



Block 9: Epidemics and contagion

ELEC 573: Network Science and Analytics

Santiago Segarra

Electrical and Computer Engineering

Rice University

segarra@rice.edu

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You are here

Wk.	Date	Topic	HW	Project
1	23-Aug	Introduction to course	HW0 out	
2	30-Aug	Graph theory	HW0 solutions posted	
3	6-Sep	LABOR DAY (no class)	HW1 out	
4	13-Sep	Centrality measures / Community detection		
5	20-Sep	Community detection		
6	27-Sep	Signal Processing and Deep learning for graphs	HW1 due	
7	4-Oct	Signal Processing and Deep learning for graphs	HW2 out	
8	11-Oct	FALL BREAK (no class)		
9	18-Oct	Network models	HW2 due	
10	25-Oct	Network models	HW3 out	Project proposal due
11	1-Nov	Inference of network topologies and features		
12	8-Nov	Inference of network topologies and features	HW3 due	
13	15-Nov	Inference of network topologies and features		
14	22-Nov	Epidemics		Project progress report
15	29-Nov	Inference of network processes		

13-Dec Project presentation (video recording) and final report due



Epidemic processes

Branching processes

Traditional epidemic modeling

Network-based epidemic modeling



Dynamic network processes

- ▶ Most systems studied from a network-based perspective are **dynamic**
⇒ Most processes on graphs are dynamic processes

Example

- ▶ Cascade of failures in the electrical power grid
- ▶ Diffusion of knowledge and spread of rumors
- ▶ Spread of a virus among a population of humans or computers
- ▶ Synchronization of behavior as neurons fire in the brain
- ▶ Interactions of species such as prey-predator dynamics



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- ▶ Interactions of species such as prey-predator dynamics
- ▶ **Dynamic process on a graph** is $\{X_i(t)\}_{i \in V}$ for $t \in \mathbb{N}$ or \mathbb{R}_+
 - ▶ Both deterministic and stochastic models commonly adopted
 - ▶ **Ex:** differential equations or time-indexed random (Markov) processes



Epidemics

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 - ▶ Encountered with contagious diseases due to biological pathogens
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 - ⇒ Pathogen e.g., contagiousness, severity, infectious period
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- ▶ Biological issues mixed with social ones. Spread patterns depend on:
 - ⇒ Pathogen e.g., contagiousness, severity, infectious period
 - ⇒ Network structures within the affected population
- ▶ Quantitative epidemic modeling concerned with three basic issues:
 - (i) Understanding the mechanisms by which epidemics spread;
 - (ii) Predicting the future course of epidemics; and
 - (iii) Gaining the ability to control the spread of epidemics



Contact networks

- ▶ **Def:** In a **contact network** the people (vertices) are connected if they come into contact so that the disease can spread among them
- ▶ Natural to represent this structure as a network graph $G(V, E)$
 - ⇒ Vertices $i \in V$ represent elements of the population
 - ⇒ Edges $(i, j) \in E$ indicate contact between elements i and j
- ▶ Contact does not indicate actual infection, only the possibility of it



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 - ▶ Dense when highly contagious e.g., airborne transmission via coughs
 - ▶ Sparser connectivity in e.g., sexually transmitted diseases



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- ▶ Often difficult to measure the structure of contact networks



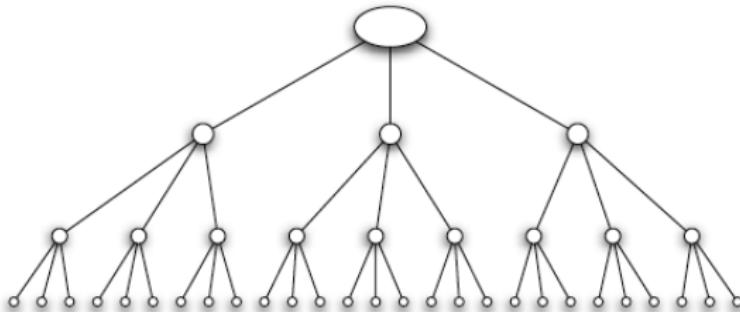
Branching processes

- ▶ The **branching process (BP)** is the simplest model for a contagion
- ▶ BP model considers different waves, i.e., discrete-time instants
 - ▶ First wave: one infective enters the population, meets k other friends
 - ▶ Wave n : each person of wave $n - 1$ meets k different new friends
- ▶ Suppose the disease is transmitted to friends independently w.p. p



