Epidemics

Introduction to Network Science Carlos Castillo Topic 16

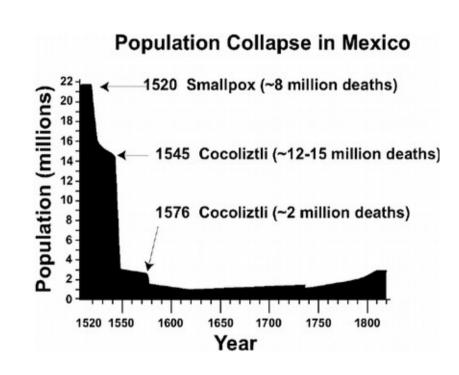


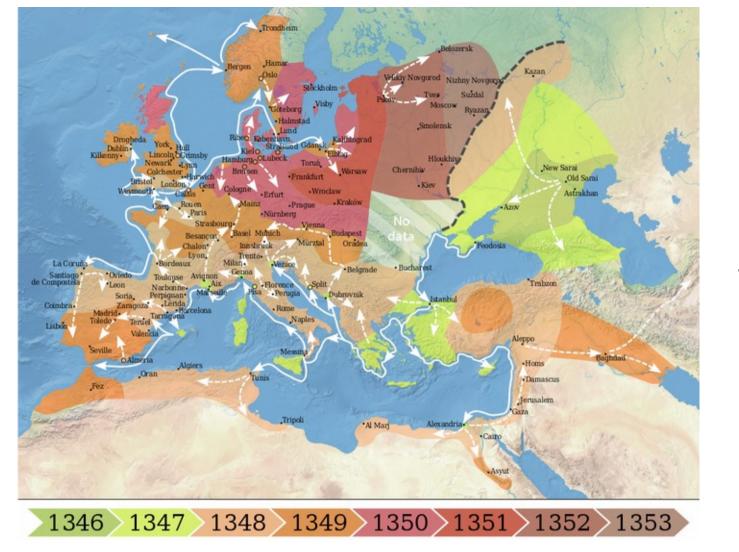
Sources

- 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





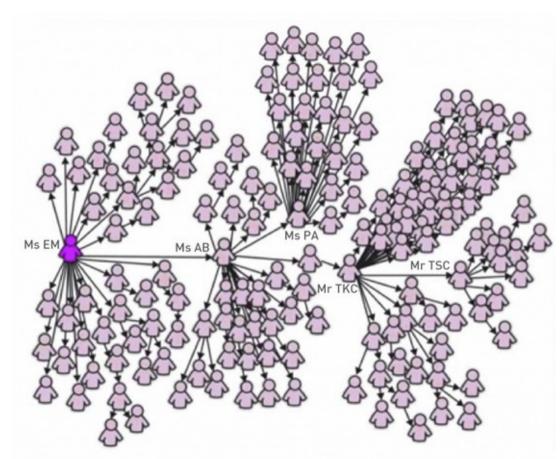
The "Black Death" (Bubonic plague)
1300s

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

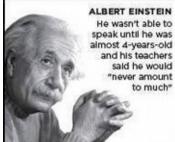


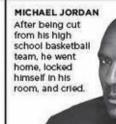
Spread of a Meme ("Famous Failures")



https://vimeo.com/50730795

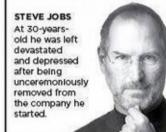
FAMOUS FAILURES



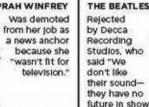




Fired from a newspaper for "lacking imagination" and "having no original ideas."





