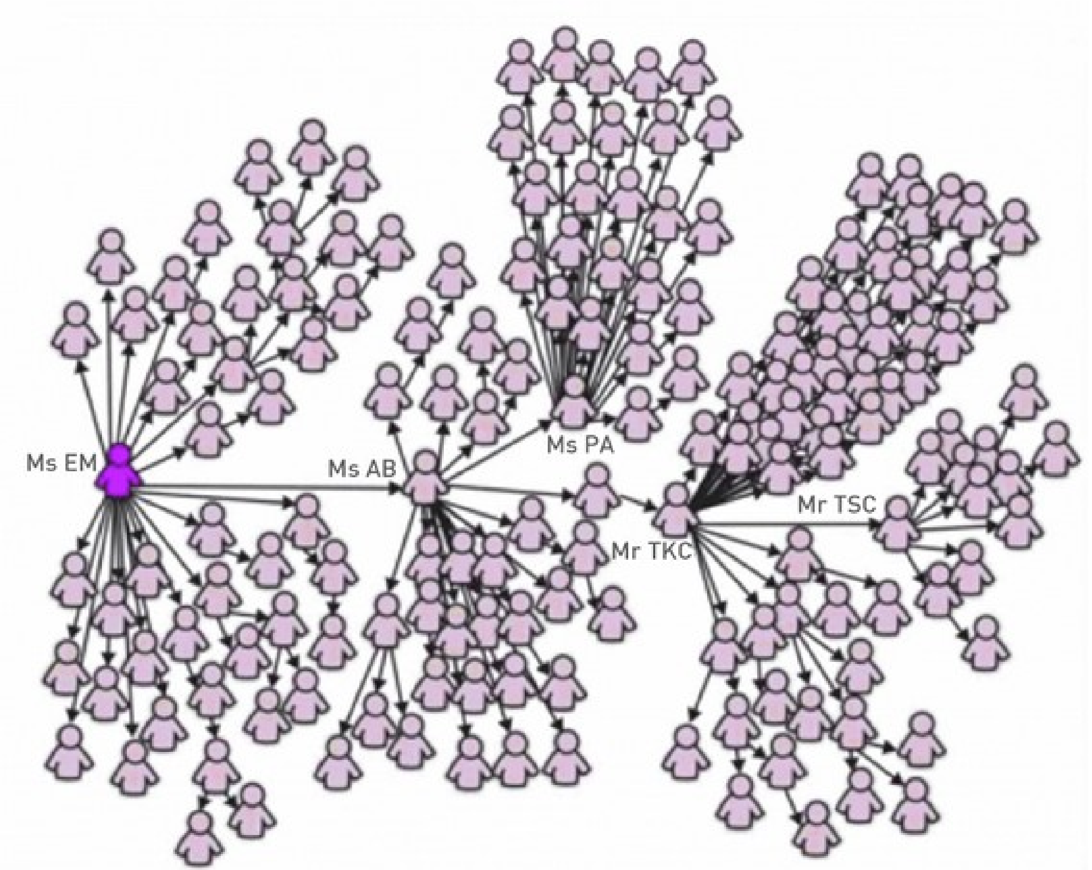
1300s

Killed 30%-60% of the total population of Europe

https://commons.wikimedia.org/wiki/File:1346-1353_spread_of_the_Black_Death_in_Europe_map.svg

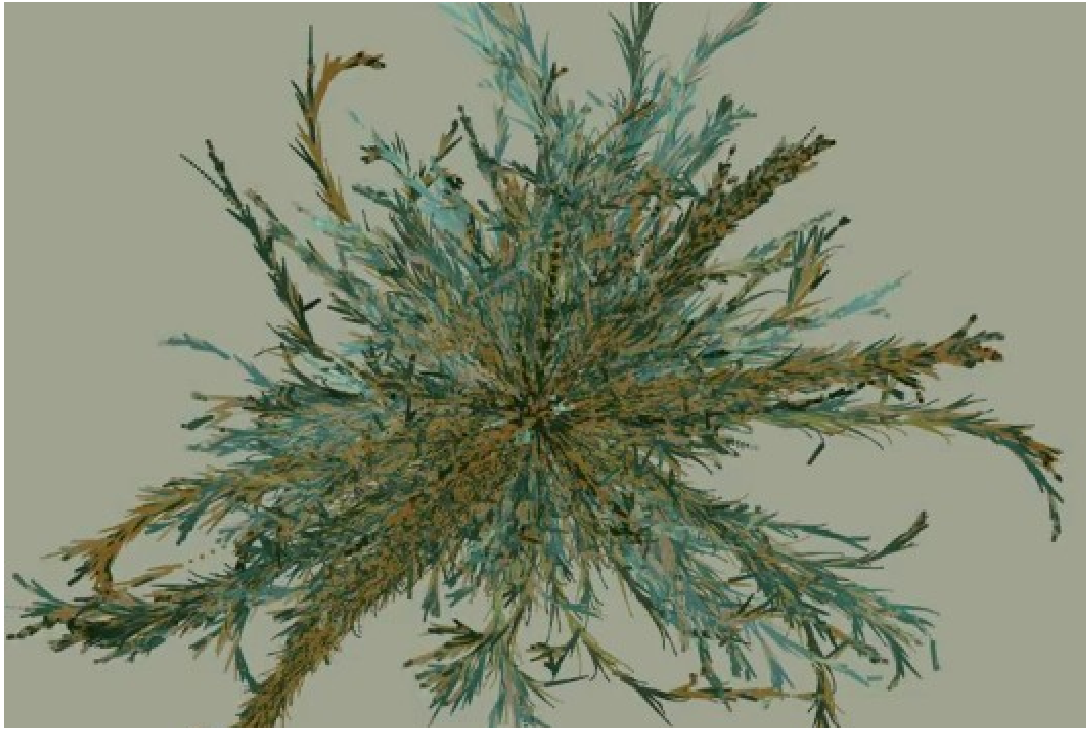
SARS Outbreak (2003)

