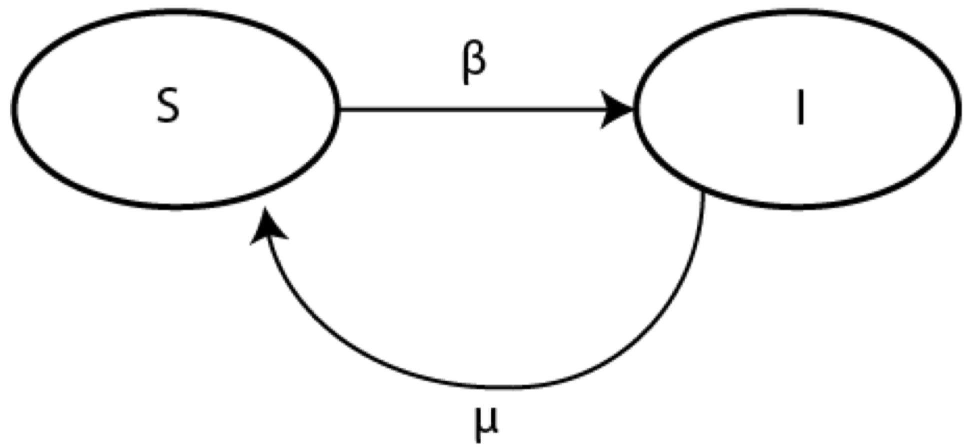
Network Dynamics

Modeling Epidemics

The bubonic plague killed 20% of the population of Europe over a seven-year period in the 1300s.

The SIS Model for Spread of Disease

Applies to diseases that do not confer long-lasting immunity, like the common cold



S = Susceptible population

I = Infected population

β = Infection rate

μ = recovery rate

For a compartmental model:

$$\frac{dS}{dt} = -\beta IS + \mu I$$

$$\frac{dI}{dt} = \beta IS - \mu I$$

The SIS Model for Spread of Disease

The contact network describes contacts between individuals in a population. Infection spreads on this network.

In each iteration, visit all nodes. For each node *i*:

If *i* is **susceptible**, loop over its neighbors. For each infected neighbor, *i* becomes infected with probability β.

If *i* is **infected**, *i* becomes susceptible with probability μ or after some number of time steps t_I.

Nodes can be visited asynchronously in random order, or synchronously.

Epidemic Threshold

Each infected person spreads the disease to an average of $\beta\langle d\rangle$ other people, where $\langle d\rangle$ is the mean degree of the network. Since there are I infected people, the number of secondary infections is $I_{\text{sec}} = \beta\langle d\rangle I$.

Over the same time period, the number expected to recover is $I_{\text{rec}} = \mu I$.

The disease will spread to become an epidemic if $I_{\text{sec}} > I_{\text{rec}}$, so the epidemic threshold condition is

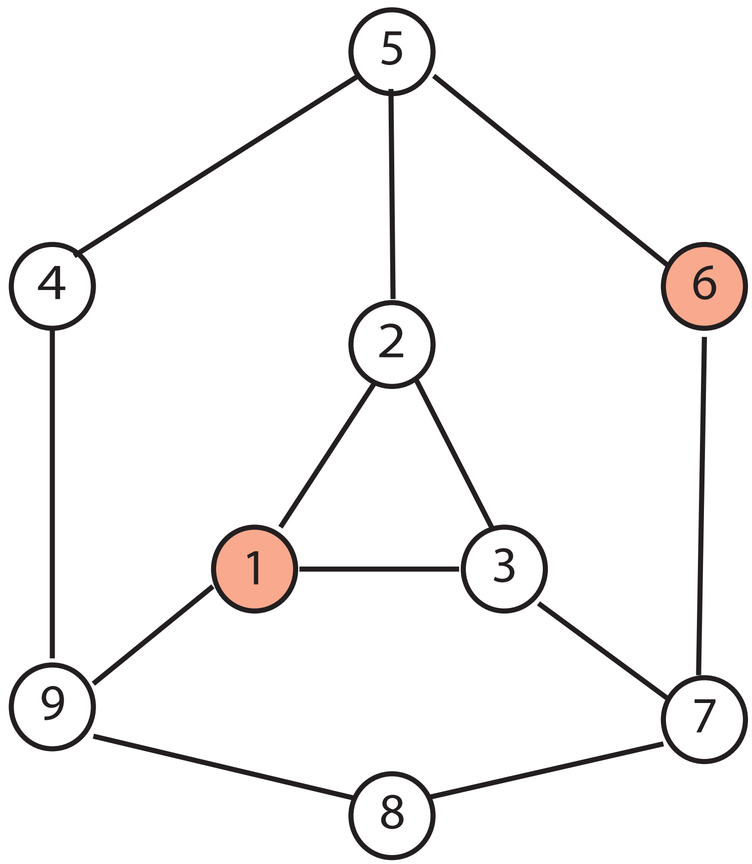
$$\boxed{R_0 = \frac{\beta}{\mu}\langle d\rangle > 1}$$

R_0 is called the basic reproduction number.

SIS Dynamics on a Network

Example with $t_I = 1$, $\beta = 0.5$ with 2 individuals initially infected.

