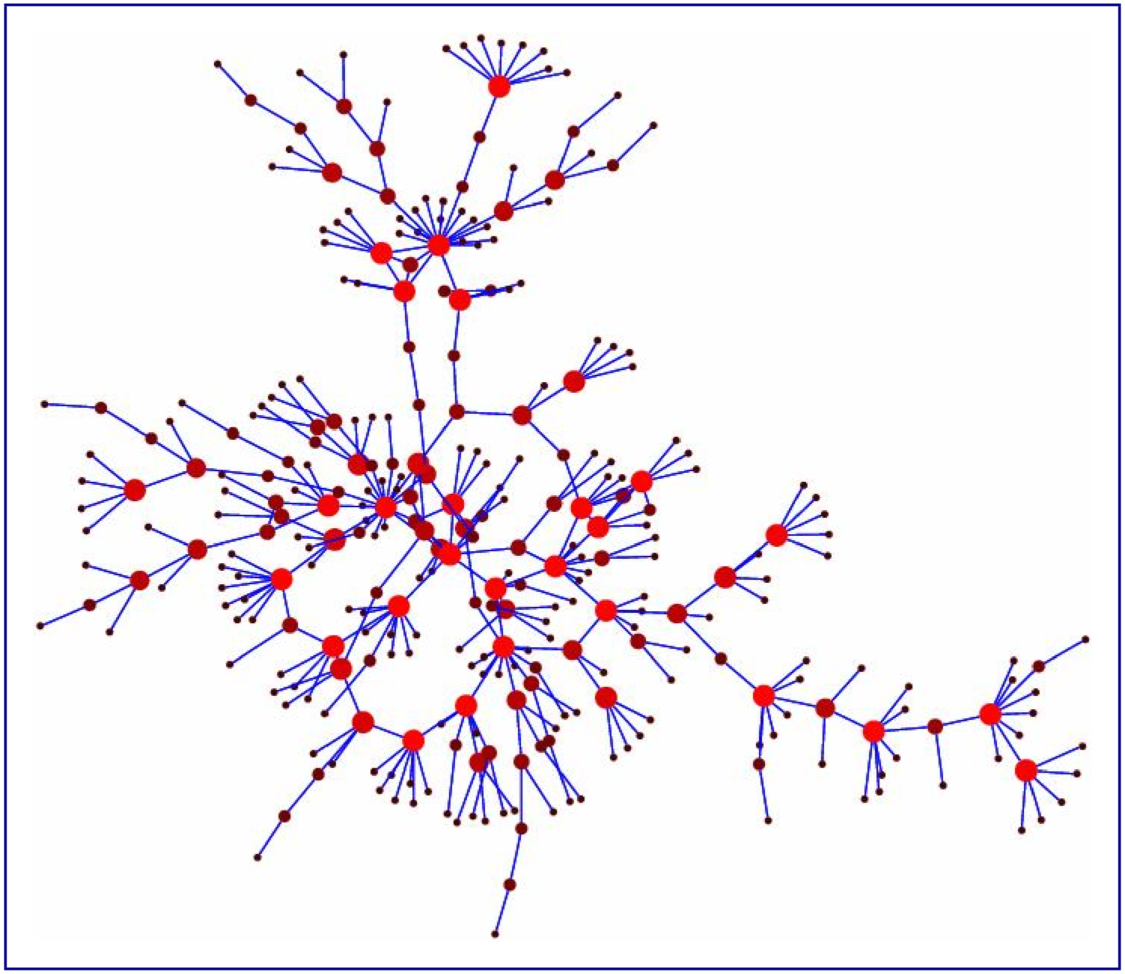
ECS 253 / MAE 253, Lecture 6

April 19, 2023



- “Percolation and Epidemiology on Networks”

Announcements

- Need help with math? Visit the
  Academic Assistance and Tutoring Center for Mathematics
  https://tutoring.ucdavis.edu/math
- HW1: Due Thurs, April 20 11:59pm via Gradescope.
- HW1b: Due Thurs, April 20 11:59pm via Gradescope.
- HW1a: Project pitch ... Due .... Friday, (at 11:50pm) via Canvas.
- See the resources for writing research papers at bottom of "Lecture" schedule.
- Canvas discussion on focus and concentration:
  Practice "Distraction free hour"

Processes on networks

- Spreading processes
- Search for information

Interplay of topology and function (see, e.g.,)

- Barrat, et al, *Dynamical processes on Complex Networks*
- Porter and Gleeson, *Dynamical systems on networks: A tutorial*

Epidemiology

- Understanding how diseases/opinions spread on networks
- Human diseases
- Computer viruses (typically spread via email networks)
  - Typically attached to an executable program.
  - Typically corrupt files on host computer
- Computer worms (spread directly from computer to computer via network connections)
  - Worms are self-contained.
  - Generally harm the network and consume bandwidth.