- February 21st: Chinese doctor who have been several treating “atypical pneumonia” cases check-ins into hotel in Hong Kong
  - Hospitalized on Feb 22nd
  - Died on March 4th
- March 1st: “Ms. E. M.” returns to Singapore after visiting Hong Kong
  - Graph depicts 144 out of the first 206 SARS patients in Singapore
  - Ms. E. M. lived, various of her family members died

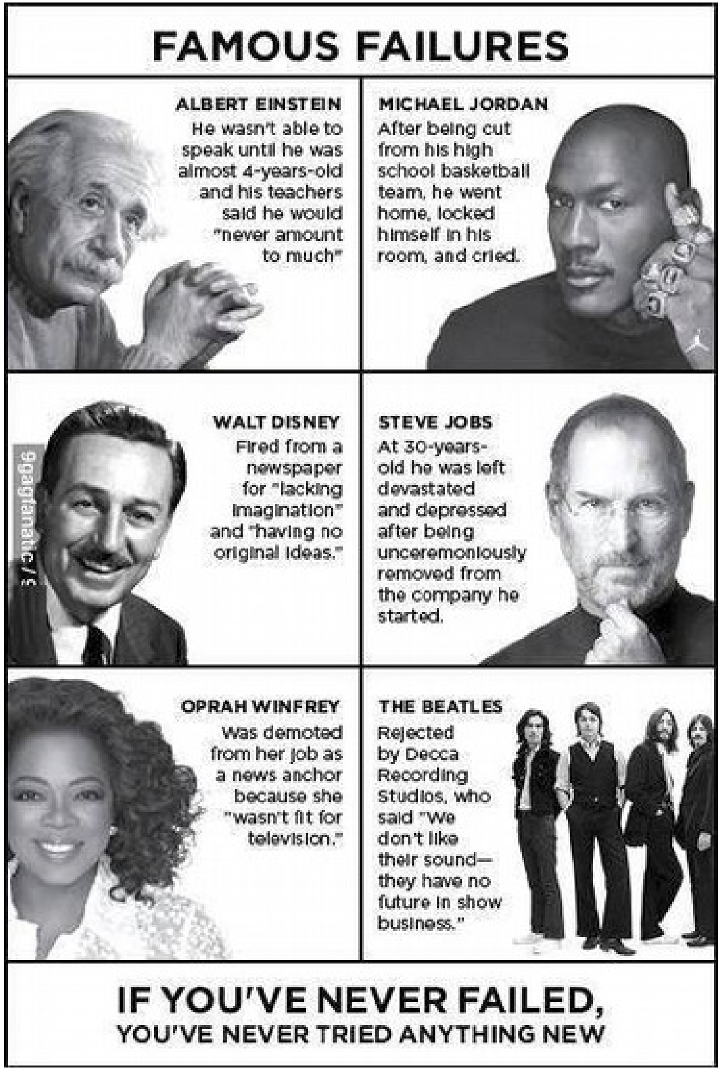


https://en.wikipedia.org/wiki/Timeline_of_the_SARS_outbreak

Spread of a Meme
(“Famous Failures”)



https://vimeo.com/50730795



Simple models for epidemics

- There are many factors:
  - Contagiousness
  - Length of infectious period,
  - Severity
  - ...
- Structure of contacts in a population

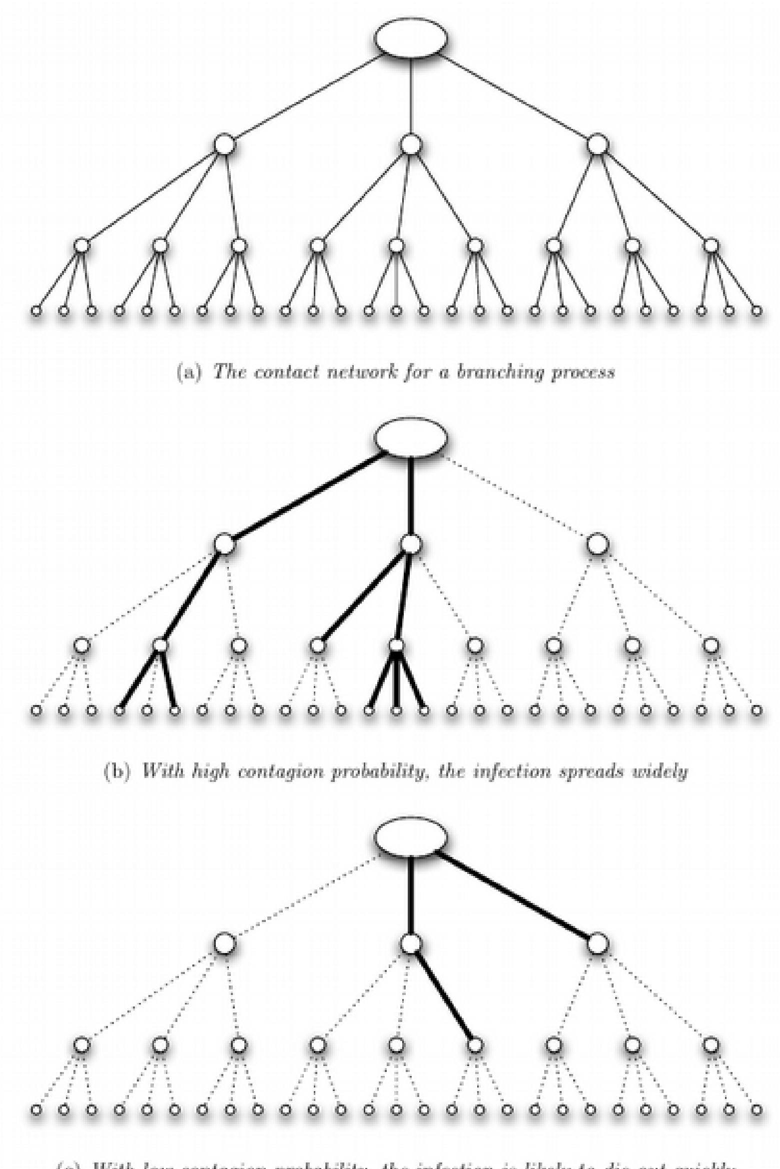
Diffusion of ideas and diseases

- Adopting a new idea, behavior, fashion, product, taste, may also spread from person to person: “social contagion”
- There is a certain agency of the receiver
- In diffusion of diseases, we assume there is no agency: each contagion is random