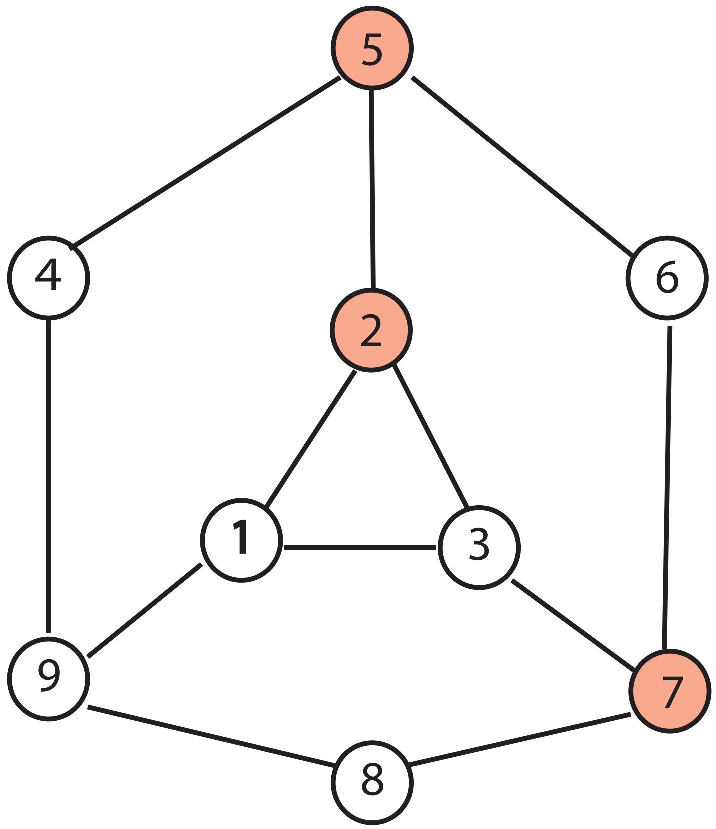
$t = 0$



SIS Dynamics on a Network

Example with $t_I = 1, \beta = 0.5$ with 2 individuals initially infected.

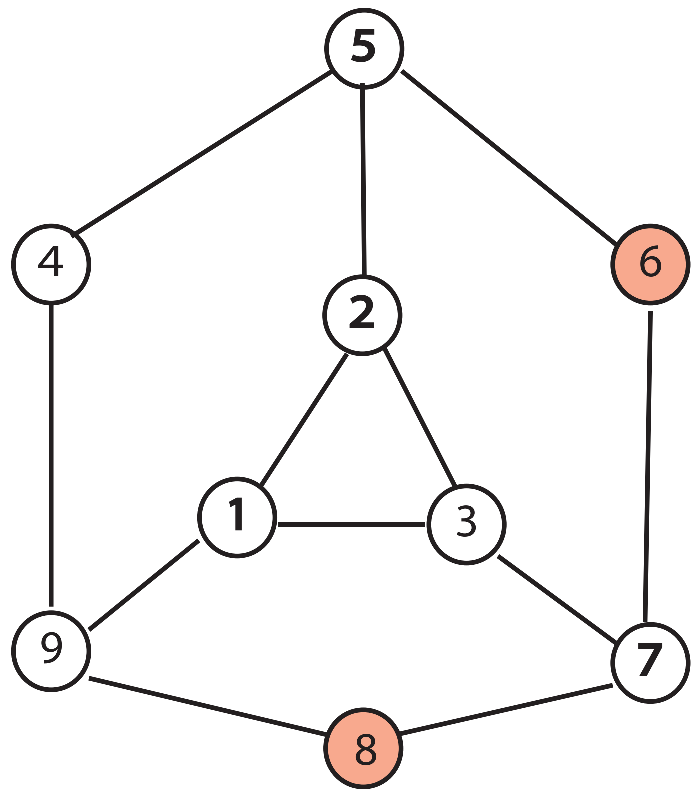
$t = 1$



SIS Dynamics on a Network

Example with $t_I = 1, \beta = 0.5$ with 2 individuals initially infected.

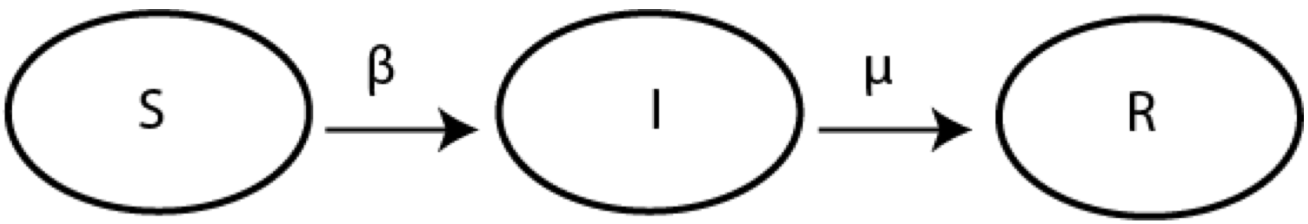
$t = 2$



Epidemic can continue indefinitely

The SIR Model for Spread of Disease

Applies to diseases that do confer long-lasting immunity, like measles and mumps.



S = Susceptible population

I = Infected population

R = Recovered population

β = Infection rate

μ = recovery rate,
or t_I time steps

For compartmental model:

$$\frac{dS}{dt} = -\beta IS$$

$$\frac{dI}{dt} = \beta IS - \mu I$$

$$\frac{dR}{dt} = \mu I$$

SIR Dynamics on a Network

Initially, some nodes are in the *I* state, others are in the *S* state.

Every node v that enters the *I* state remains infectious for a fixed number of time steps t_I.