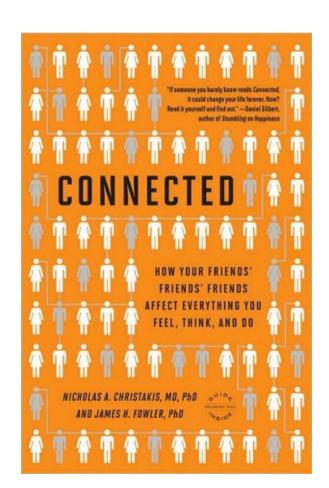




IF YOU'VE NEVER FAILED, YOU'VE NEVER TRIED ANYTHING NEW

Non-trivial examples

- Back pain: spread from West to East in Germany after fall of Berlin Wall
- Suicide: well known to spread throughout communities on occasion
- Sex practices: e.g., increase in prevalence of oral sex among teenagers
- Politics: the denser your connections, the more intense your convictions



Simple models for epidemics

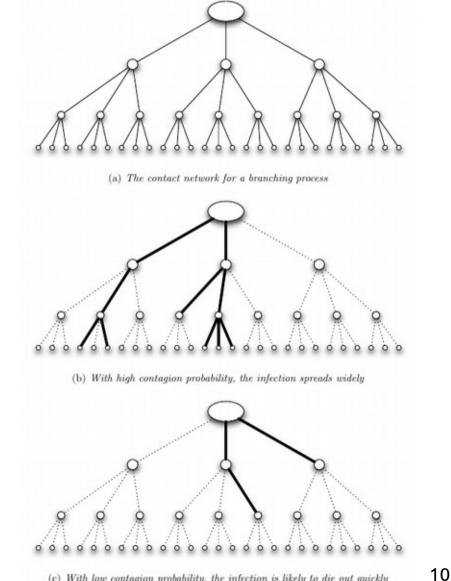
- There are many factors:
 - Contagiousness
 - Length of infectious period,
 - Severity
 - ...
- Structure of contacts in a population

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

Transmission rate or "Basic reproductive number" R_o

- 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 _O
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 (HEALTHY)

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

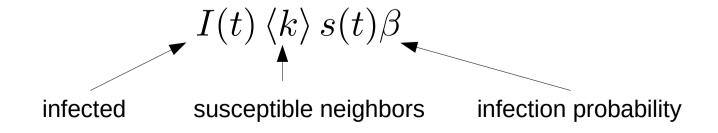
- Number of susceptible S(t)
 - Fraction of susceptible s(t) = S(t) / N
- Number of infected I(t)
 - Fraction of infected i(t) = I(t) / N
- s(t) + i(t) = 1

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)



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

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

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

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

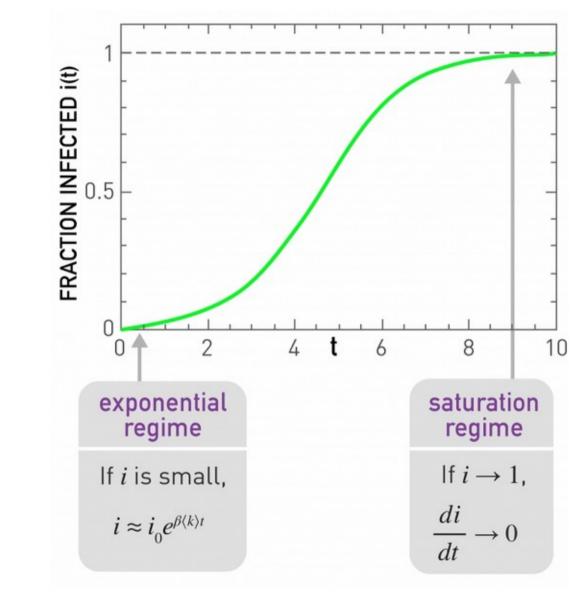
$$\int \frac{1}{x} dx = \log x + C \qquad \int \frac{1}{1-x} dx = -\log(1-x) + C$$

Infected as a function of time (SI)

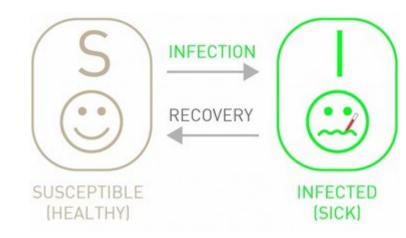
$$i(t) = \frac{i_0 e^{\beta \langle k \rangle t}}{1 - i_0 + i_0 e^{\beta \langle k \rangle t}}$$