Simple model: branching process

- Each person interacts with other k people
- Each interaction ends in infection with probability β

Example: k=3



(a) The contact network for a branching process

(b) With high contagion probability, the infection spreads widely

(c) With low contagion probability, the infection is likely to die out quickly

Transmission rate or "Basic reproductive number" R_0

- Each person interacts with other k people
- Each interaction ends in infection with probability β

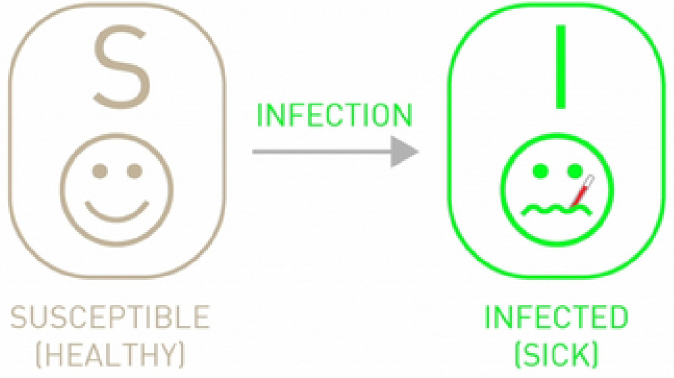
- What is the expected number of cases caused by a single individual?
- What do you think happens if $R_0 < 1$?
- What do you think happens if $R_0 > 1$?

Disease	Transmission	R_0
Measles	Airborne	12-18
Pertussis	Airborne droplet	12-17
Diptheria	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 (1918 strain)	Airborne droplet	2-3

Changing $R_0 = \beta k$

- Sanitary practices (reduce β)
- Quarantine (reduces k)

The SI model



- Susceptible:
  - The node can catch the disease
- Infected:
  - The node has the disease and can spread it
  - It will stay sick forever

Notation

- Number of susceptible $S(t)$
  - Fraction of susceptible $s(t) = S(t) / N$
- Number of infected $I(t)$
  - Fraction of infected $i(t) = I(t) / N$
- $s(t) + i(t) = 1$

How many susceptible neighbors a node has?

$$\langle k \rangle \, \frac{S(t)}{N} = \langle k \rangle \, s(t)$$

How many new infections are produced?

(for every infected, iterate through its susceptible neighbors, infect with probability β)

$$I(t) \, \langle k \rangle \, s(t) \beta$$

infected susceptible neighbors infection probability

Prove that $i(t) = \dfrac{i_0 e^{\beta\langle k\rangle t}}{1 - i_0 + i_0 e^{\beta\langle k\rangle t}}$

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

Use $\dfrac{1}{i(1-i)} = \dfrac{1}{i} + \dfrac{1}{1-i}$ and integrate from t = 0 to t

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

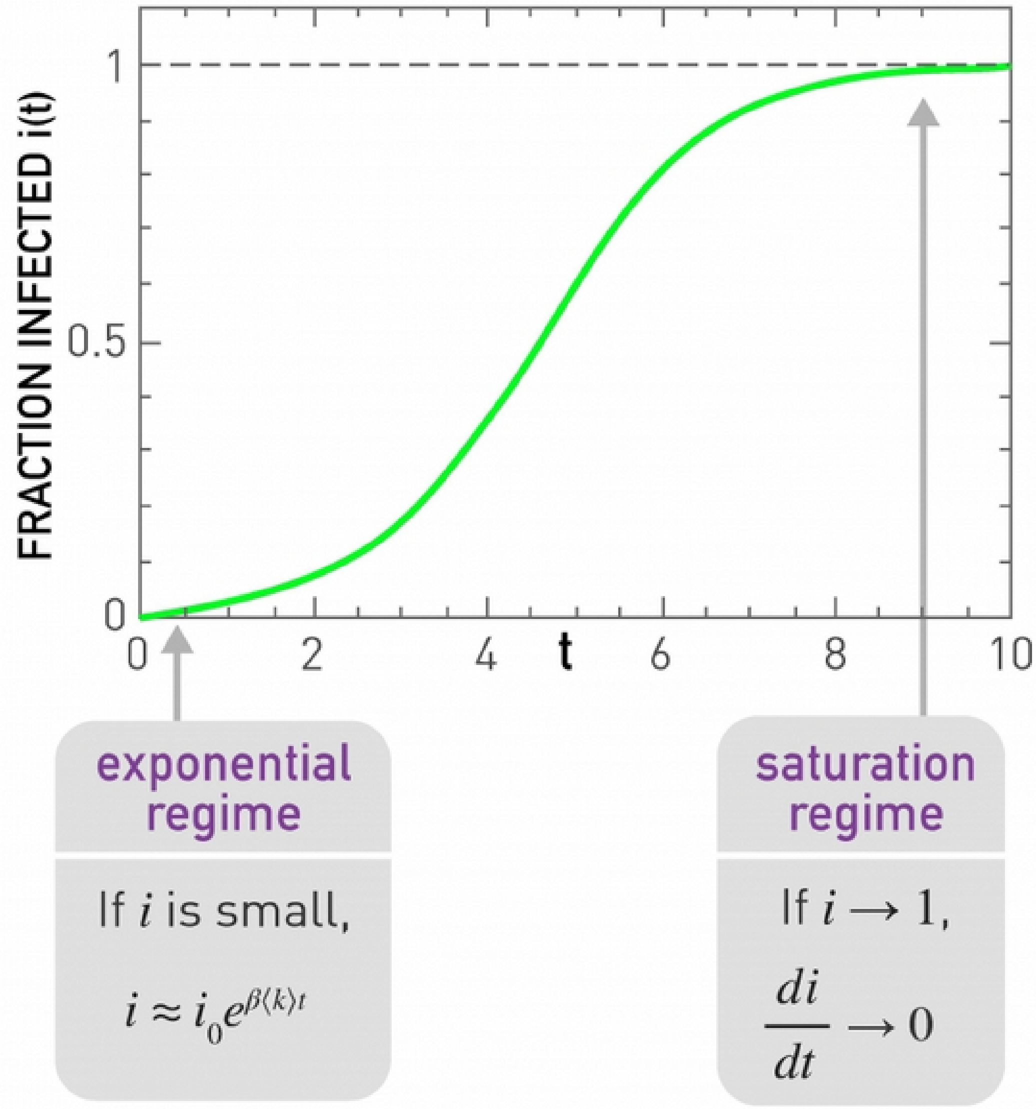
$$\int \frac{1}{x} dx = \log x + C \qquad \int \frac{1}{1-x} dx = -\log(1-x) + C$$