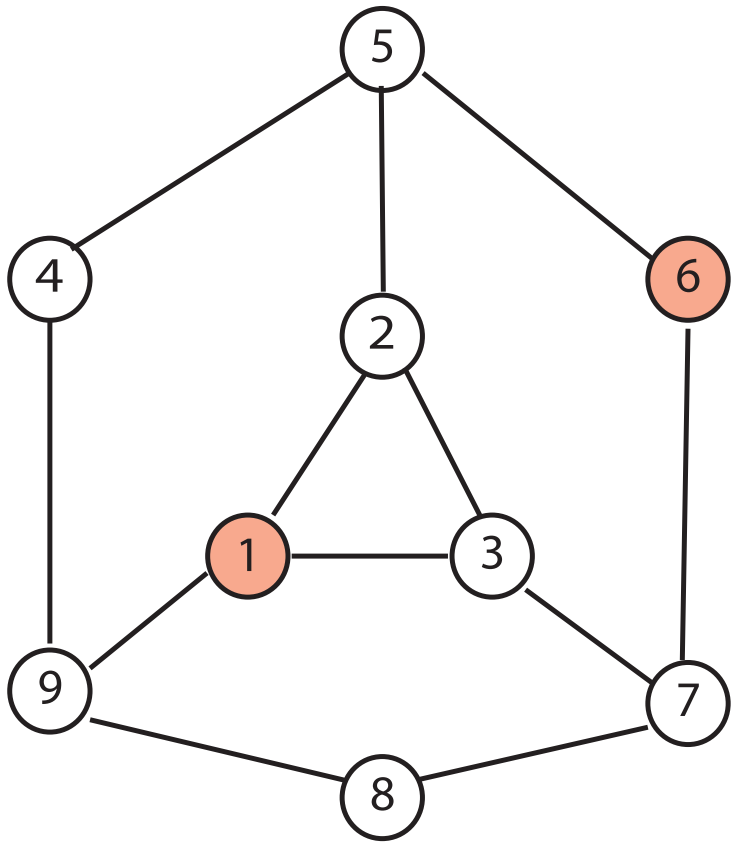
During each of the t_I steps, node v has a probability β of passing the disease to each of its susceptible neighbors.

After t_I steps, node v is no longer infectious or susceptible, and moves to state *R*.

SIR Dynamics on a Network

Example with $t_I = 1, \beta = 0.5$ with 2 individuals initially infected.

$t = 0$

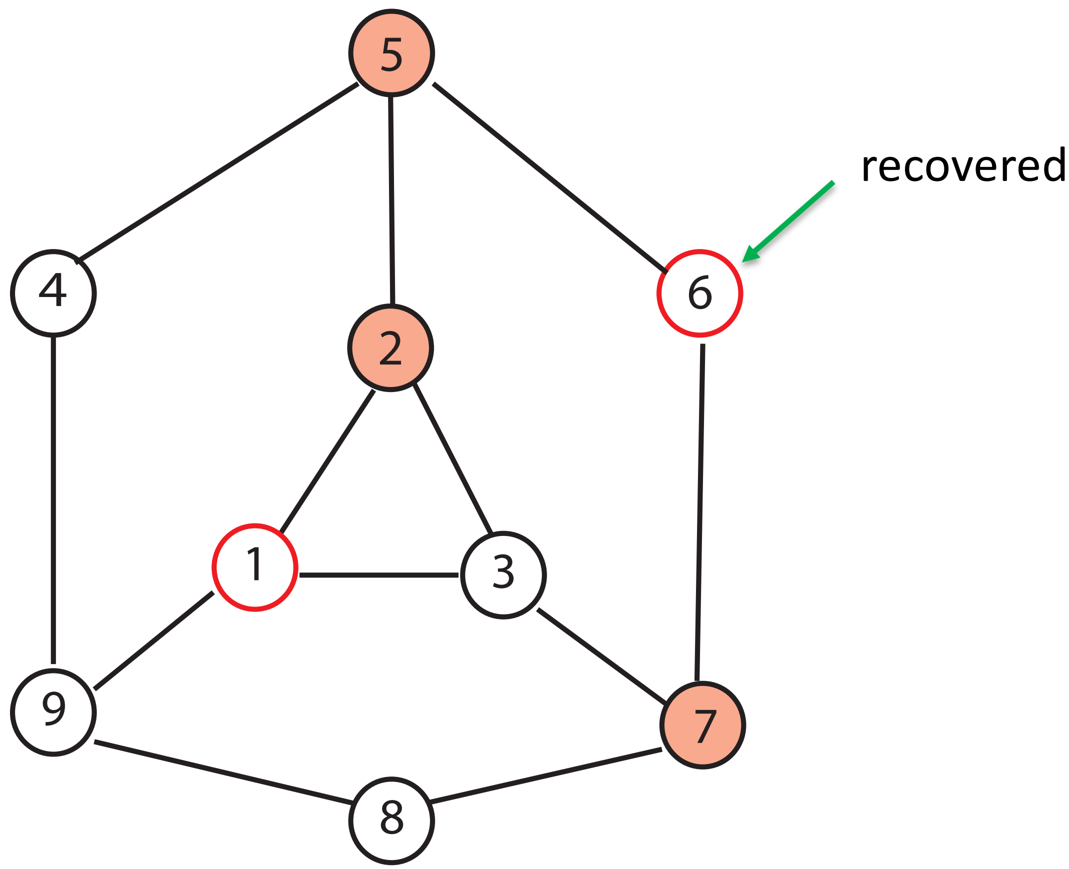


Nodes 1 and 6 infect neighbors with probability β

SIR Dynamics on a Network

Example with $t_I = 1, \beta = 0.5$ with 2 individuals initially infected.

