Epidemics

Introduction to Network Science

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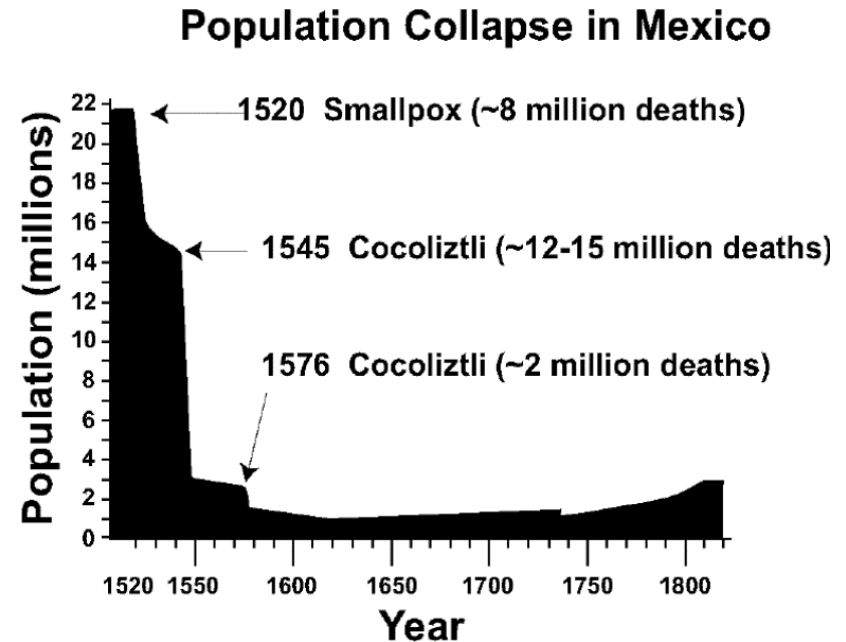
Topic 13

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

Population Collapse in Mexico

1520 Smallpox (~8 million deaths)

1545 Cocoliztli (~12-15 million deaths)

1576 Cocoliztli (~2 million deaths)

Population (millions) vs Year

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

1346 1347 1348 1349 1350 1351 1352 1353

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

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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

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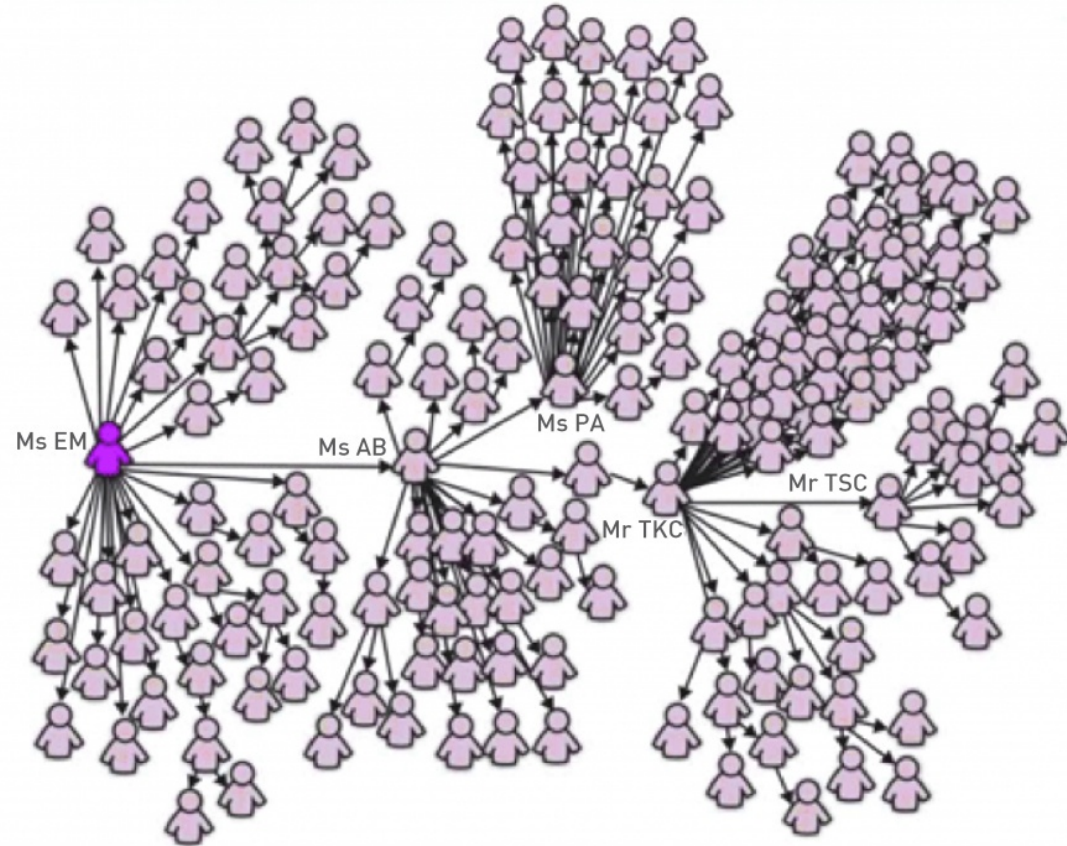
Diffusion of ideas vs diseases