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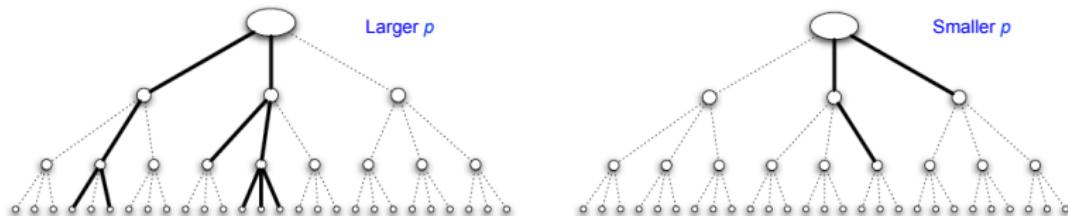
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- ▶ Contact network naturally represented by a **k -ary tree** ($k = 3$ below)





Relevant questions

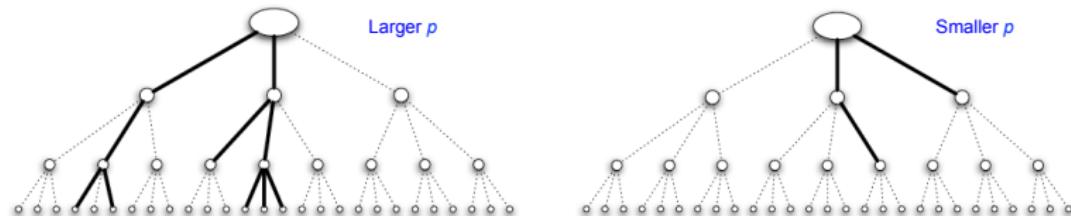
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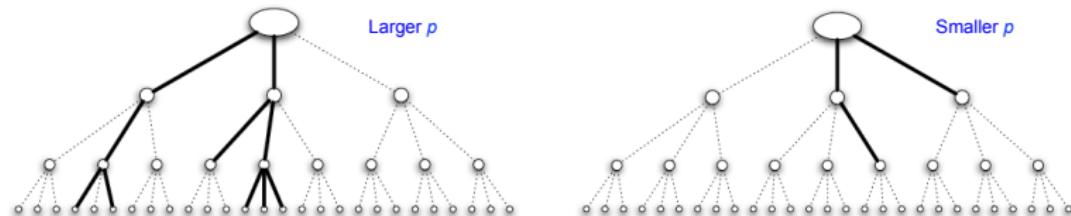


- ▶ Interesting questions we can answer under this simple model
 - ▶ Q1: Does the epidemic eventually die out?
 - ▶ Q2: Is the infected number of individuals infinite?
 - ▶ Q3: If it dies out, how long does it take until it goes extinct?



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 - ▶ **Q1:** Does the epidemic eventually die out?
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 - ▶ **Q3:** If it dies out, how long does it take until it goes extinct?
- ▶ **Dichotomy:** the epidemic dies out for finite n or goes on forever



Reproductive number

- ▶ **Def:** The reproductive number R_0 is the expected number of new infected cases with the disease caused by a single individual
- ▶ **BP:** number of infected friends of each individual is a $\text{Bino}(k, p)$ RV
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Theorem

Consider a branching process with parameters k and p

- a) If $R_0 < 1$, the disease dies out w.p. 1*
- b) If $R_0 > 1$, w.p. $q^* > 0$ the disease persists for infinitely many waves*



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- If $R_0 < 1$, the disease dies out w.p. 1
 - If $R_0 > 1$, w.p. $q^* > 0$ the disease persists for infinitely many waves
- ▶ Two basic kinds of public health measures to yield $R_0 < 1$
 - ⇒ Reduce k by quarantining people; and
 - ⇒ Reduce p by encouraging better sanitary practices



Proof of a)

- ▶ Easier if we consider the number of infected individuals. Define:
 - ▶ $Y(n)$ as the number of infected individuals at wave n
 - ▶ J_n as the number of individuals in wave n , i.e., $J_n = k^n$
 - ▶ $X_i(n) = \mathbb{I}\{i \text{ is infected}\}$, for $i = 1, \dots, J_n$



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- ▶ For $R_0 < 1$ it follows that $\lim_{n \rightarrow \infty} \mathbb{E}[Y(n)] = 0$



Proof of a) (cont.)