Starting simply

Understand flow of one virus on a static network.

- SIR (Susceptible, Infected, Removed)
- SIS (Susceptible, Infected, Susceptible)

- S = don't have the disease but can catch it if exposed.
- I = have the disease and can pass it on.
- R = recovered with permanent immunity (or "removed").

Traditional mathematical epidemiology

- β – probability of an S catching disease from an I.
- γ – probability of an I recovering and becoming an R.

Neglect any spatial structure, and assume *fully mixed* (i.e., any individual is equally likely to come into contact with any other).

- In graph theory terms, this would be the complete graph.
- Also called “mean-field” in physics.

The resulting rate equations:

The Kermack-McKendrick model:

[Kermack and McKendrick, “A Contribution to the Mathematical Theory of Epidemics.” Proc. Roy. Soc. Lond. A 115, 1927]

[Anderson and May, “Population Biology of Infectious Diseases: Part I.” Nature 280, 1979]

Three coupled ordinary differential equations:

1. $\frac{dS}{dt} = -\beta I S,$
2. $\frac{dI}{dt} = \beta I S - \gamma I,$
3. $\frac{dR}{dt} = \gamma I.$

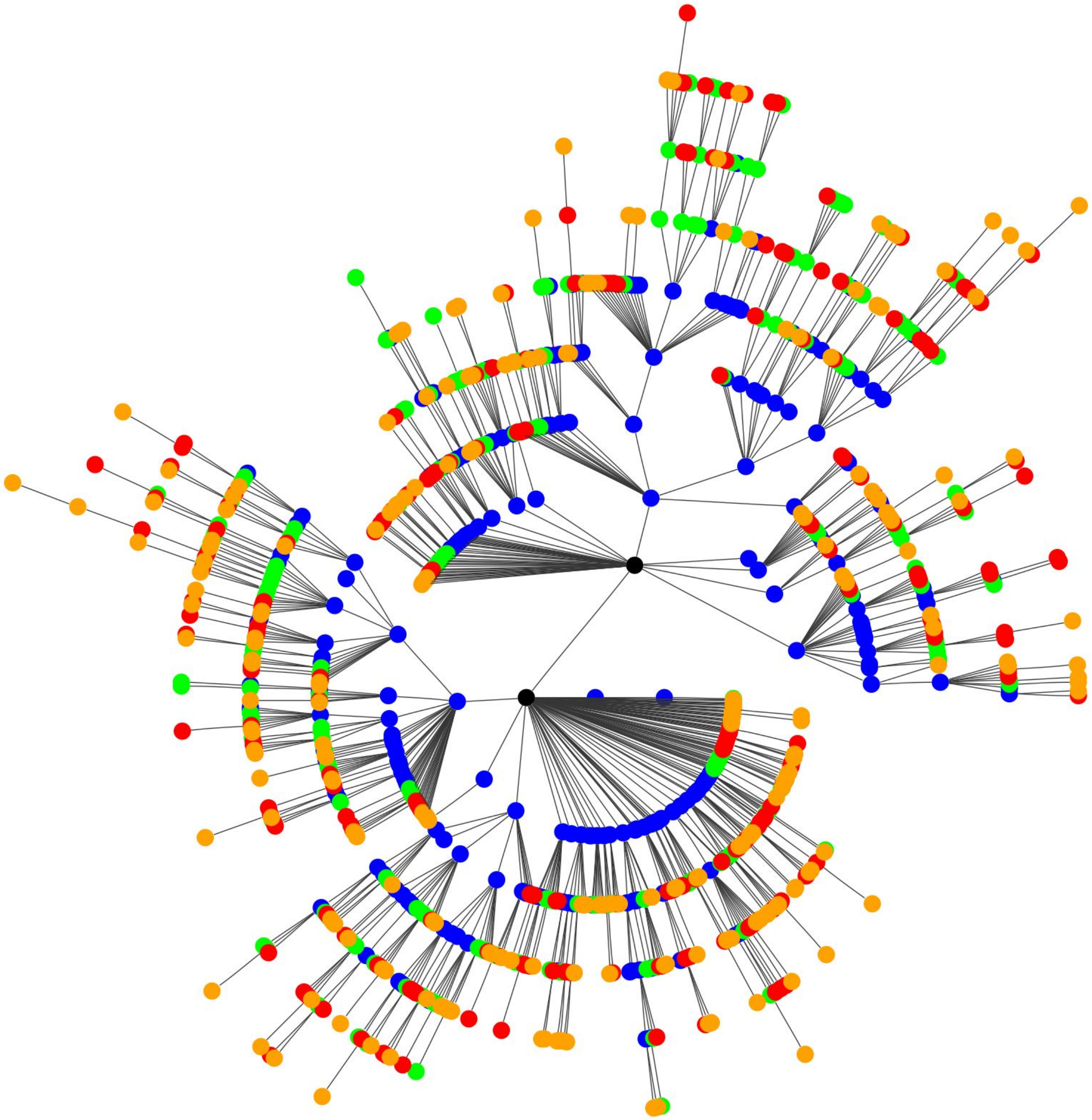
Epidemiological threshold

$$\boxed{T_c = \frac{\beta S_0}{\gamma}}$$

- Where S_0 is initial size of susceptible population.
- For $T_c < 1$ disease dies out, $dI/dt < 0$.
  (An I infects less than one S before recovering or dying).
- For $T_c > 1$ disease will spread until full population gets infected, $dI/dt > 0$.
  (An I infects more than one S).