- 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**

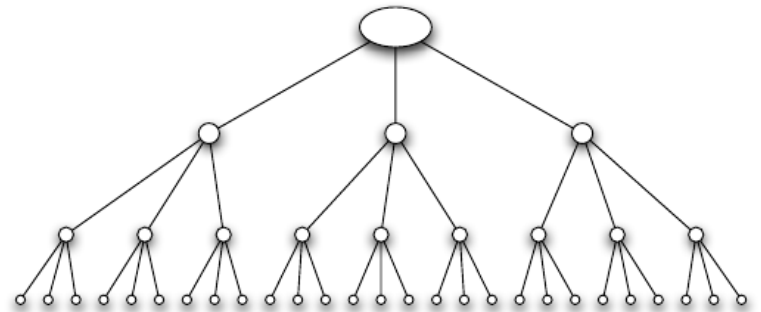# Simple model: branching process

Modeling epidemics

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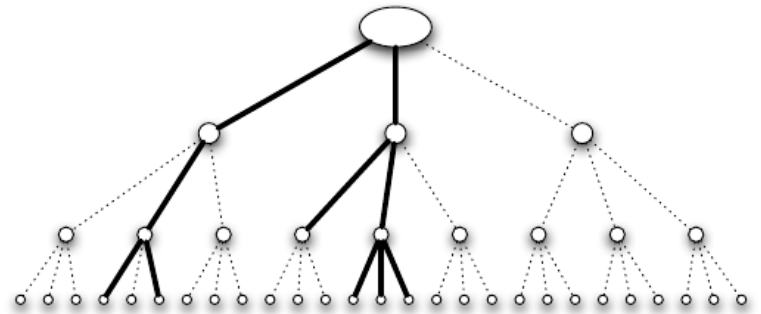- Structure of contacts in a population

Simple model: branching process

(a) *The contact network for a branching process*

- Each person interacts with other k people

- Each interaction ends in infection with probability β

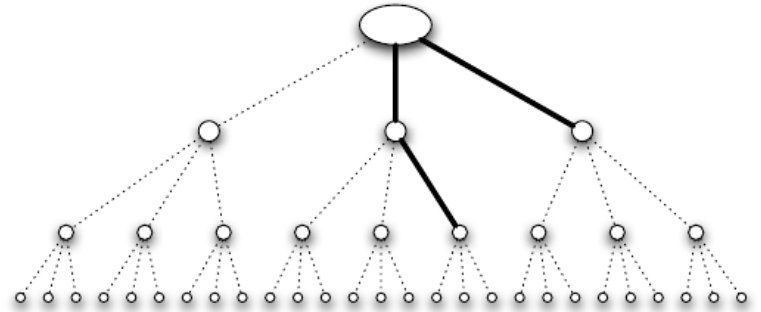(b) *With high contagion probability, the infection spreads widely*

Example: k=3

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

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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, R_0?

- 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
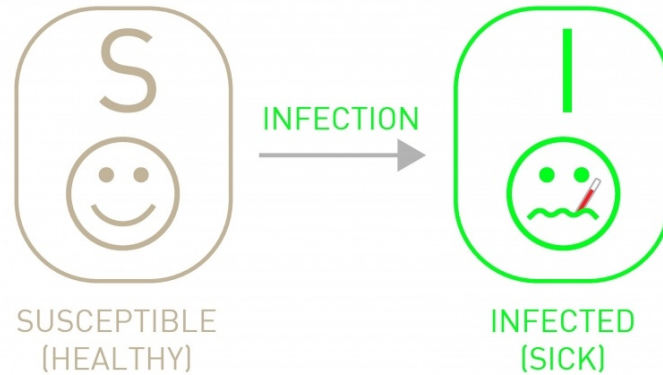
The SI model

SUSCEPTIBLE (HEALTHY) → INFECTION → INFECTED (SICK)