Infected as a function of time (SI)

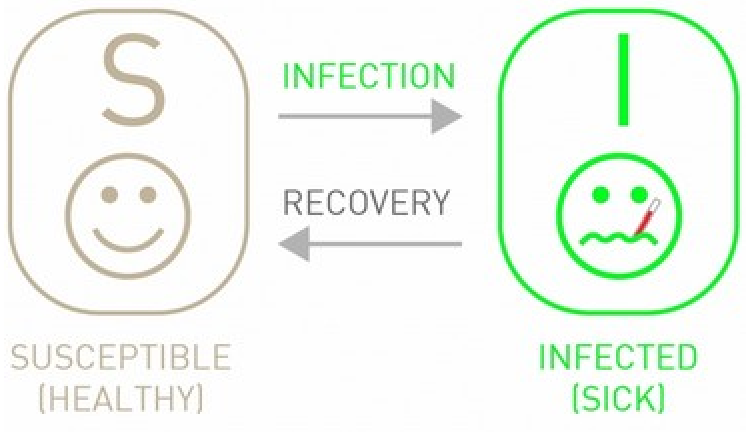
$$i(t) = \frac{i_0 e^{\beta \langle k \rangle t}}{1 - i_0 + i_0 e^{\beta \langle k \rangle t}}$$

Characteristic time
(to infect 1/e ≃ 36% of people):

$$\tau = \frac{1}{\beta \langle k \rangle}$$



The SIS model



- Susceptible:
  - The node can catch the disease
- Infected:
  - The node has the disease and can spread it
  - After some time, it recovers … but it becomes susceptible again

Infection dynamics

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

- μ is the recovery rate, i.e., the probability of becoming susceptible again in an unit of time