Disease spread on a network

(No longer mean field)



Wave-like spreading in the distant past

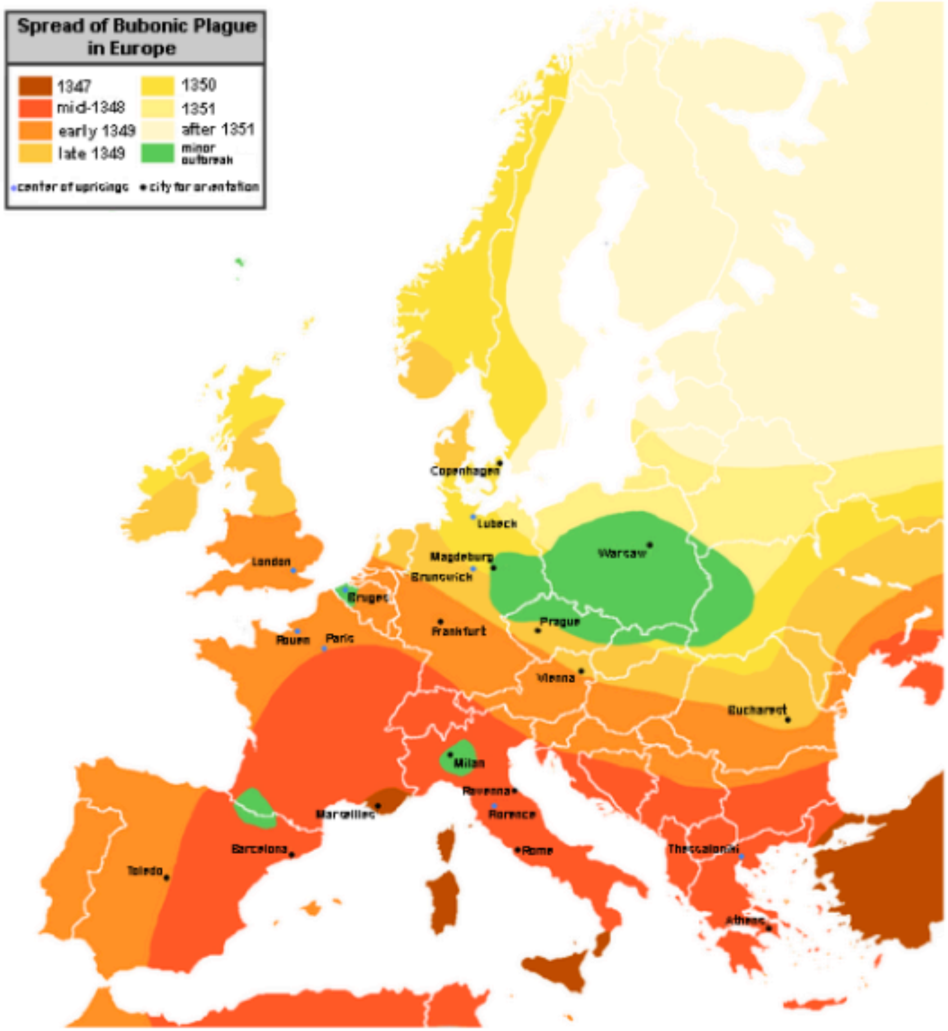


Figure 10.9 The Great Plague

From Barabasi, Network Science book

Network structure matters!

- GLEAMviz.org

  see. e.g.,

- Colizza, V., Barrat, A., Barthelemy, M., & Vespignani, A. “The role of the airline transportation network in the prediction and predictability of global epidemics”. *PNAS*, 103(7), (2006).