- Susceptible:
  - The node can catch the disease

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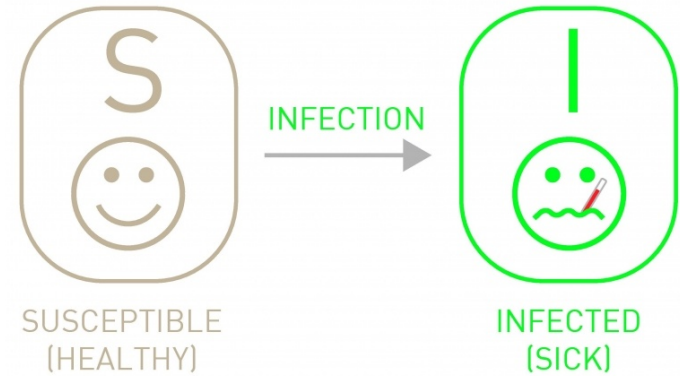
Notation

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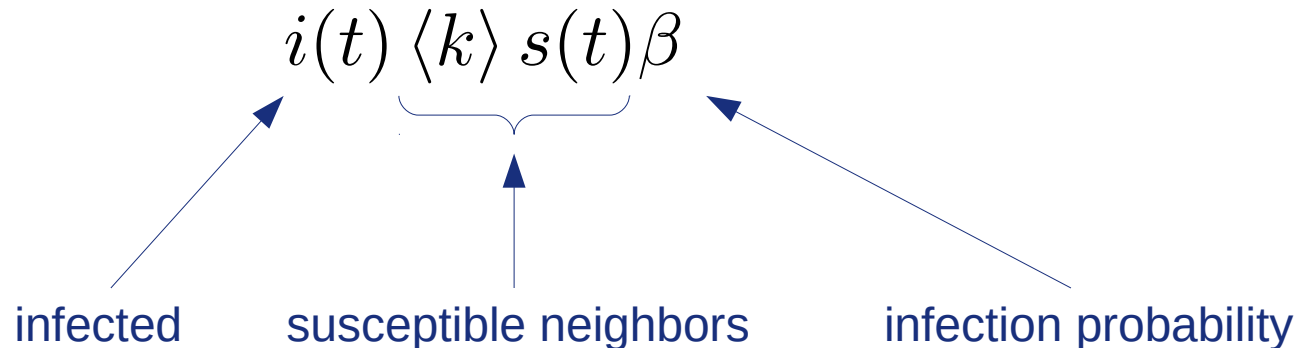
Prove that $i(t) = \dfrac{i_0 e^{\beta \langle k \rangle t}}{1 - i_0 + i_0 e^{\beta \langle k \rangle t}}$

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

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

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

$$\int \frac{1}{x} dx = \log x + C \qquad \int \frac{1}{1 - x} dx = -\log(1 - x) + C$$
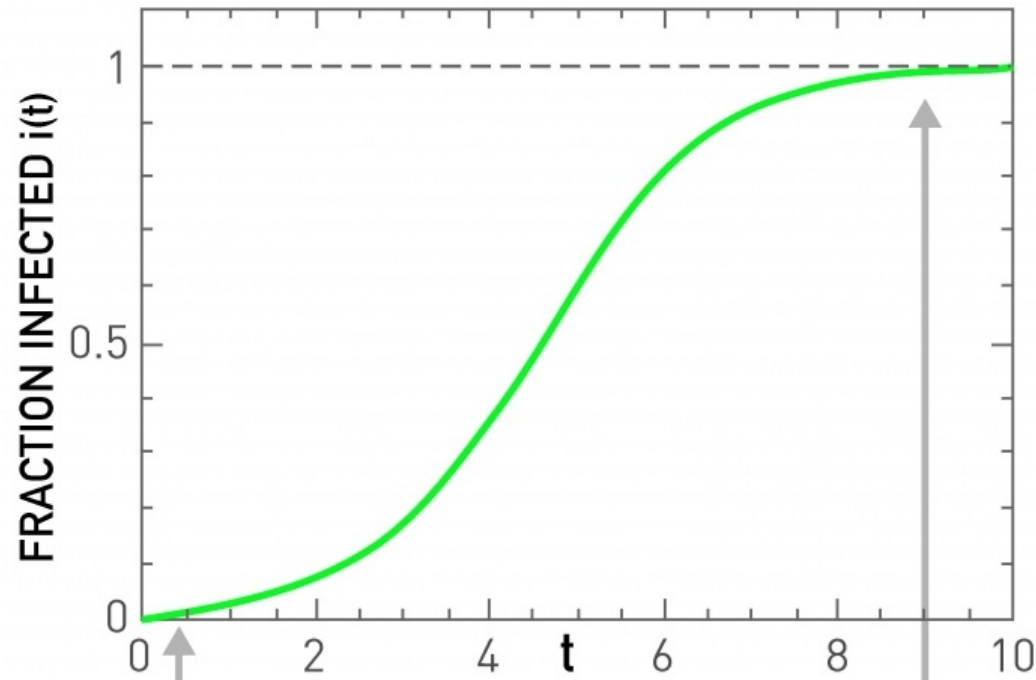
Behavior in the limit $t \to \infty$

- What is the limit of $i(t) = \dfrac{i_0 e^{\beta \langle k \rangle t}}{1 - i_0 + i_0 e^{\beta \langle k \rangle t}}$ when $t \to \infty$?