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

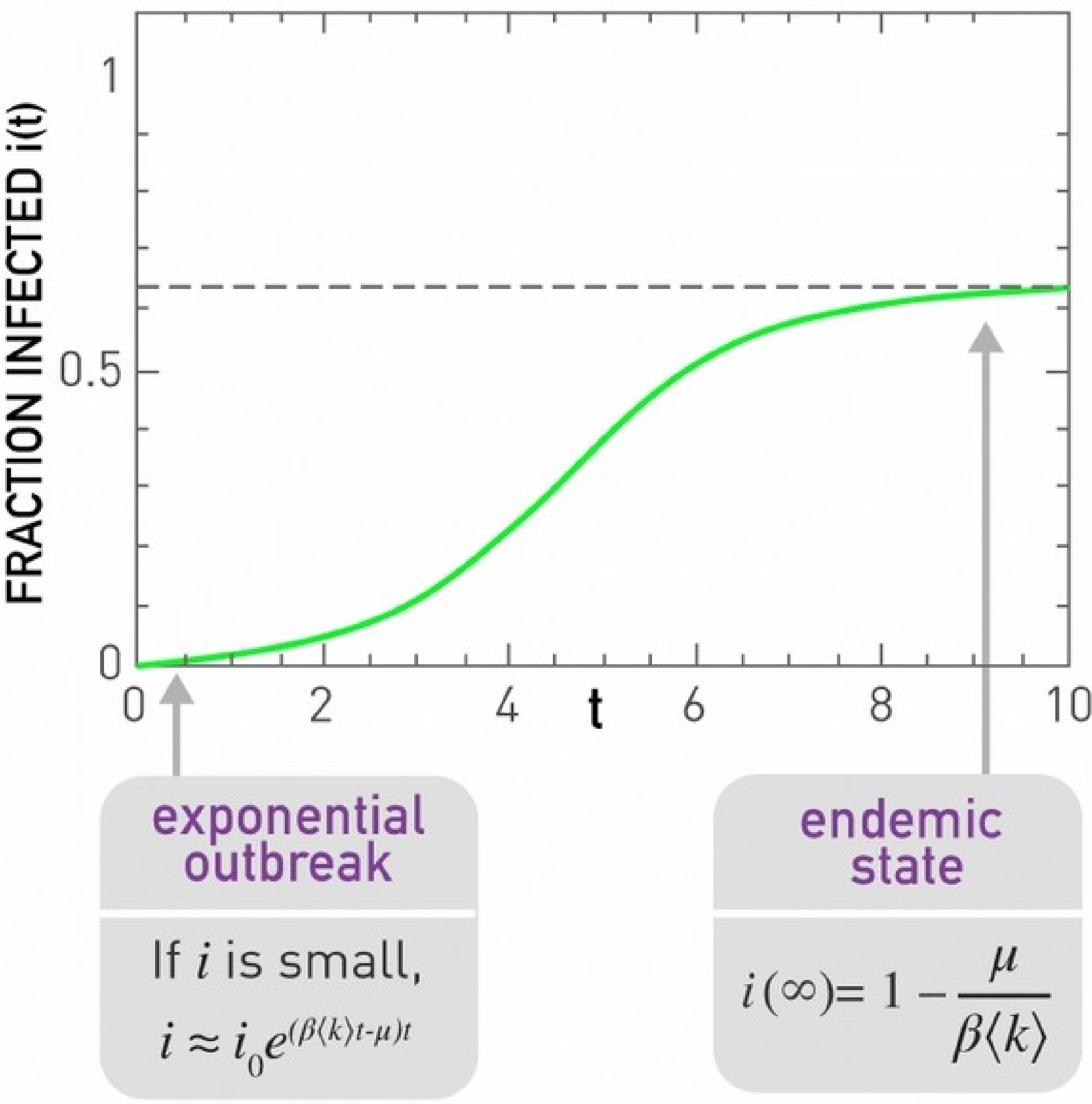
- C is a constant that depends on i_0

Infected as a function of time (SIS)

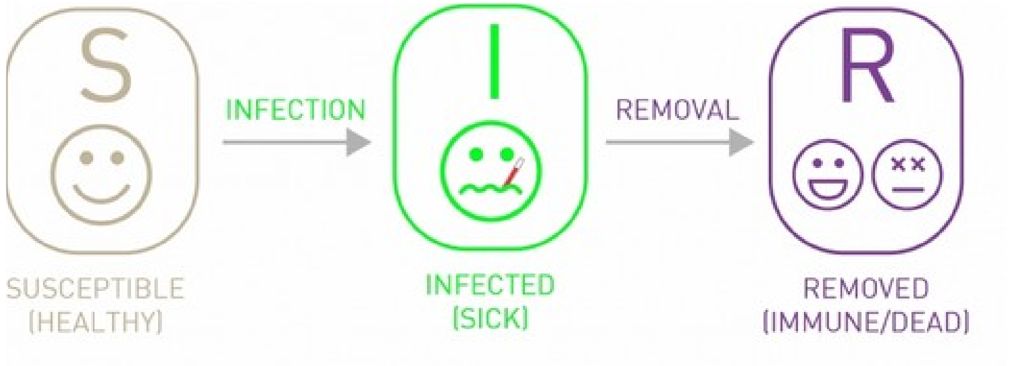
$$i(t) = \left(1 - \frac{\mu}{\beta \langle k \rangle}\right) \frac{Ce^{(\beta\langle k\rangle - \mu)t}}{1 + Ce^{(\beta\langle k\rangle - \mu)t}}$$

This is in the case $\mu < \beta \langle k \rangle$

In the case $\mu > \beta \langle k \rangle$ the infection dies out



The SIR model



- Susceptible:
  - The node can catch the disease
- Infected:
  - The node has the disease and can spread it
- Removed:
  - The node no longer has the disease, and cannot catch it or propagate it again (could be dead, could be immune)

Infection dynamics in SIR

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

$$\frac{dr(t)}{dt} = \mu i(t)$$

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

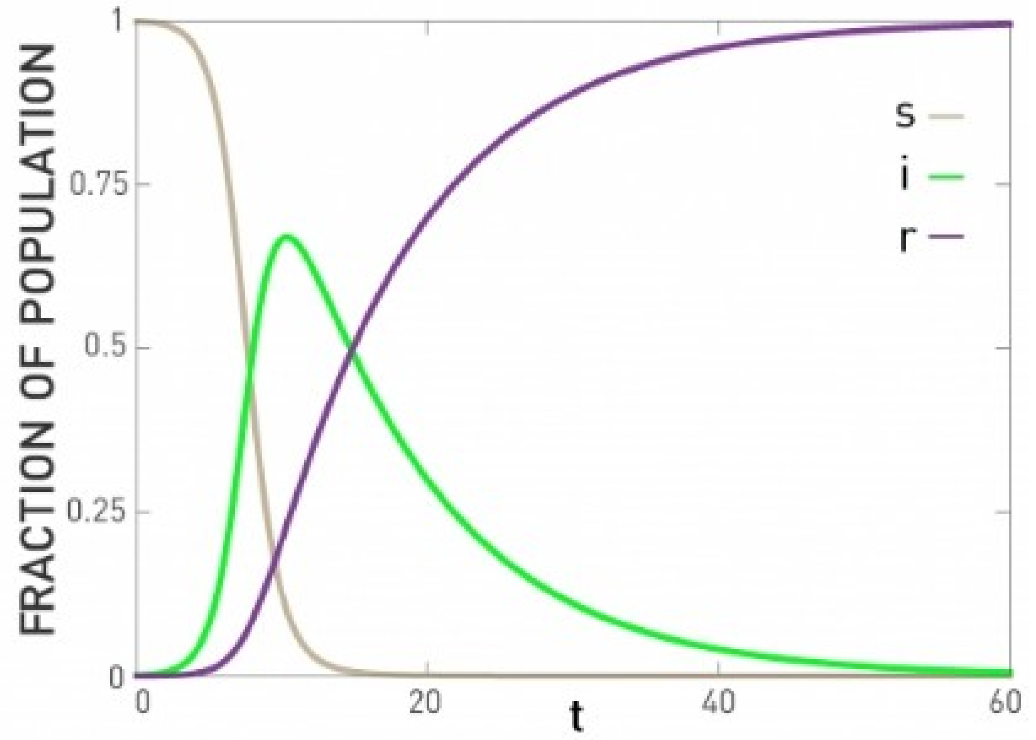
- No closed form solution

Infection dynamics (SIR)