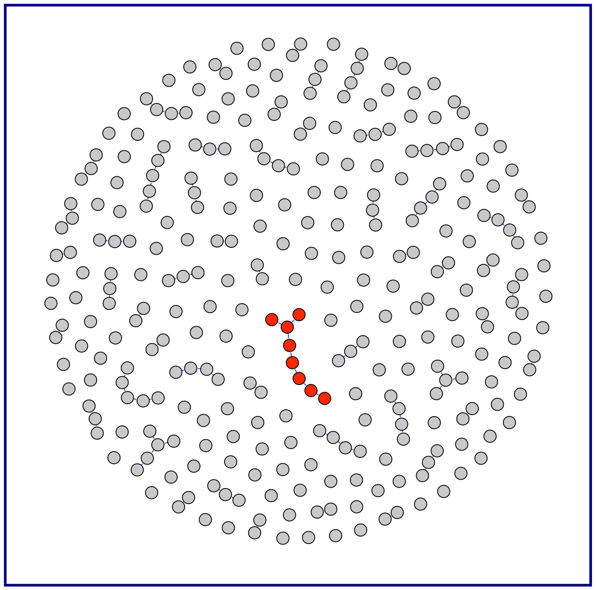
- Colizza, Vittoria, Romualdo Pastor-Satorras, and Alessandro Vespignani. “Reaction-diffusion processes and metapopulation models in heterogeneous networks.” *Nature Physics* 3 (2007).

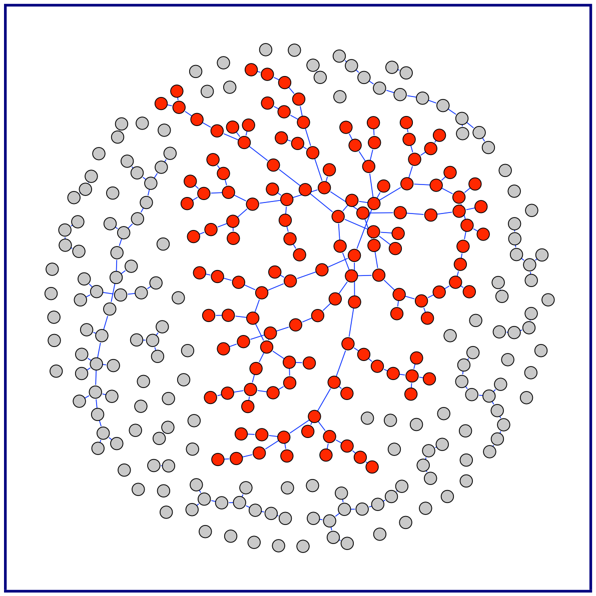
Incorporating network structure in mathematical models:

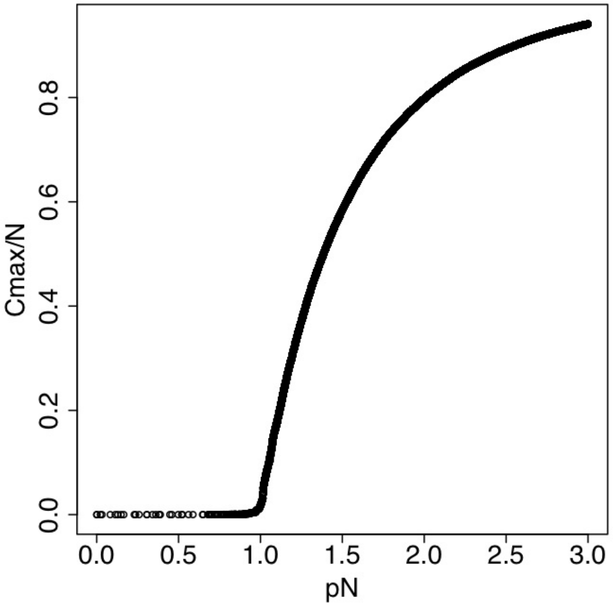
- Simpler than SIS/SIR:
  Percolation on a network; an “SI” model

- SIS/SIR models

ER onset of the giant component: “Percolation”







Bond Percolation (Contact processes)

[Grassberger, "On the critical behavior of the general epidemic process and dynamical percolation", Math. Biosci., 63, 1983.]

- Start out with the complete graph as the underlying structure
- Assume random distribution of initial carriers
- Probability disease is transmitted corresponds to the edge occupancy probability, p.
- The size of the largest connected component is the size of the largest outbreak (the number of Infecteds)
- (Recall the Erdös-Renyi random graph)

Aside:
Bond percolation versus site percolation on a lattice

Useful java applets:

- http://stp.clarku.edu/simulations/percolation/
- http://www.math.colostate.edu/$\sim$achter/

Incorporating network structure:

Bond Percolation (Contact processes)

[Grassberger, “On the critical behavior of the general epidemic process and dynamical percolation”, Math. Biosci., 63, 1983.]

- Assume randomly chosen initial carrier.
- Probability disease is transmitted corresponds roughly to the edge occupancy probability. Remember the Erdös-Renyi random graph, but here we are given an underlying network and are “activating” selected edges.

Bond percolation, cont.

- Look at **distribution of cluster sizes**. These correspond to extent of disease spread. Note all we get are the final I and S values. Says nothing about the dynamics of spreading! Just the final state.

- **The percolation transition corresponds to the epidemic threshold.** The size of the giant component corresponds to the size of the epidemic.