- Hint: similar to $f(t) = \dfrac{e^t}{1 + e^t}$

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):

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

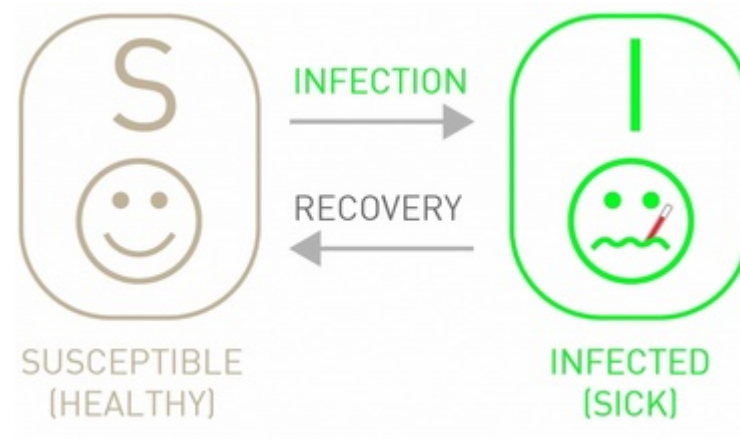

FRACTION INFECTED i(t)

exponential regime

If i is small,

$$i \approx i_0 e^{\beta \langle k \rangle t}$$

saturation regime

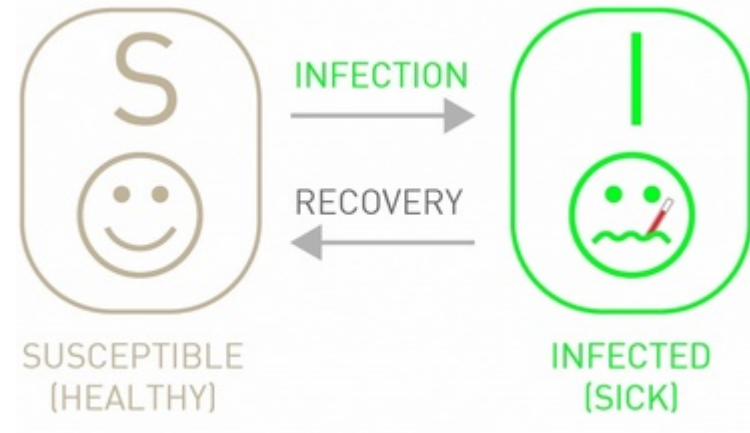If $i \to 1$,

$$\frac{di}{dt} \to 0$$

The SIS model

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

$$i(t) = \left(1 - \frac{\mu}{\beta \langle k \rangle}\right) \frac{Ce^{(\beta \langle k \rangle - \mu)t}}{1 + Ce^{(\beta \langle k \rangle - \mu)t}}$$
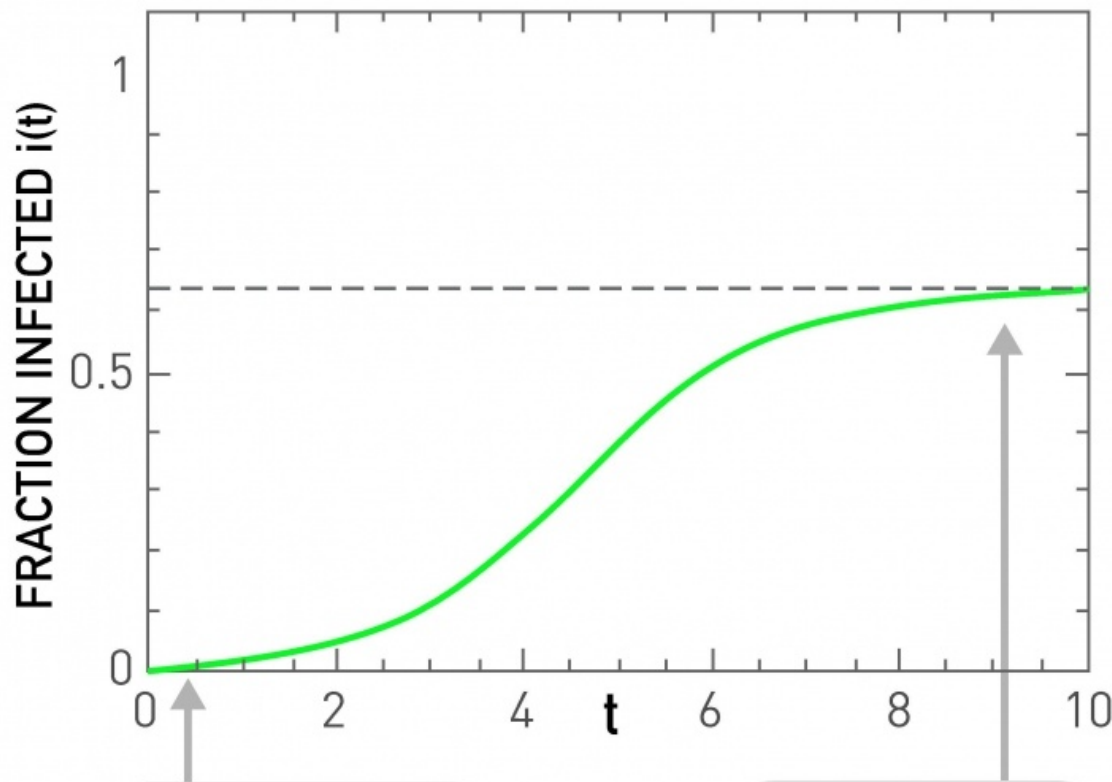
- C is a constant that depends on i_0