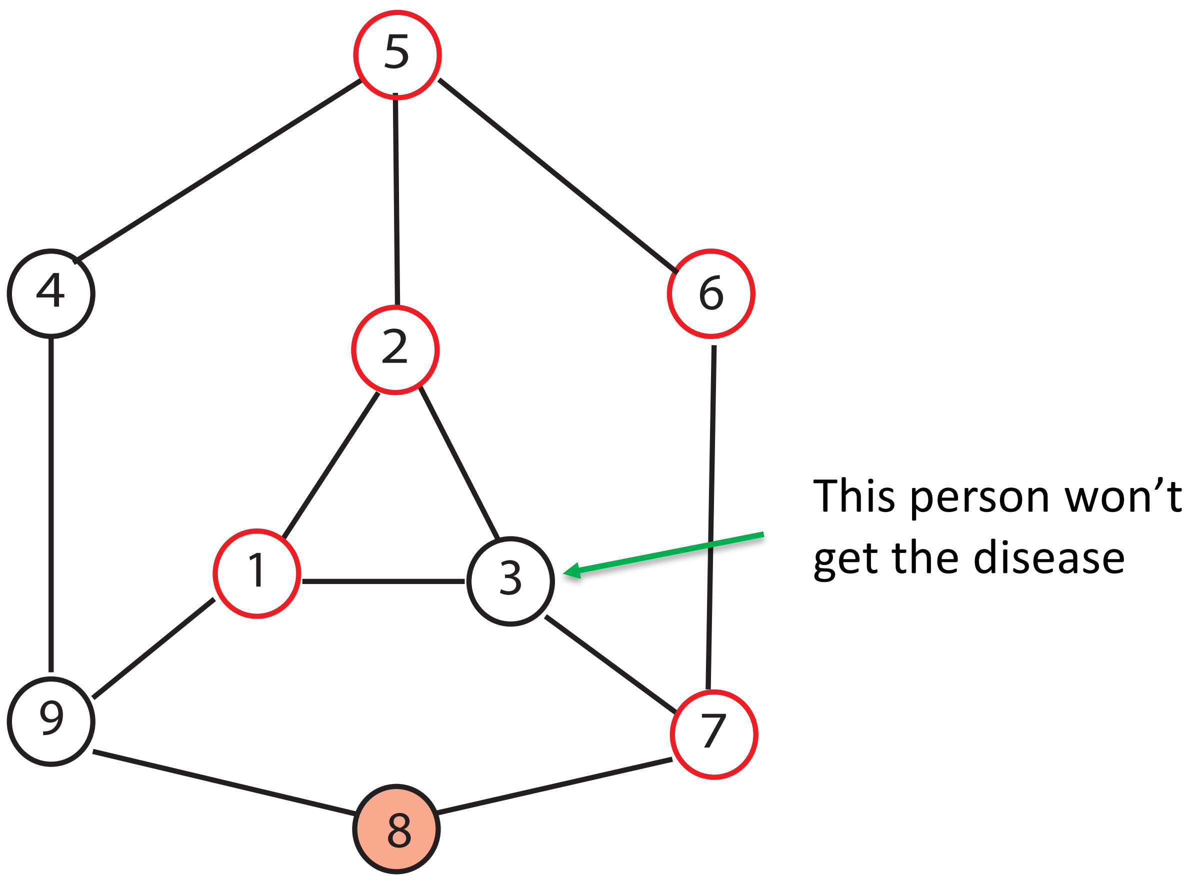
$t = 1$



SIR Dynamics on a Network

Example with $t_I = 1, \beta = 0.5$ with 2 individuals initially infected.

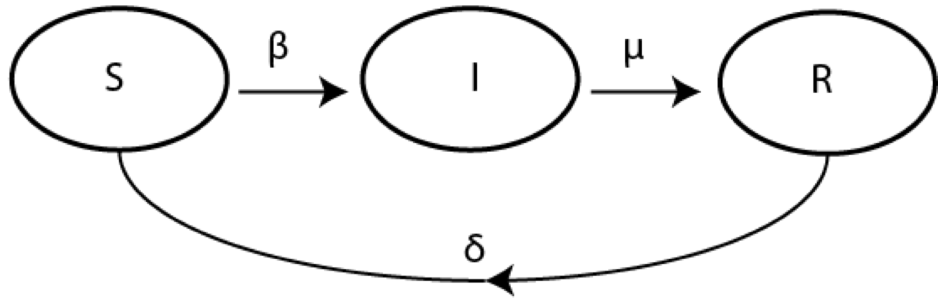
$t = 2$



The epidemic will eventually die out as enough individuals enter the recovered state, establishing herd immunity.

The SIRS Model for Spread of Disease

Applies to diseases that do confer shorter immunity, like COVID.



S = Susceptible population

I = Infected population

R = Recovered population

β = Infection rate

μ = recovery rate,
or t_I time steps

δ = rate of immunity loss

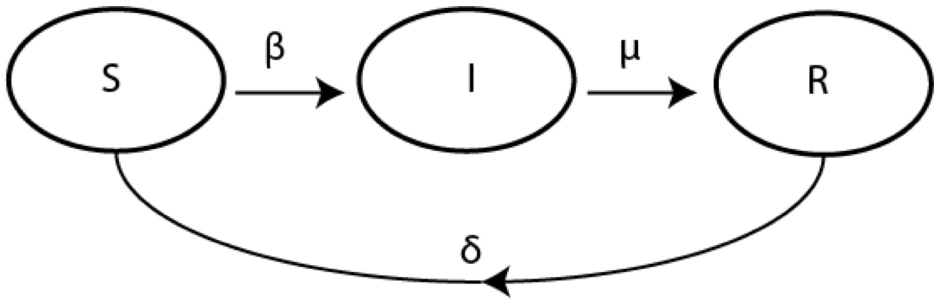
For compartmental model:

$$\frac{dS}{dt} = -\beta IS + \delta R$$

$$\frac{dI}{dt} = \beta IS - \mu I$$

$$\frac{dR}{dt} = \mu I - \delta R$$

SIRS Models: Disease Spread With Time-Limited Immunity



Initially, some nodes are in the *I* state, others are in the *S* state.