- ▶ Recall that for a nonnegative RV X with $\mathbb{E}[X] < \infty$, constant $a > 0$
⇒ Markov's inequality states → $P[X \geq a] \leq \frac{\mathbb{E}[X]}{a}$



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- ▶ Let Y be the total number of infected individuals. What is $\mathbb{E}[Y]$?

$$\mathbb{E}[Y] = \sum_{n=0}^{\infty} \mathbb{E}[Y(n)] = \sum_{n=0}^{\infty} R_0^n = \frac{1}{1 - R_0}$$

- ▶ Calculating the expected duration of the disease is more involved
⇒ Leverage standard tools since $\{Y(n)\}_{n=0}^{\infty}$ is a Markov chain



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⇒ Recursion $q_n = 1 - (1 - pq_{n-1})^k$ holds for $n = 0, 1, \dots$

- ▶ **Claim** regarding the recursion's fixed point q^* as $n \rightarrow \infty$, i.e.,

$$q^* = 1 - (1 - pq^*)^k$$

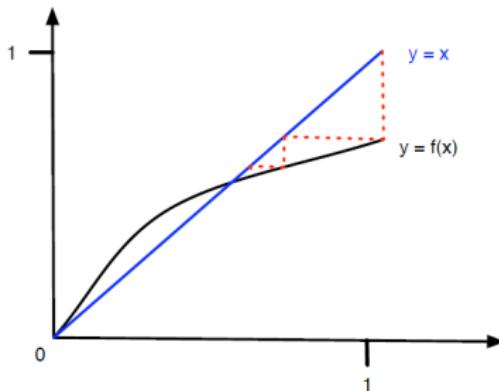
⇒ If $R_0 \leq 1$, then the only solution in $[0, 1]$ is $q^* = 0$

⇒ If $R_0 > 1$, there is also a nonzero solution in $[0, 1]$



Proof of b) (cont.)

- To establish the **claim**, define $f(x) = 1 - (1 - px)^k$. Properties:
 - $f(x)$ is increasing and continuous
 - $f(x)$ is differentiable with $f'(x) = R_0(1 - px)^{k-1}$
 - $f(0) = 0$, $f(1) < 1$ and $f'(0) = R_0$



- If $R_0 > 1$ then $f'(0) > 1$ and $y = f(x)$ intersects the line $y = x$
⇒ A solution q^* exists in the open interval $(0, 1)$

□



Closing remarks on BP model

- ▶ Simple BP model suffices to capture basic effects of the epidemic
- ▶ The spread of the disease depends on both
 - ▶ Properties of the pathogen via p
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- ▶ Dichotomous behavior depending on the reproductive number R_0
 - ▶ When $R_0 \leq 1$ the disease is not able to replenish itself
 - ▶ When $R_0 > 1$ the outbreak is constantly trending upward
- ▶ 'Knife-edge' behavior around $R_0 = 1$ implies high sensitivity
 - ▶ Even when $R_0 > 1$, the probability q^* of persistence is less than one
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- ▶ Up next: more general models applicable to any contact network
 - ⇒ Reproductive number R_0 still important for intuition



Modeling epidemics

Branching processes

Traditional epidemic modeling

Network-based epidemic modeling



SIR model

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- ▶ Stochastic formulation of simplest case with **no contact network**
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- ▶ Consider a closed population of $N + 1$ elements. At any time $t \in \mathbb{R}_+$
 - ▶ $N_S(t)$ elements are susceptible to infection (called 'susceptibles')
 - ▶ $N_I(t)$ elements are infected (called 'infectives')
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- ▶ Given $N_S(t)$ and $N_I(t)$, can determine $N_R(t)$ due to the constraint

$$N_S(t) + N_I(t) + N_R(t) = N + 1$$

⇒ $\{N_S(t), N_I(t), N_R(t)\}_{t=0}^{\infty}$ is a continuous-time random process
⇒ Need to specify the probabilistic law for their evolution