Behavior in the limit $t \rightarrow \infty$

- What is the limit of $i(t) = \left(1 - \dfrac{\mu}{\beta \langle k \rangle} \right) \dfrac{Ce^{(\beta \langle k \rangle - \mu)t}}{1 + Ce^{(\beta \langle k \rangle - \mu)t}}$ when $t \rightarrow \infty$?

- Hint: similar to $f(t) = \alpha \dfrac{e^t}{1 + e^t}$

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 $\mu < \beta \langle k \rangle$

FRACTION INFECTED i(t) vs **t**

exponential outbreak

If i is small,

$i \approx i_0 e^{(\beta\langle k \rangle t - \mu)t}$

endemic state

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

What happens if $\mu > \beta \langle k \rangle$?

- Remember: $\dfrac{di(t)}{dt} = \beta \langle k \rangle \, i(t)(1 - i(t)) - \mu i(t)$

The SIR model

The SIR model

SUSCEPTIBLE (HEALTHY) → INFECTION → INFECTED (SICK) → REMOVAL → REMOVED (IMMUNE/DEAD)

- 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

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

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

$$\frac{ds(t)}{dt} = -\frac{di(t)}{dt} - \frac{dr(t)}{dt} = -\beta \langle k \rangle i(t)(1 - r(t) - i(t))$$
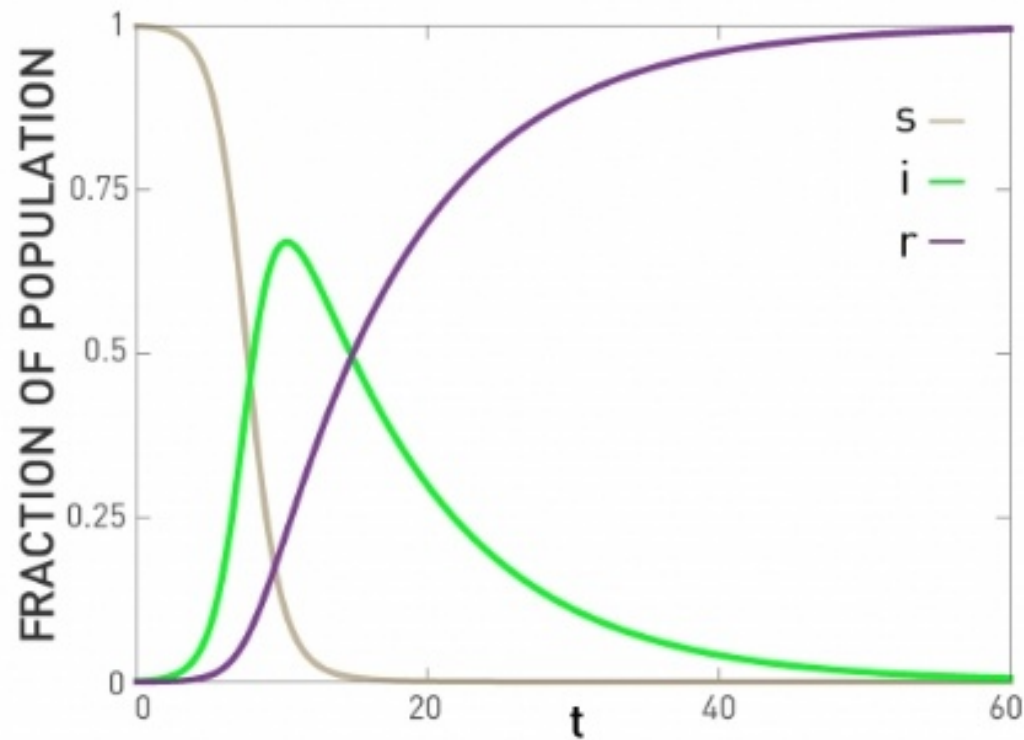
- No closed form solution
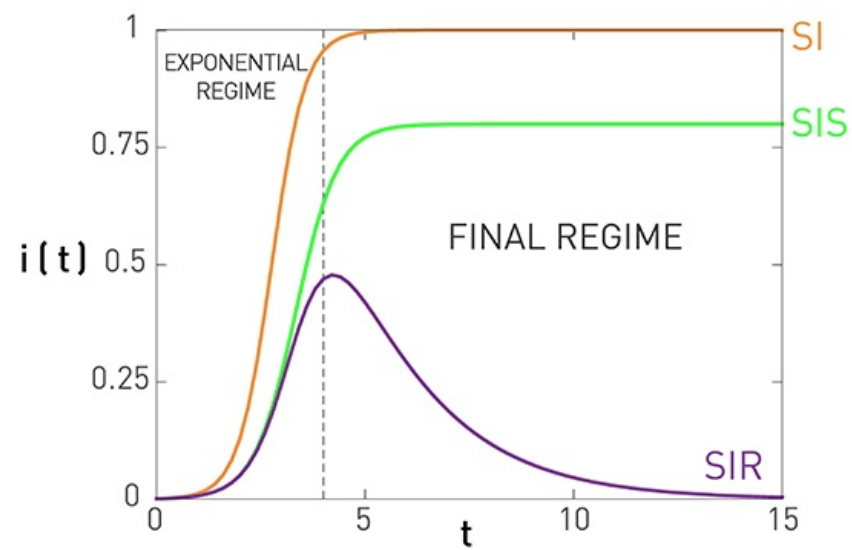
Infection dynamics (SIR)