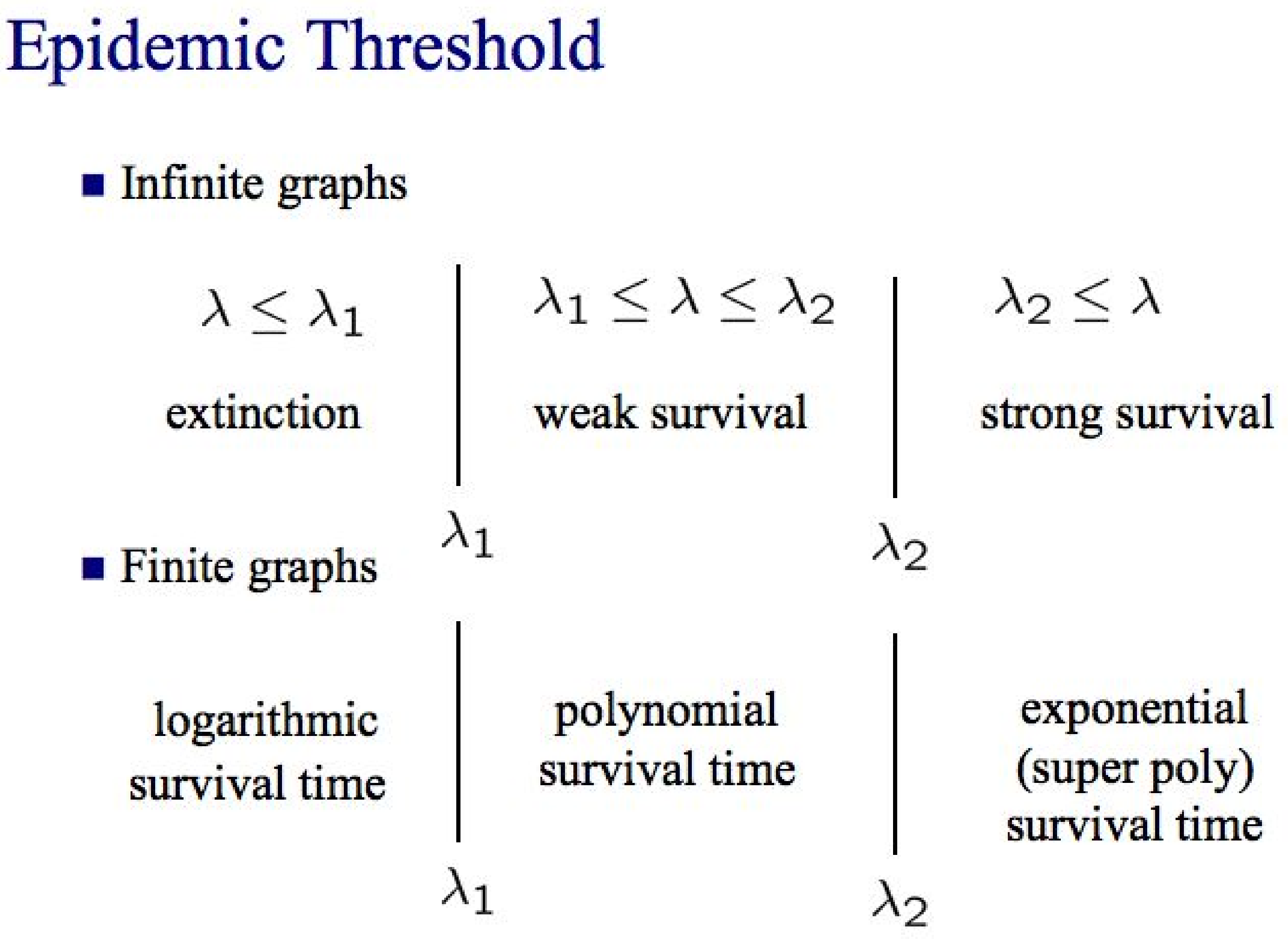
- How do we choose the underlying graph?

  – Almost every social network studied shows heavy-tailed distribution.

  – The Internet has a highly right-skewed degree distribution.

  – Power law random graphs relatively easy to analyze.

Behavior on ER random graphs:
(λ is infection rate)



Epidemic Threshold

- Infinite graphs

$\lambda \leq \lambda_1$ | $\lambda_1 \leq \lambda \leq \lambda_2$ | $\lambda_2 \leq \lambda$

extinction | weak survival | strong survival

λ_1 λ_2

- Finite graphs

logarithmic survival time | polynomial survival time | exponential (super poly) survival time

λ_1 λ_2

Slide courtesy of Amin Saberi

Percolation/epidemic threshold on power law random graphs, $P(k) \sim k^{-\gamma}$ for $2 < \gamma \leq 3$

- "Network robustness and fragility: Percolation on random graphs", Callaway, Newman, Strogatz and Watts, *Phys. Rev. Lett.*, 85 (2000).
- "Epidemic Spreading in Scale-Free Networks", R. Pastor-Satorras and A. Vespignani *Phys. Rev. Lett.* **86** (2001).
- "The Epidemic Threshold in Scale-Free Graphs", N. Berger, C. Borgs, J. Chayes, and A. Saberi, *Symposium on Discrete Algorithms (SODA)*, (2005).