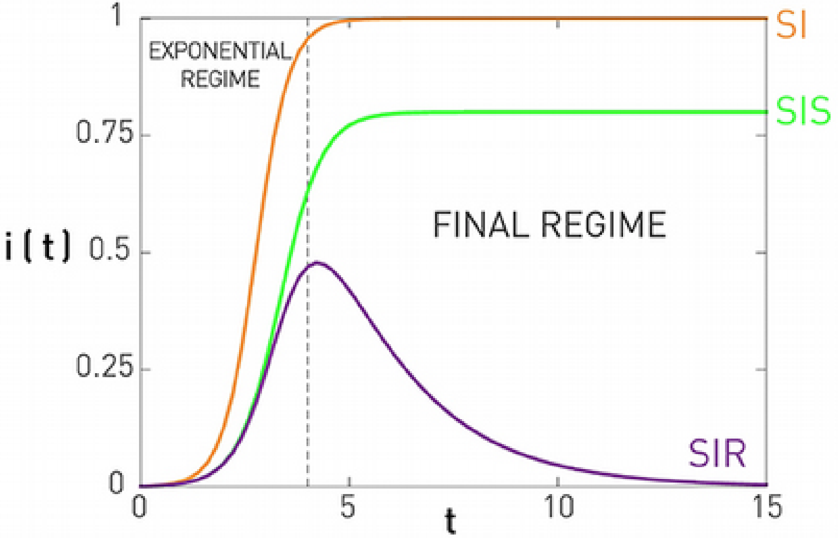
$$\frac{di(t)}{dt} = \beta \langle k \rangle i(t)(1 - r(t) - i(t)) - \mu i(t)$$

$$\frac{dr(t)}{dt} = \mu i(t)$$

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



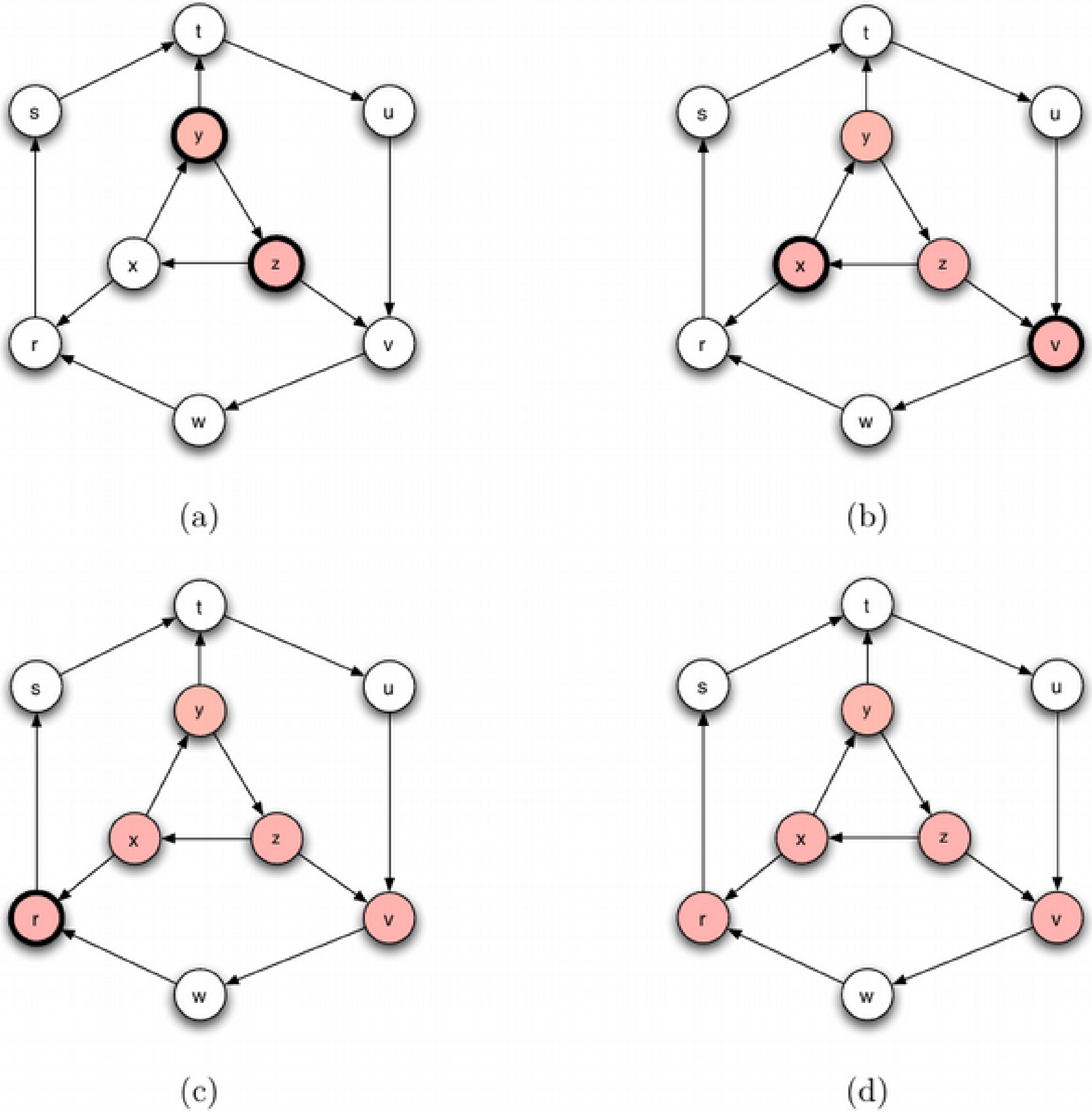
Comparison of *i(t)*



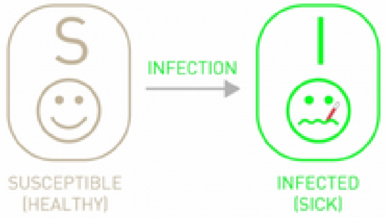
	SI	SIS	SIR
Exponential Regime: Number of infected individuals grows exponentially	$i=\frac{i_0 e^{\beta\langle k\rangle t}}{1-i_0+i_0 e^{\beta\langle k\rangle t}}$	$i=\left(1-\frac{\mu}{\beta\langle k\rangle}\right)\frac{Ce^{(\beta\langle k\rangle-\mu)t}}{1+Ce^{(\beta\langle k\rangle-\mu)t}}$	No closed solution
Final Regime: Saturation at t→=∞	$i(\infty)=1$	$i(\infty)=1-\frac{\mu}{\beta\langle k\rangle}$	$i(\infty)=0$
Epidemic Threshold: Disease does not always spread	No threshold	$R_0=1$	$R_0=1$