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

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

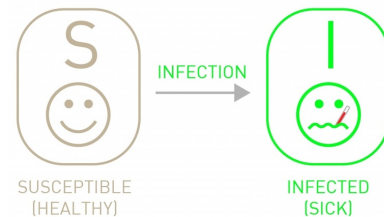$$\frac{ds(t)}{dt} = -\beta \langle k \rangle i(t)(1 - r(t) - i(t))$$

Comparison of $i(t)$

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

SI and SIS **on a graph**
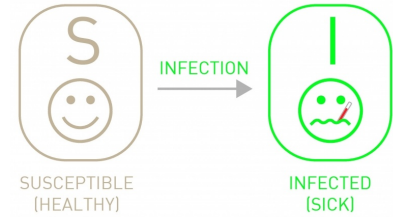
SI dynamics on a graph

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

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

$$i(t) = \sum_k i_k(t) p_k$$
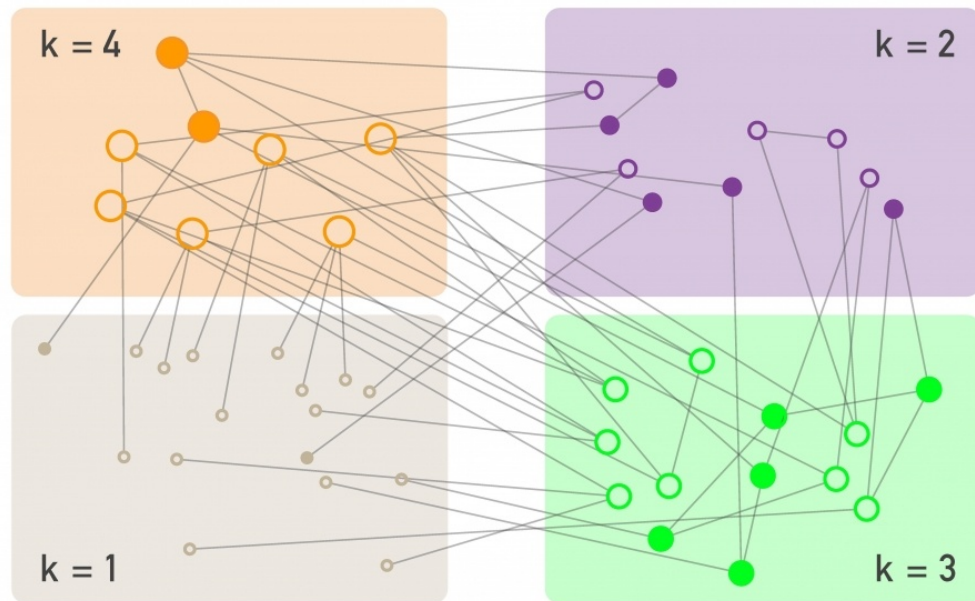
SI dynamics on a graph