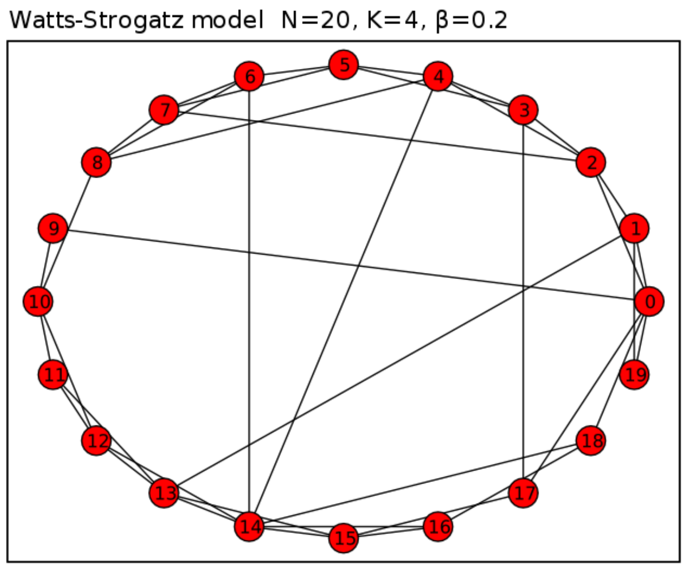
Every node *v* that enters the *I* state remains infectious for a fixed number of time steps t_I.

During each of the t_I steps, node *v* has a probability β of passing the disease to each of its susceptible neighbors.

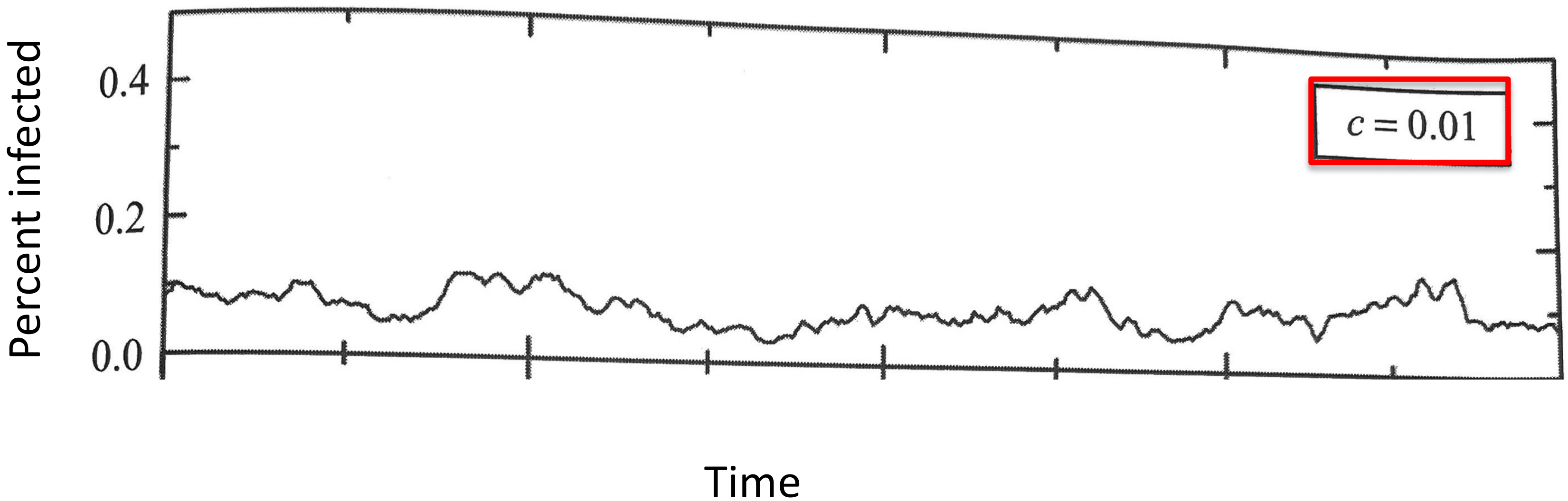
After t_I steps, node *v* is no longer infectious and enters the *R* state and moves back to *S* with probability δ or after t_R time steps.

SIRS on a Small-World Network

Studies of the SIRS model have been performed using the Watts-Strogatz model as a contact network