SIR on a graph

- In this simulation we assume recovery takes one timestep
- Infected nodes have thick borders
- Recovered nodes have thin borders



SI dynamics on a graph



- Degree block approximation: all nodes with the same degree are jointly analyzed

$$i_k(t) = \frac{I_k(t)}{N_k}$$

$$i(t) = \sum_k i_k(t) p_k$$

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

for every infected,

iterate through its susceptible neighbors,

infect with probability β

Θ_k is the fraction of infected nodes of a susceptible node of degree k

SI model on a graph: infected as a function of time

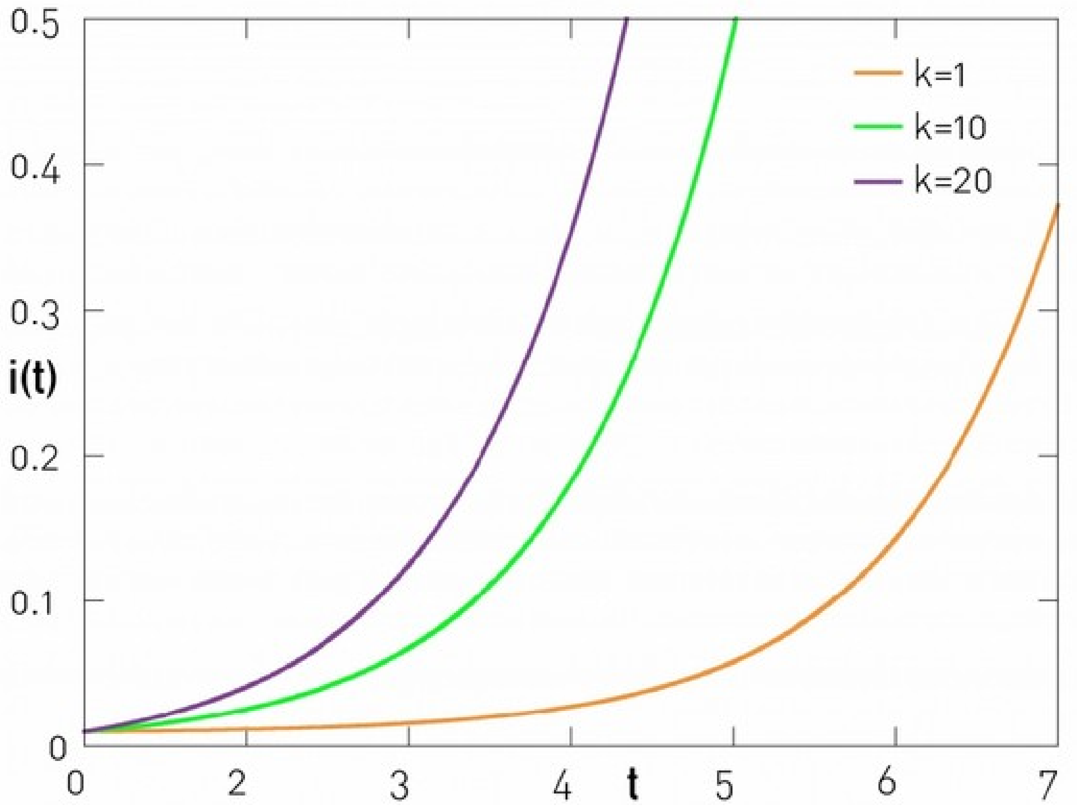
$$i_k(t) \approx i_0 \left(1 + k \frac{\langle k \rangle - 1}{\langle k^2 \rangle - \langle k \rangle} \left(e^{t/\tau^{SI}} - 1\right)\right)$$

What can you say about $i_k(t)$?

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

Characteristic time, i.e., the time to infect 1/e ≃ 36% of nodes

Higher degree nodes are more likely to become infected



$$i_k(t) = i_0 \left(1 + \frac{k\left(\langle k \rangle - 1\right)}{\langle k^2 \rangle - \langle k \rangle}\left(e^{t/\tau^{SI}} - 1\right)\right)$$

Characteristic time

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

- Random network

$$\left\langle k^2 \right\rangle = \langle k \rangle \left(\langle k \rangle + 1 \right) \Rightarrow \tau^{SI}_{ER} = \frac{1}{\beta \langle k \rangle}$$

- Scale-free network with $\gamma \geq 3$

$$\langle k \rangle, \left\langle k^2 \right\rangle \text{ are finite} \Rightarrow \tau^{SI} \text{ is finite}$$

- Scale-free network with $\gamma < 3$

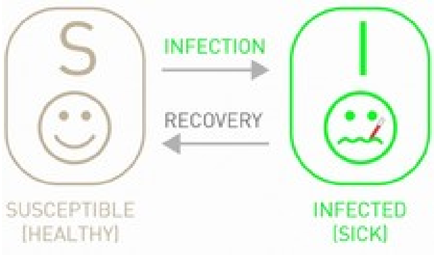
$$\left\langle k^2 \right\rangle \xrightarrow[N \to \infty]{} \infty \Rightarrow \lim_{N \to \infty} \tau^{SI} = 0$$