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

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

Similar to simple SI model, except:

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

Compare with simple SI model:

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

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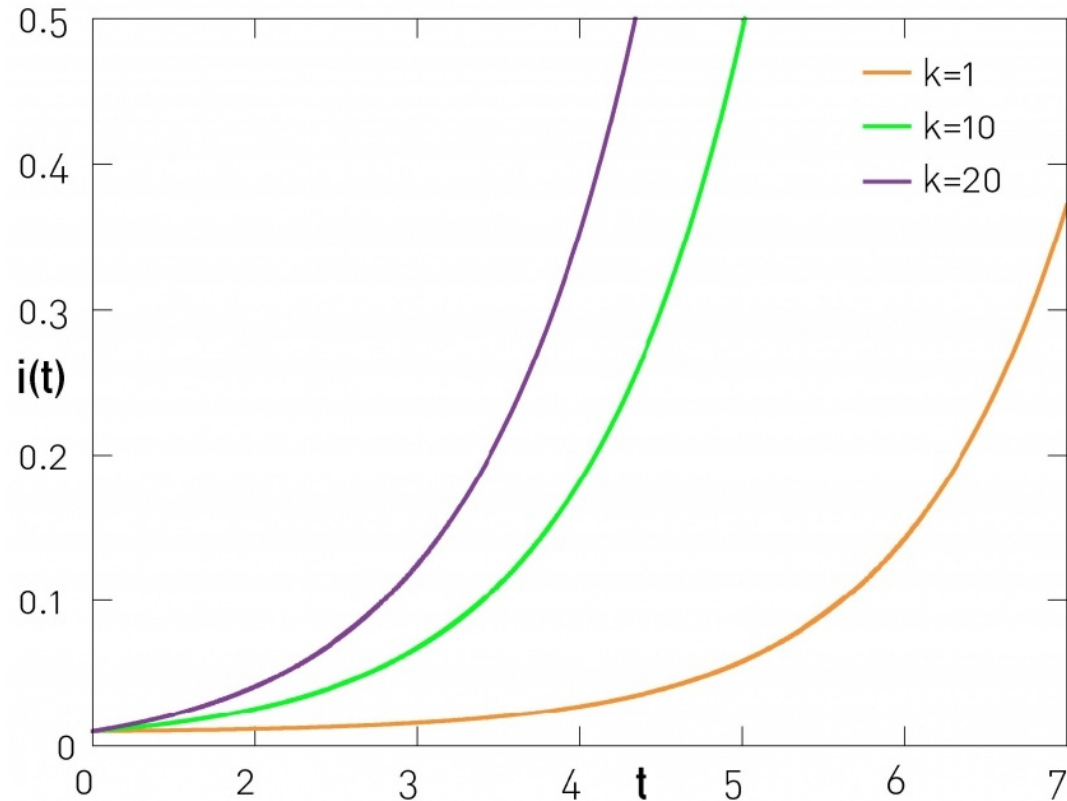# infected as a function of time

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

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

(time to infect *1/e ≃ 36%* of nodes)

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

- Random network

$$\left\langle k^2 \right\rangle = \langle k \rangle \left(\langle k \rangle + 1 \right) \Rightarrow$$

- Scale-free network with *γ ≥ 3*

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

- Scale-free network with *γ < 3*

$$\left\langle k^2 \right\rangle \xrightarrow[N \to \infty]{} \infty \Rightarrow$$

Characteristic time

(time to infect *1/e ≃ 36%* of nodes)

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

- Random network

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

- Scale-free network with *γ ≥ 3*

$$\langle k \rangle, \langle k^2 \rangle \ \text{are finite} \Rightarrow \tau_{BA}^{SI} \ \text{is finite}$$
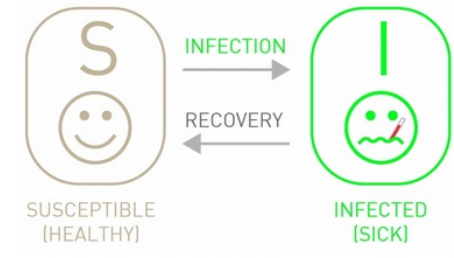
- Scale-free network with *γ < 3*

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

Vanishing characteristic time

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

- If $\lim\limits_{N \to \infty} \dfrac{\langle k \rangle}{\langle k^2 \rangle} = 0$ 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 … unless $\langle k^2 \rangle \to \infty$