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- ▶ Susceptible infected by infective on chance encounter
 - ⇒ β = Rate of encounters between susceptible and infective
 - ⇒ S susceptibles and I infectives ⇒ βSI = rate of first reaction
- ▶ Each infective recovers (and is removed) at rate γ
 - ⇒ Population of I infectives ⇒ γI = rate of second reaction



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- ▶ Each infective recovers (and is removed) at rate γ
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- ▶ Model assumption: 'homogenous mixing' among population members
 - ⇒ All pairs of members equally likely to interact with one another



State transition probabilities

- ▶ Consider the bivariate state $[N_S(t), N_I(t)]^\top$ ($N_R(t)$ uniquely defined)
 - ⇒ Process starts with one infective and N susceptibles, i.e.,

$$N_I(0) = 1, N_S(0) = N, \text{ and } N_R(0) = 0$$



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- ▶ Process evolves according to **instantaneous transition probabilities**

Infection with rate β :

$$P[N_S(t + \delta t) = s - 1, N_I(t + \delta t) = i + 1 \mid N_S(t) = s, N_I(t) = i] \approx \beta s i \delta t$$

Recovery with rate γ :

$$P[N_S(t + \delta t) = s, N_I(t + \delta t) = i - 1 \mid N_S(t) = s, N_I(t) = i] \approx \gamma i \delta t$$

Unchanged state:

$$P[N_S(t + \delta t) = s, N_I(t + \delta t) = i \mid N_S(t) = s, N_I(t) = i] \approx 1 - (\beta s + \gamma) i \delta t$$



Continuous-time Markov chain

- ▶ Process $\{N_S(t), N_I(t)\}_{t=0}^{\infty}$ is a **continuous-time Markov chain (CTMC)**



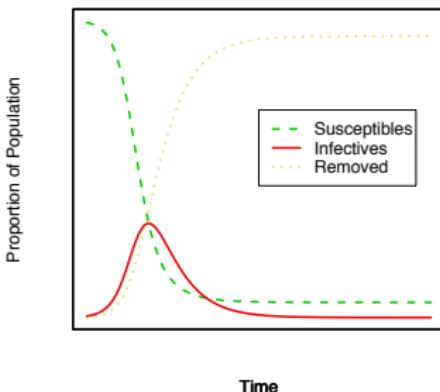
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- ▶ Equivalently implies that given $N_I(t) = i, N_S(t) = s$, then the CTMC
 - ⇒ Transitions from state (s, i) after time $T \sim \exp((\beta s + \gamma)i)$
 - ⇒ **Infection:** to state $(s - 1, i + 1)$ w.p. $\beta si/[(\beta s + \gamma)i]$
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 - ⇒ **Recovery:** to state $(s, i - 1)$ w.p. $\gamma i/[(\beta s + \gamma)i]$
- ▶ This formulation of the model facilitates the **simulation of realizations**





Transition-probability functions

- ▶ CTMC evolution given by matrix of **transition-probability functions**

$$P_{s,i}(t) = \mathbb{P} [N_S(t) = s, N_I(t) = i \mid N_S(0) = N, N_I(0) = 1]$$

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- ▶ Transition probability functions satisfy the differential equations

$$\frac{\partial P_{N,1}(t)}{\partial t} = -(\beta N + \gamma)P_{N,1}(t)$$

$$\frac{\partial P_{s,i}(t)}{\partial t} = \beta(s+1)(i-1)P_{s+1,i-1}(t) - i(\beta s + \gamma)P_{s,i}(t) + \gamma(i+1)P_{s,i+1}(t)$$

- ▶ Initial conditions $P_{N,1}(0) = 1$ and $P_{s,i}(0) = 0$ for all $(s, i) \neq (N, 1)$