Find $T_c = 0$, in other words absence of epidemiological threshold.

For all $\beta > 0$ and $S_0 > 0$, the steady-state result is that some non-zero, fraction of the population has the disease.

Results from Callaway et al

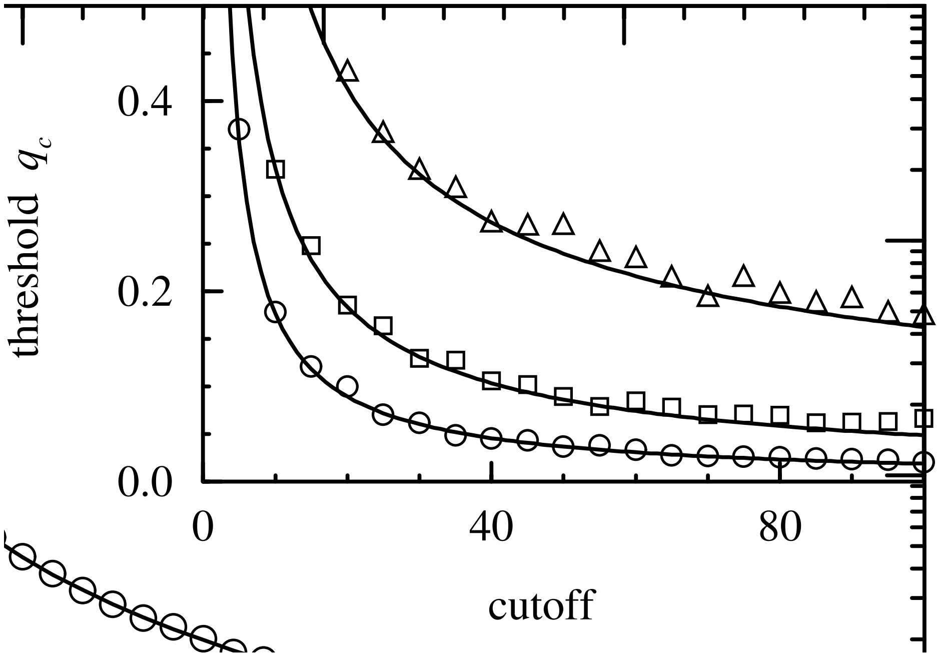
- Degree dist, $p_k \sim k^{-\gamma} e^{-k/C}$ (power law with cutoff).
- Let q_k be probability that a vertex of degree k is “infected”. For simplicity they analyze $q_k = q$ (independent of k).
- Then $p_k q$ is probability of having degree k and being infected.
- Calculate $\langle s \rangle$, the mean cluster size. Find (via generating functions ... details omitted here) that

$$\langle s \rangle = q + \frac{q^2 \langle k \rangle}{1 - (q \langle k^2 \rangle / \langle k \rangle)}$$

- $\langle s \rangle \to \infty$ when denominator $1 - q \left\langle k^2 \right\rangle / \langle k \rangle = 0$, i.e.,

$$\boxed{q_c = \frac{\langle k \rangle}{\left\langle k^2 \right\rangle}}$$

q_c versus C, the cutoff



Critical infection probability for epidemic outbreak $q_c \to 0$ as the graph becomes a true power law.

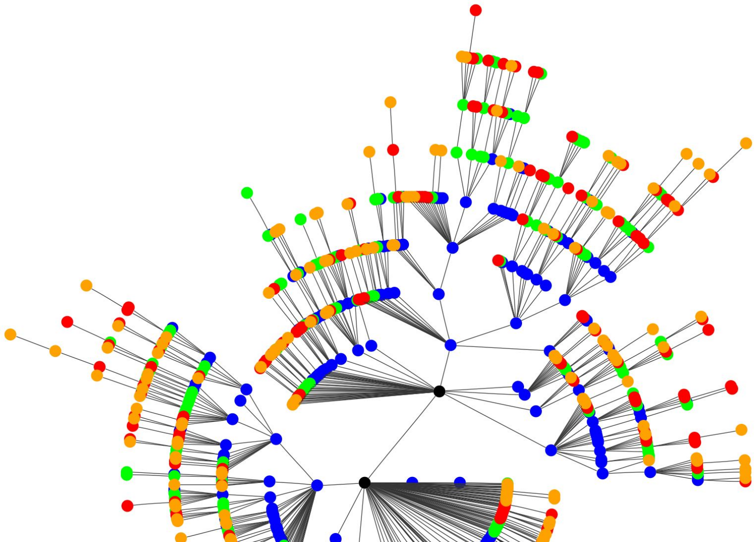
(Epidemic if $q > q_c = \frac{\langle k \rangle}{\langle k^2 \rangle}$. Also means expected number of second neighbors $\langle k^2 \rangle$ exceeds expected number of first $\langle k \rangle$ for “locally tree-like” networks.)