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 $\tau > 0$
- Spreading rate larger than epidemic threshold:
  - infection becomes endemic
- Spreading rate smaller than epidemic threshold:
  - 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 $\langle k^2 \rangle = \langle k \rangle \left(\langle k \rangle + 1 \right)$

$$\tau^{SIS} = \frac{\langle k \rangle}{\beta \langle k^2 \rangle - \mu \langle k \rangle}$$
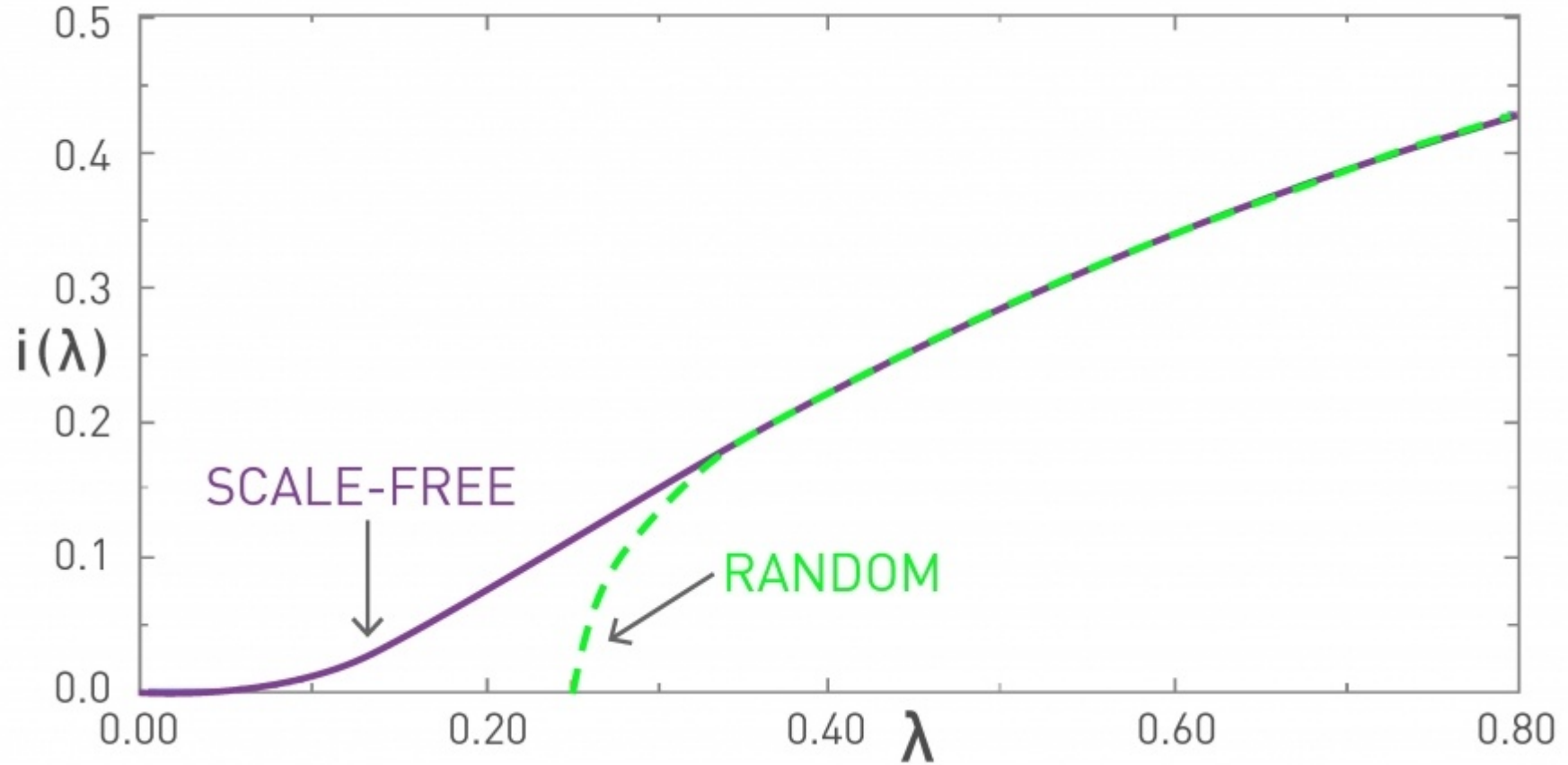
Epidemic threshold in a scale-free network

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

Epidemic threshold in BA graph

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

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

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

Two key results for
SI and SIS models on a BA graph

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: $\lambda_c = 0$

Summary

Things to remember

- SI, SIS, SIR models

- Which are the states in each process and which are the possible transitions

- Equations for number of nodes in each state

- Regimes under different parameters

- Practice executing by hand and write code if it helps you remember better each process