Characteristic time (to infect $1/e \approx 36\%$ of people):

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



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

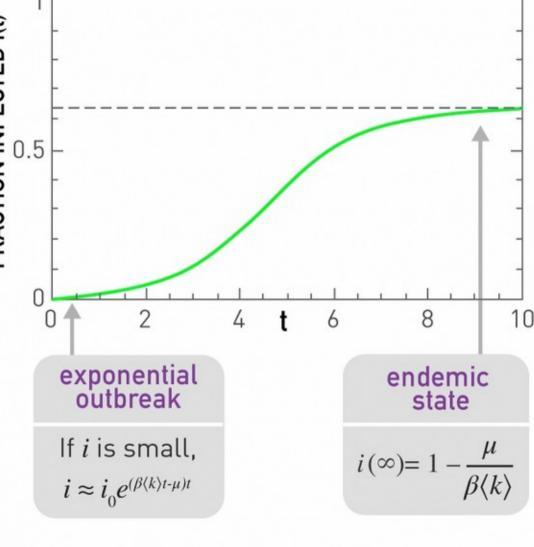
$$i(t) = \left(1 - \frac{\mu}{\beta \langle k \rangle}\right) \frac{Ce^{(\beta \langle k \rangle - \mu)t}}{1 + Ce^{(\beta \langle k \rangle - \mu)t}}$$

C is a constant that depends on i₀

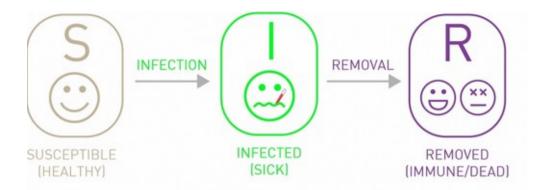
Infected as a function of time (SIS)

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

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

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

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

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

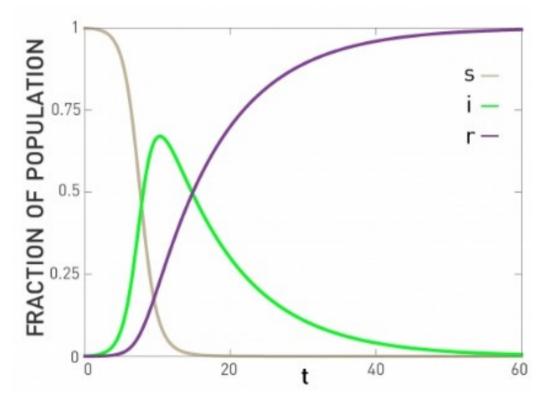
No closed form solution

Infection dynamics (SIR)

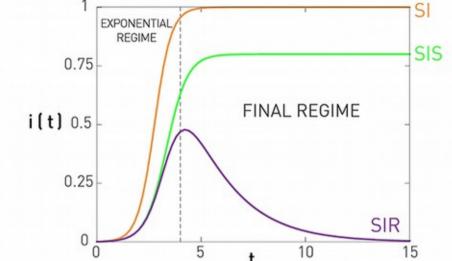
$$\frac{di(t)}{dt} = \beta \langle k \rangle i(t)(1 - r(t) - i(t)) - \mu i(t)$$