From Percolation to SIS dynamics on a network

SIS $\equiv$ Susceptible-Infected-Susceptible

- Epidemic Spreading in Scale-Free Networks, R. Pastor-Satorras and A. Vespignani *Phys. Rev. Lett.* **86** (2001).
- Rigorous proof:
  The Epidemic Threshold in Scale-Free Graphs, N. Berger, C. Borgs, J. Chayes, and A. Saberi, *Symposium on Discrete Algorithms (SODA)*, (2005).

  (Always enough hubs that disease on a hub's neighbor and reinfects hub. (Recall this is SIS))



Following Pastor-Satorras and A. Vespignani

- $\rho_k(t)$ is density of infected nodes of degree k at time t. (Hence $[1-\rho_k(t)]$ is probability a node of degree k is NOT infected.)

- $\lambda = \beta/\gamma$, the effective spreading rate. Set $\gamma = 1$.
  (Recall β is infection rate, γ is recovery.)

- The time evolution (a “master equation”/ “rate equation”):

$$\frac{d\rho_k(t)}{dt} = -\rho_k(t) + \lambda k \left[1-\rho_k(t)\right] \Theta(\rho(t))$$

- First term: nodes recover with unit rate ($\gamma = 1$)

- Second term: Infection rate λ, times number of neighbors k, times prob node of degree k is healthy, times prob of being connected to an infected node $\Theta(\rho(t))$.

Edge following probability

- Prob of following an edge to a node of degree k is $k\ p_k$

- So probability of neighbor being infected ($\rho_k(t)$ density of infected):

$$\Theta(\rho(t)) = \frac{\sum_k k\ p_k\ \rho_k(t)}{\sum_k k\ p_k} = \frac{1}{\langle k \rangle} \sum_k k\ p_k\ \rho_k(t)$$

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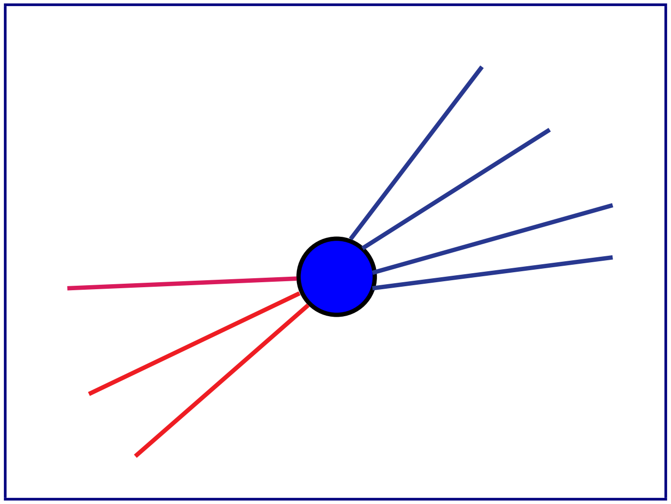
k edges reach node of degree k:



- Steady state of master eqn, $\frac{d\rho_k}{dt} = 0$ implies:

$$\rho_k = \frac{\lambda\, k\, \Theta}{1 + \lambda\, \Theta}$$

- Inserting into expression for Θ:

$$\Theta = \frac{1}{\langle k \rangle} \sum_k k\; p_k\, \frac{\lambda\, k\, \Theta}{1 + \lambda\, \Theta}$$

(Note $\Theta = 0$ always satisfies, but is quite dull! ... $\rho_k = 0$)

Searching for more solutions to last equation, in interval $0 < \Theta \leq 1$

- Taking derivative w.r.t. Θ of both sides of last equation:

$$\frac{d}{d\Theta}\left[\frac{1}{\langle k\rangle}\sum_k k\ p_k\ \frac{\lambda\ k\ \Theta}{1+\lambda\ \Theta}\right]\Bigg|_{\Theta=0} = 1, \quad \text{at} \quad \lambda = \lambda_c$$

- solving this:

$$\frac{1}{\langle k\rangle}\sum_k k\ p_k\ \lambda_c\ k = \frac{\langle k^2\rangle}{\langle k\rangle}\lambda_c = 1$$

Critical spreading rate: $\boxed{\lambda_c = \frac{\langle k\rangle}{\langle k^2\rangle}}$

If $\langle k^2\rangle \to \infty$ but $\langle k\rangle$ finite, then $\lambda_c \to 0$.