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- ▶ Transition probability functions satisfy the differential equations

$$\frac{\partial P_{N,1}(t)}{\partial t} = -(\beta N + \gamma)P_{N,1}(t)$$

$$\frac{\partial P_{s,i}(t)}{\partial t} = \beta(s+1)(i-1)P_{s+1,i-1}(t) - i(\beta s + \gamma)P_{s,i}(t) + \gamma(i+1)P_{s,i+1}(t)$$

- ▶ Initial conditions $P_{N,1}(0) = 1$ and $P_{s,i}(0) = 0$ for all $(s, i) \neq (N, 1)$
- ▶ These are known as the **Kolmogorov forward equations**
 - ⇒ Exact analytical solution possible, but form is quite complicated

Reproductive number of the general SIR model



- ▶ Can still derive basic results without explicit formulas for $P_{s,i}(t)$
- ▶ For the general epidemic SIR model, the **reproductive number** is

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Theorem

Consider a generic SIR model with infection rate β and recovery rate γ

- If $R_0 = N\beta/\gamma \leq 1$, the disease dies out after finite time
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- ▶ Again, threshold theorems useful to design epidemic control procedures
- Ex: reduce R_0 to less than unity via vaccination, education, quarantine



Inference of model parameters

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- ▶ If $\{N_S(t), N_I(t)\}_{t=0}^\tau$ observed in $(0, \tau)$, ML rate estimates given by

$$\hat{\beta} = \frac{N - N_S(\tau)}{\int_0^\tau N_S(t)N_I(t)dt} \quad \text{and} \quad \hat{\gamma} = \frac{N_R(\tau)}{\int_0^\tau N_I(t)dt}$$

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- ▶ Unfortunately, rarely are such complete measurements available
- ▶ Often only the final state of the epidemic is observed, i.e., $N_R(\tau)$
⇒ Impossible to estimate β and γ since they relate to time
- ▶ There are also methods to estimate R_0 based on the method of moments



Incorporating the contact network

Branching processes

Traditional epidemic modeling

Network-based epidemic modeling



Structured population models

- ▶ So far assumed ‘homogenous mixing’ among population members
 - ⇒ All pairs of members equally likely to interact with one another
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 - ⇒ Assumed contact patterns take into account population structure
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- ▶ Epidemic models on graphs study dynamic processes $\mathbf{X}(t) = \{X_i(t)\}_{i \in V}$



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 - ⇒ Infective has infectious contacts **independently** with each neighbor
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- ▶ Each infective recovers (and is removed) at rate γ
 - ⇒ Time till recovery is exponentially distributed with parameter γ
- ▶ Define the stochastic process $\mathbf{X}(t) = \{X_i(t)\}_{i \in V}$, where

$$X_i(t) = \begin{cases} 0, & \text{if vertex } i \text{ is susceptible at time } t \\ 1, & \text{if vertex } i \text{ is infected at time } t \\ 2, & \text{if vertex } i \text{ is recovered at time } t \end{cases}$$



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$$P[\mathbf{X}(t + \delta t) = \mathbf{x}' | \mathbf{X}(t) = \mathbf{x}] \approx \begin{cases} \beta M_i(\mathbf{x}) \delta t, & \text{if } x_i = 0 \text{ and } x'_i = 1 \\ \gamma \delta t, & \text{if } x_i = 1 \text{ and } x'_i = 2 \\ 1 - [\beta M_i(\mathbf{x}) + \gamma] \delta t, & \text{if } x_i = 2 \text{ and } x'_i = 2 \end{cases}$$