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

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



Comparison of i(t)



i(t) 0.5	FINAL REGIME	
0.25	5 t	SIR 15
	SI	SIS
Exponential Regime: Number of infected individ- uals grows exponentially	$i = \frac{i_0 e^{\beta(k)t}}{1 - i_0 + i_0 e^{\beta(k)t}}$	$i = \left(1 - \frac{\mu}{\beta \langle k \rangle}\right) \frac{Ce^{(\beta \langle k \rangle - \mu)t}}{1 + Ce^{(\beta \langle k \rangle - \mu)t}}$
Final Regime: Saturation at t→=∞	$i(\infty) = 1$	$i(\infty) = 1 - \frac{\mu}{\beta \langle k \rangle}$

$$R_0 = 1$$

$$R_0 = 1$$

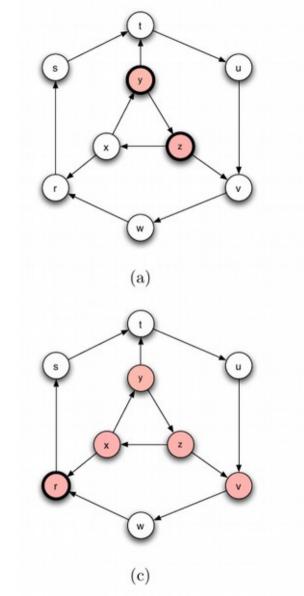
SIR

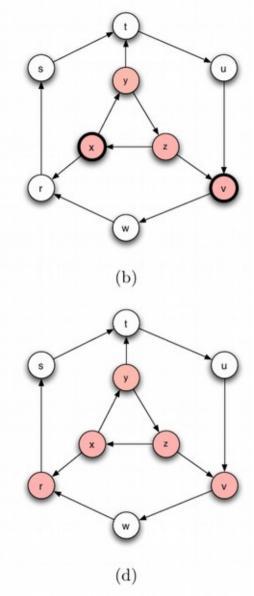
No closed solution

 $i(\infty) = 0$

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 eta

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

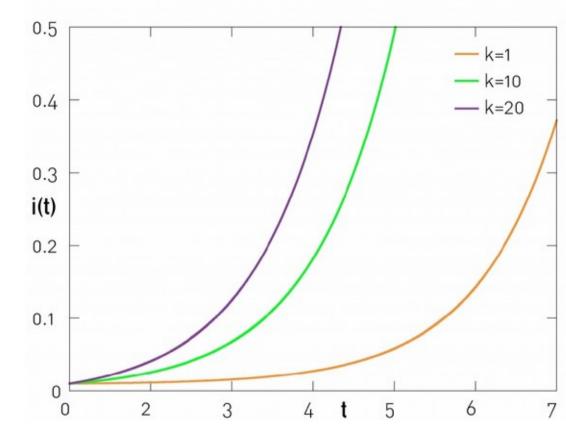
SI model on a graph: infected as a function of time

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

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

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

Random network

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

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

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

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

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

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, au < 0 and the infection dies out

Epidemic threshold

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

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

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

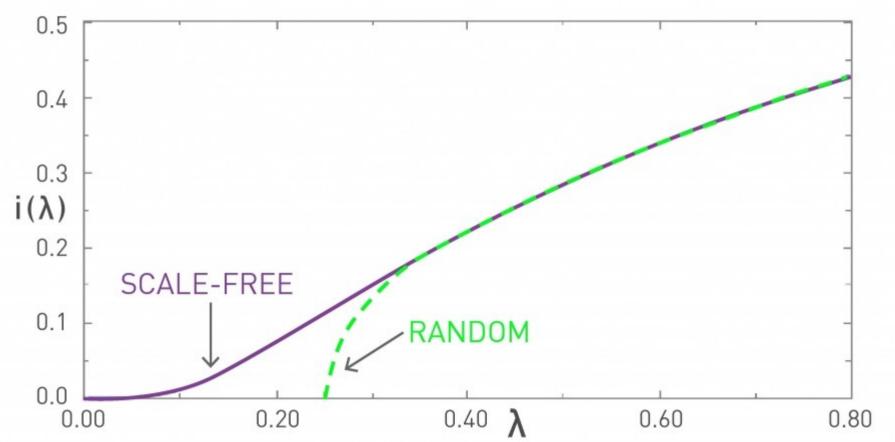
Epidemic threshold in a scale-free network

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

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

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

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



Two key results

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: $\lambda_c=0$