Last three slides, actually pieced from three papers

- Epidemic Spreading in Scale-Free Networks, R. Pastor-Satorras and A. Vespignani *Phys. Rev. Lett.* **86** (2001).

- Epidemic dynamics in finite size scale-free networks, R Pastor-Satorras, A Vespignani *Physical Review E* (2002).

- Immunization of complex networks, R Pastor-Satorras, A Vespignani *Physical Review E* (2002).

From SIS to SIR

- PSV’01 and BBCS’05 consider SIS.
- R. M. May, A. L. Lloyd “Infection dynamics on scale-free networks” *Phys. Rev. E*, (2001). Show similar results hold for SIR. (Lord Robert May, founder of theoretical ecology/population biology/evolutionary game theory... great wiki entry)

Immunization

- Many subsequent papers on immunization by knocking out nodes.
- But the **recovery rate** depends on other attributes of node (age, medical history....) and can override network structure. (i.e., less overall infected or less overall fatalities important?)

Implications for disease spread?

- Are human contact networks and the Internet really like power law random graphs?

- Yes, they have the power law degree disribution.

- But usually, also more structure:
  - Geographic correlation.
  - Degree-degree correlations.
  - High transitivity for social networks.

- Each of the three factors alone can make $T_c > 0$.

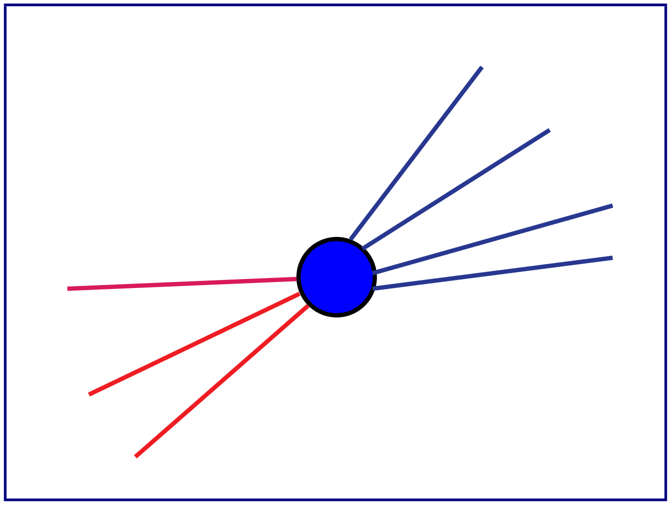
Developing a model that accurately captures human connectivity still in the works.

Immunization:
Coupling percolation and network resilience

- View vaccination as removing a particular set of vertices from the network.
- As we saw previously, removing the high-degree nodes from a power law random graph, quickly destroys connectivity.
- How to find these “hubs” in a social network, for instance a network for sexually transmitted diseases?

Identifying Hubs

- Want to sample *edges* rather than *nodes*.
- Choose node at random, probability of choosing node of degree k is p_k.
- Choose an edge at random, probability of it leading to a node of degree k proportional to kp_k.
- How to chose an edge at random?



Acquaintance vaccination

- Choose a person at random.
- Then choose a *friend* of that person to vaccinate.

Cohen, ben-Avraham, and Havlin, “Efficient Immunization of Populations and Computers”, Phys. Rev. Lett. 91, 247901 (2003)

Show by computer simulation and analytic calculations that this is much more effective than random vaccination.

This type of acquaintance vaccination actually used to control small pox and foot-and-mouth (“ring vaccination”)

How to model a real human population?
(Using census data)

[Bansal, Pourbohloul, Meyers, “The Spread of Infectious Disease through Contact Networks”, Talk given at MSRI, April 2005.]

Not published, but a video can be viewed at:

http://angelina.msri.org/VMath/show_speakertalks?field_pid=900000033

See further references at the end.

Take actually census data from the city of Vancouver.

Constructing connectivity via census data

- Households
- Classrooms
- Businesses
- “Shopping”

Who to immunize?

Strategy one: Immunize the “hubs”

- Receptionists
- Bus drivers
- School teachers

This results in the least number of people becoming infected.

Strategy two: Immunize the most frail

- Elderly and children.

More people overall get infected, but less people overall die as a result of the disease!

Further work on network epidemiology

- Bansal S, Pourbohloul B, Meyers LA (2006) A Comparative Analysis of Influenza Vaccination Programs. PLoS Med 3(10)

- http://bansallab.com

- http://www.biosci.utexas.edu/ib/faculty/meyers.htm

- http://www.erikvolz.info/

- Brockman/Vespignani work on influenza (including “where’s George” mobility tracking, and transportation nets spreading disease),
  http://rocs.northwestern.edu/
  http://mobs.soic.indiana.edu/media

- Effects of clustering on epidemic thresholds (Newman, Gleeson, Volz alternate calculations and implications)