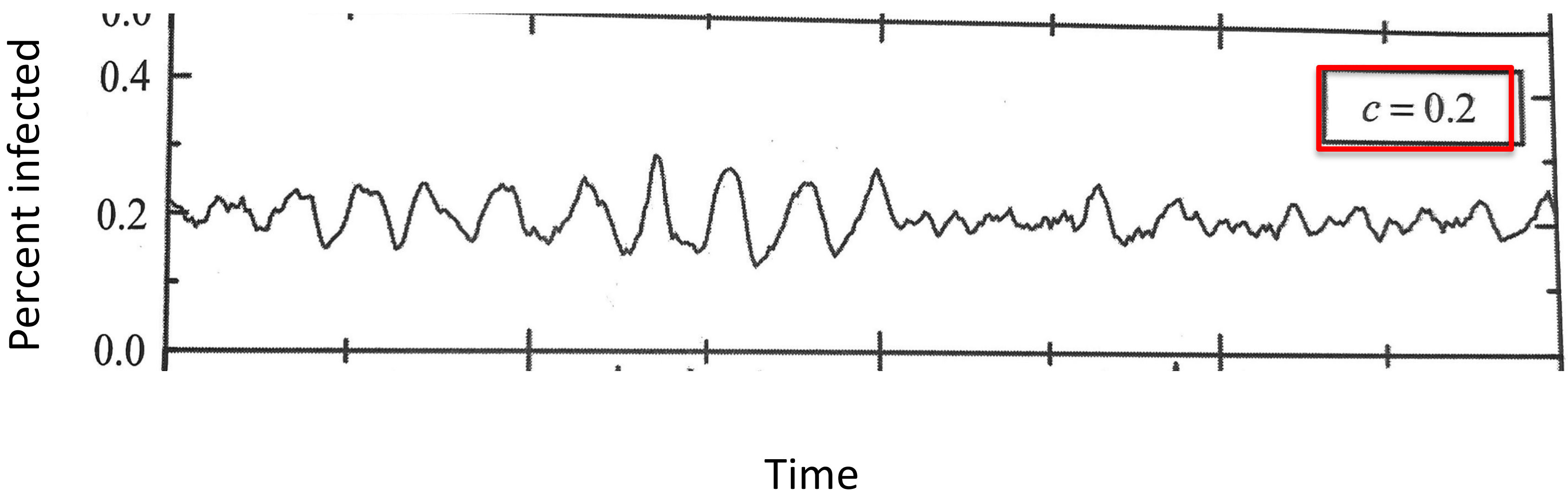


SIRS on a Small-World Network



c is the rewiring probability

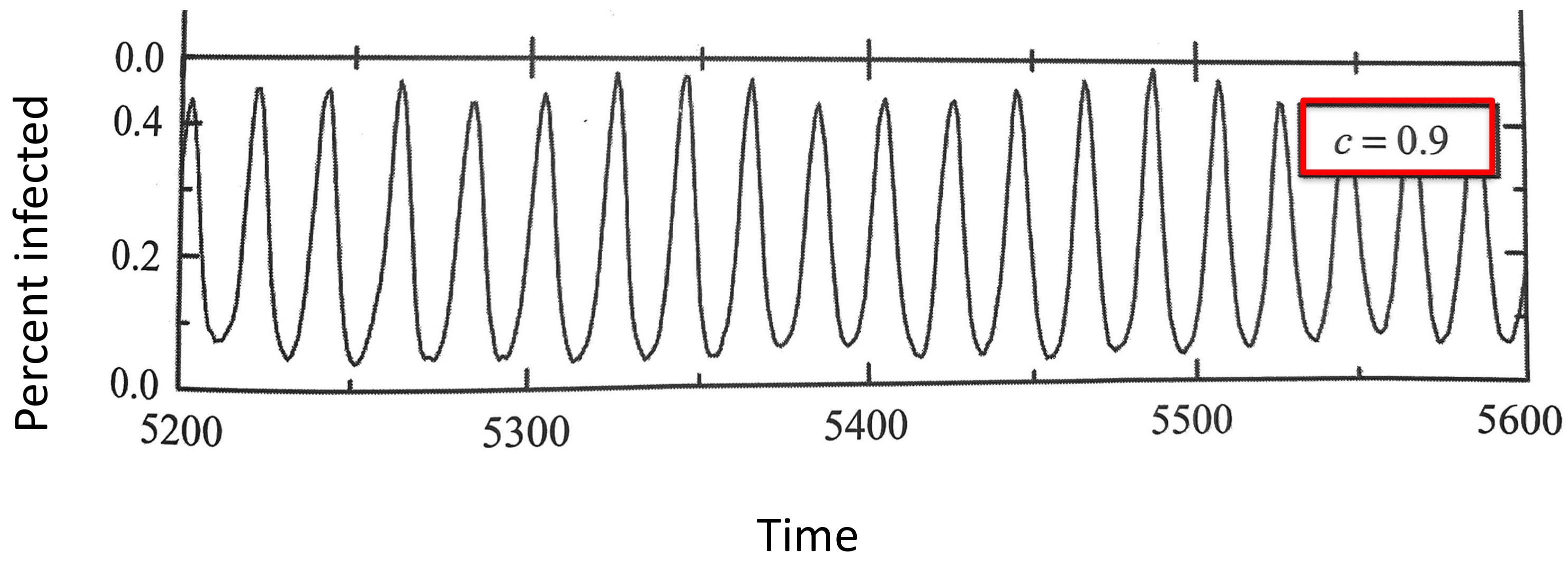
SIRS on a Small-World Network



There are some intermittent waves of infection

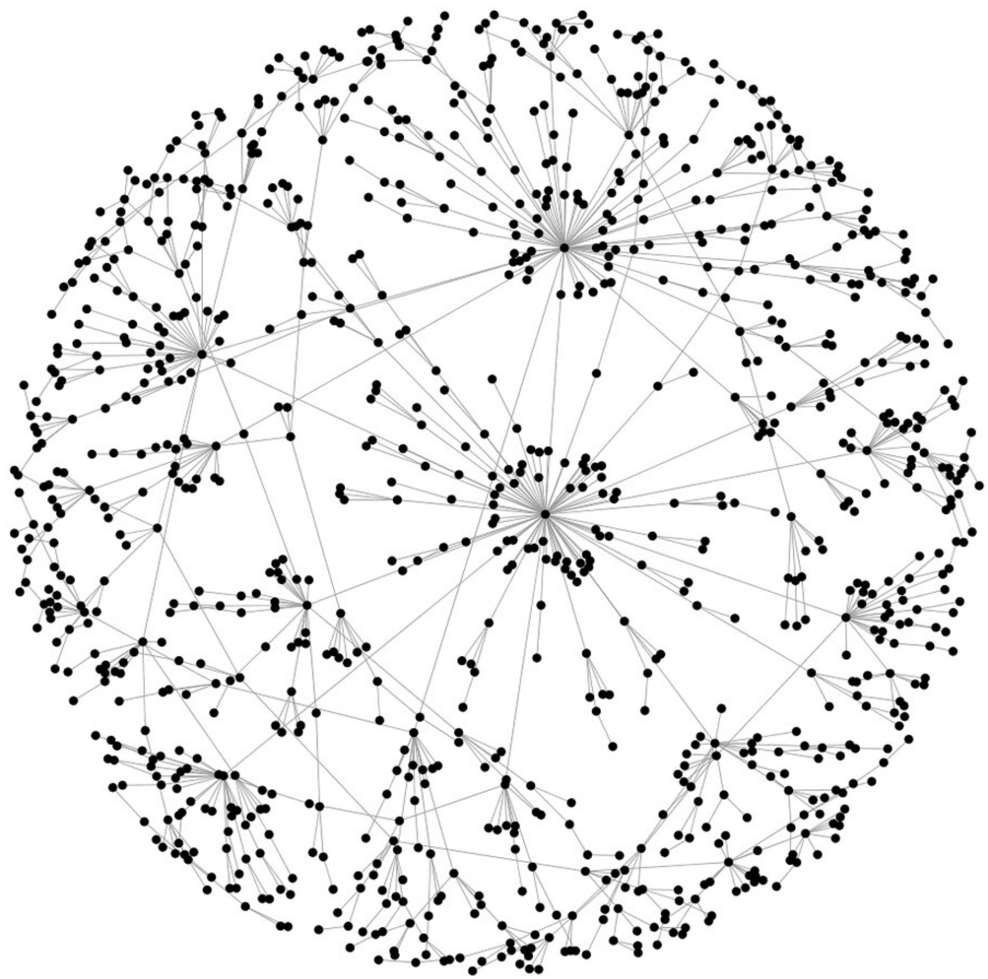
SIRS on a Small-World Network Can Produce Waves of Infection

Easley & Kleinberg



These waves of infection are due to combination of a refractory period (the time-limited immunity) and long-range connections that link together groupings and facilitate coordinated behavior.