Vanishing characteristic time

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

- If $\lim_{N \to \infty} \frac{\langle k \rangle}{\langle k^2 \rangle} = 0$ the characteristic time goes to 0
- Networks with skewed degree distributions allow infections with the same β to spread faster

SIS dynamics on a graph



Similar to SI dynamics but allowing recovery

$$\frac{di_k(t)}{dt} = k(1 - i_k(t))\Theta_k \beta - \mu i_k(t) \qquad \tau^{SIS} = \frac{\langle k \rangle}{\beta \langle k^2 \rangle - \mu \langle k \rangle}$$

If people recover quickly, $\tau < 0$ and the infection dies out

Epidemic threshold

- A key quantity is the spreading rate $\lambda = \dfrac{\beta}{\mu}$
- The critical spreading rate λ_c called the epidemic threshold, is such that $\tau > 0$

Compute the epidemic threshold for an ER graph where $\langle k^2 \rangle = \langle k \rangle \left(\langle k \rangle + 1 \right)$

$$\tau^{SIS} = \frac{\langle k \rangle}{\beta \langle k^2 \rangle - \mu \langle k \rangle}$$

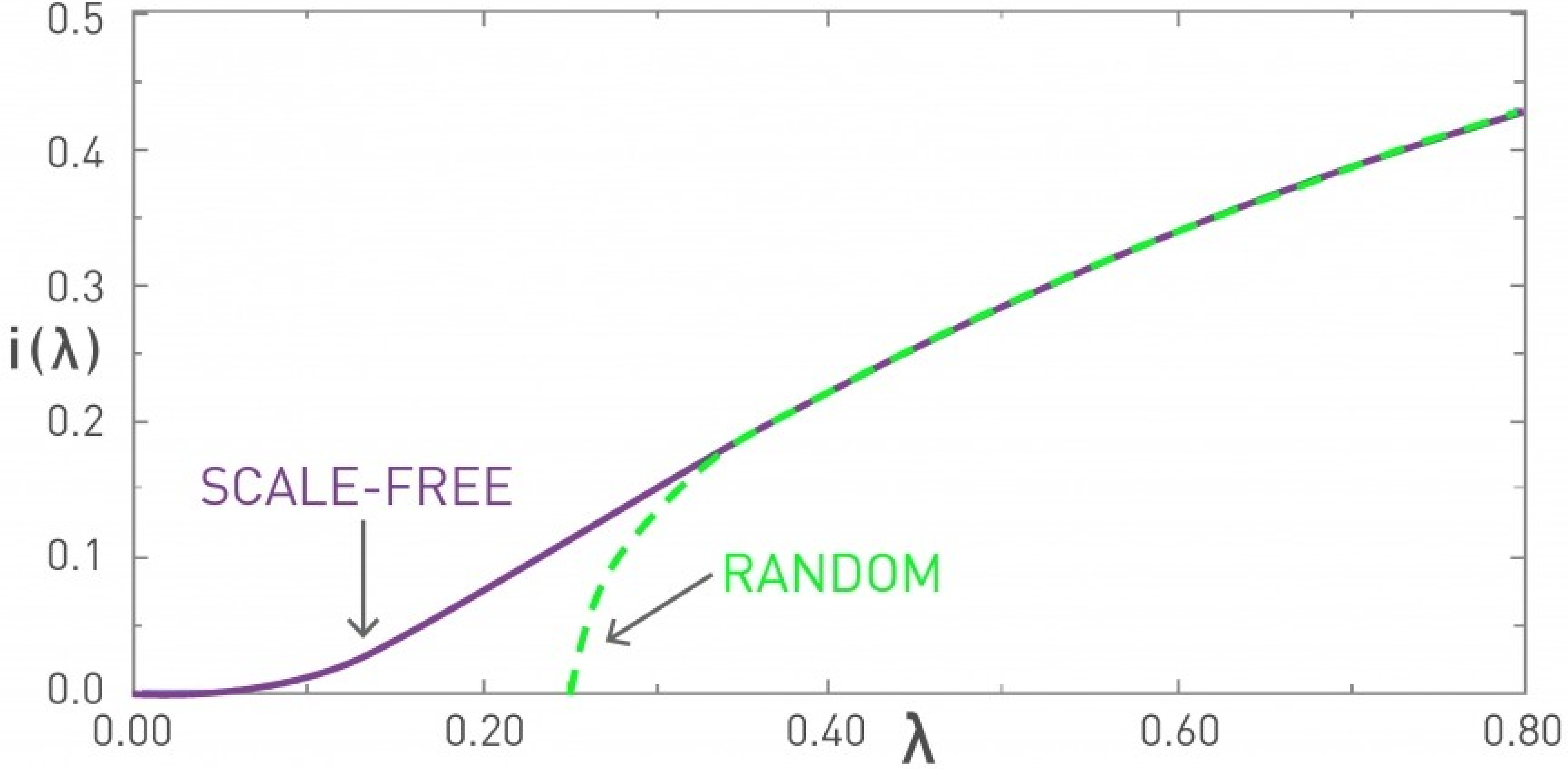
Epidemic threshold in a scale-free network

$$\tau^{SIS} = \frac{\langle k \rangle}{\beta \langle k^2 \rangle - \mu \langle k \rangle} > 0 \Rightarrow \frac{\beta}{\mu} > \frac{\langle k \rangle}{\langle k^2 \rangle} = \lambda_c$$

- In a scale-free network with $\gamma < 3$

$$\left\langle k^2 \right\rangle \xrightarrow[N \to \infty]{} \infty \Rightarrow \lim_{N \to \infty} \tau^{SIS} = 0$$

Infected (in the limit) as a function of the epidemic threshold



Two key results

In a large scale-free network with $\gamma < 3$

- An infection may reach everybody in a very short time: $\tau = 0$
- An infection may become endemic even if it is not very contagious and even if people recover fast: $\lambda_c = 0$