- ▶ Defined $M_i(\mathbf{x})$ as the number of infective neighbors of vertex i , i.e.,

$$M_i(\mathbf{x}) := |\{j : (i, j) \in E, x_j = 1\}|$$

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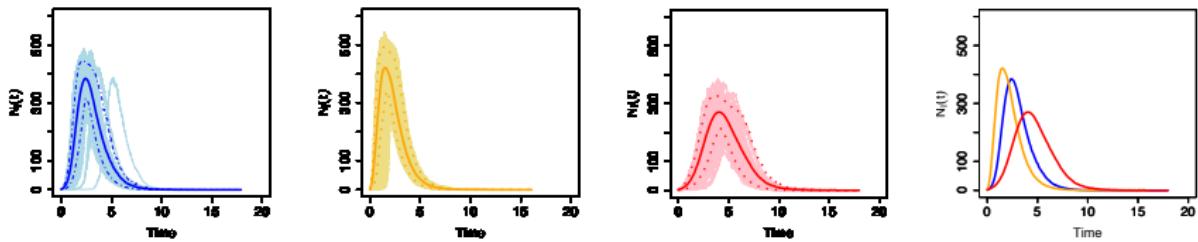
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- ▶ Given $\mathbf{X}(t)$ can define the processes $\{N_S(t), N_I(t), N_R(t)\}$ by counting
Ex: number of susceptibles $N_S(t) = \sum_{i=1}^{N_v} \mathbb{I}\{X_i(t) = 0\}$



Effect of the contact network

- ▶ Simulated the CTMC for contact networks with $N_v = 1000$ and $\bar{d} \approx 10$
 - ▶ Erdős-Rényi (blue), Barabási-Albert (yellow), Watts-Strogatz (red)
 - ▶ Plot 100 sample paths of $N_I(t)$ and the average over 1000 epidemics



- ▶ Curves $\mathbb{E}[N_I(t)]$ have the same general form as when $G = K_{N_v}$
- ▶ Different rates of growth and decay, effective duration of the epidemic
⇒ Characteristics of the epidemic process are affected by the network



Reproductive number

- ▶ Suppose G drawn from \mathcal{G} with fixed degree distribution $\{f_d\}$
⇒ Reproductive number for the SIR model can be shown to equal

$$R_0 = \frac{\beta}{\beta + \gamma} \left(\frac{\mathbb{E}[d^2]}{\mathbb{E}[d]} - 1 \right)$$

- ▶ Probability that an infective transmits the disease before recovering
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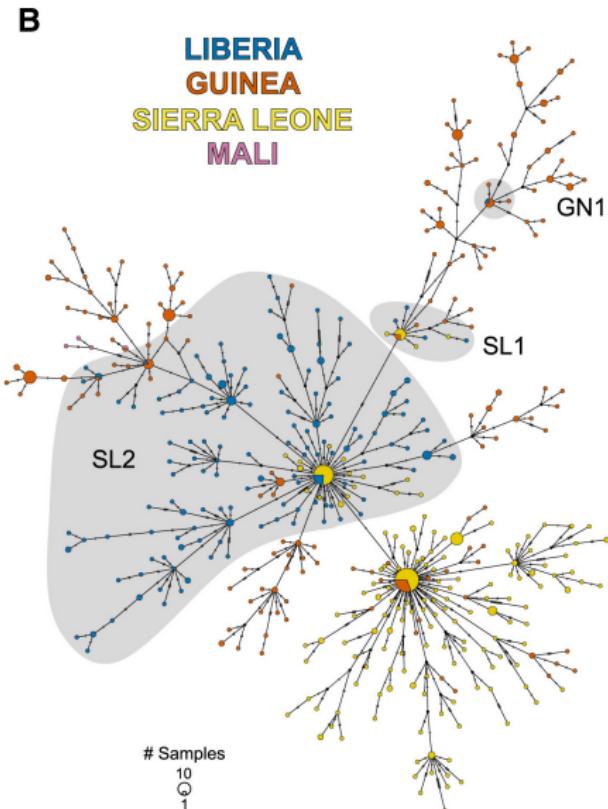
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- ▶ Ex: Power-law $\{f_d\}$ for which we can expect $\mathbb{E}[d^2] \gg \mathbb{E}[d]$
 - ⇒ Increases R_0 , easier for epidemics to occur than for $\mathcal{G}_{N_v, p}$
 - ⇒ Suffices to infect a small number of high-degree vertices
- ▶ H. Anderson and T. Britton, *Stochastic Epidemic Models and Their Statistical Analysis*. Springer, 2000.



Network of the week





Network of the week

- ▶ “Evolution and Spread of Ebola Virus in Liberia, 2014–2015” Ladner et al.