Epidemics on a Scale-Free Network: the Curse of the Superspreaders

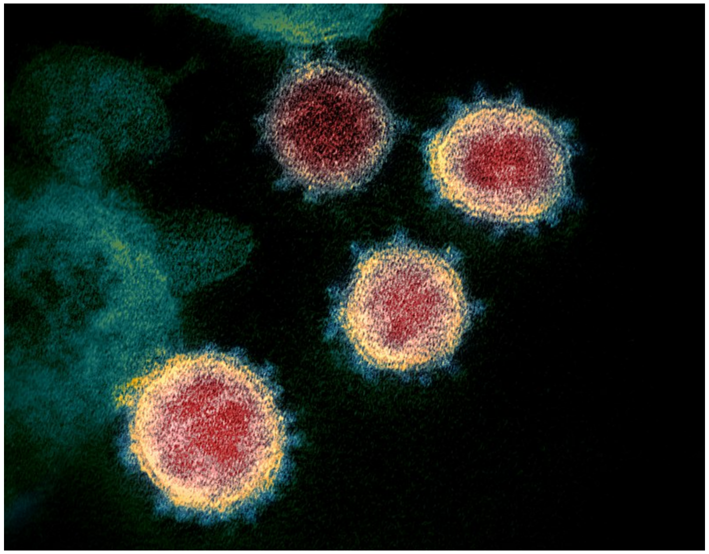


Hubs Can Be Superspreaders

An infected individual who is a network hub has a better chance of spreading the disease than most individuals in the contact network.

A network hub also has a better chance of catching the disease.

These two facts are what make hubs in contact networks superspreaders. How do superspreaders influence the spread of an epidemic like the novel coronavirus on a contact network?

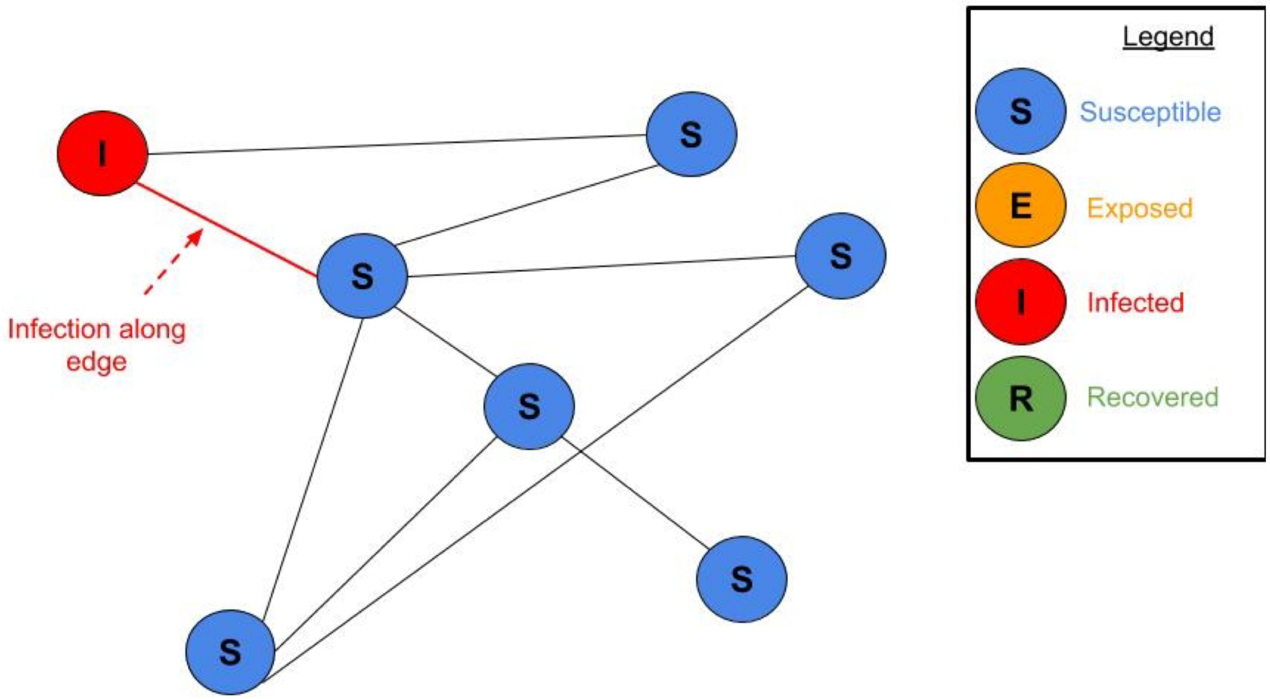


Case Study of Covid-19

We will follow a very recent study by Ofir Reich, Guy Shalev, and Rom Kalvari titled “Modeling COVID-19 on a network: super-spreaders, testing and containment”, MedRxiv preprint, doi: 10.1101/2020.04.30.20081828

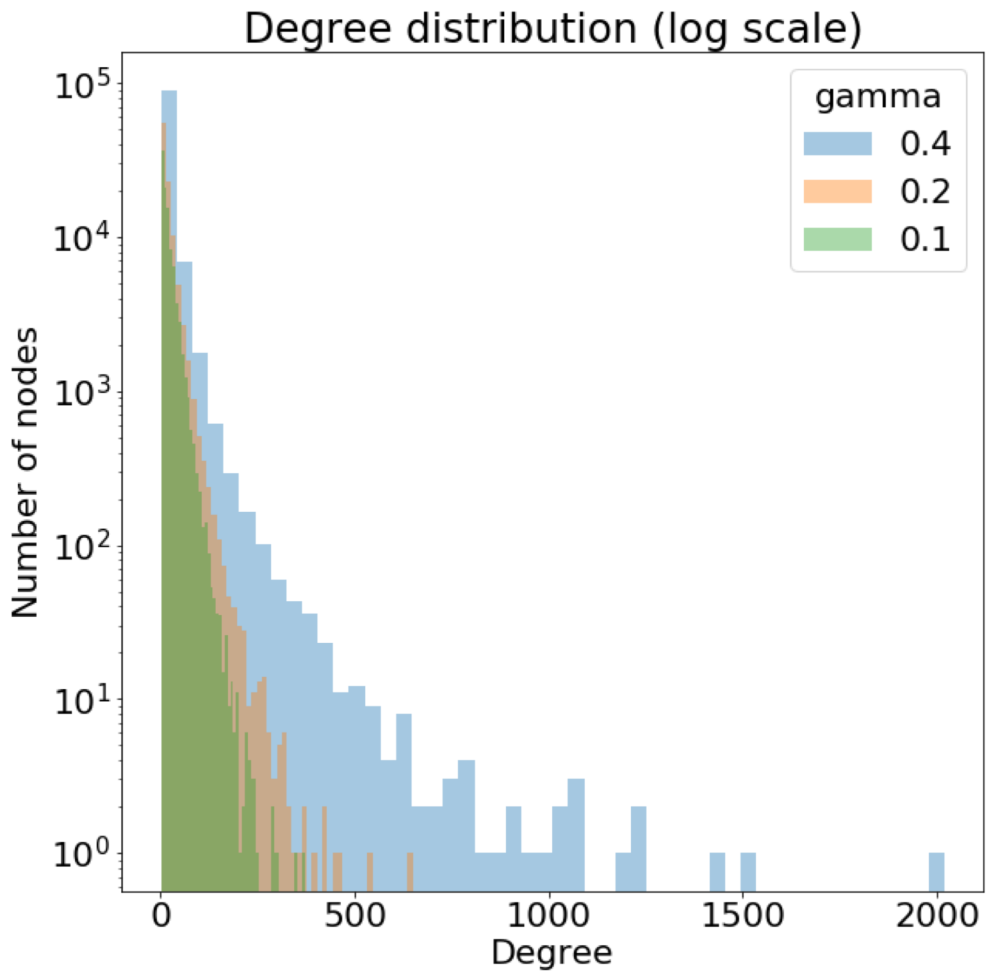
Case Study of COVID-19

They used an SEIR model on a connection network. The new state, *E*, represents individuals that are infected and are now in their presymptomatic incubation period. They become infectious two days prior to entering the Infected (*I*) state. Once in the *I* state, an individual is more infectious than when in the *E* state.



Use the Configuration Model with 10^5 Nodes

They established a contact network using the configuration model with a power-law degree distribution, with different values for the exponent γ.



Transmission Parameters

Assume that the transmission probability, ϕ, is uniform over the network.

Let $r_j = \phi k$ be the expected number of susceptibles that an infectious node will infect, where k is the number of susceptible neighbors. For most nodes, k will be small, but for hubs it will be large.

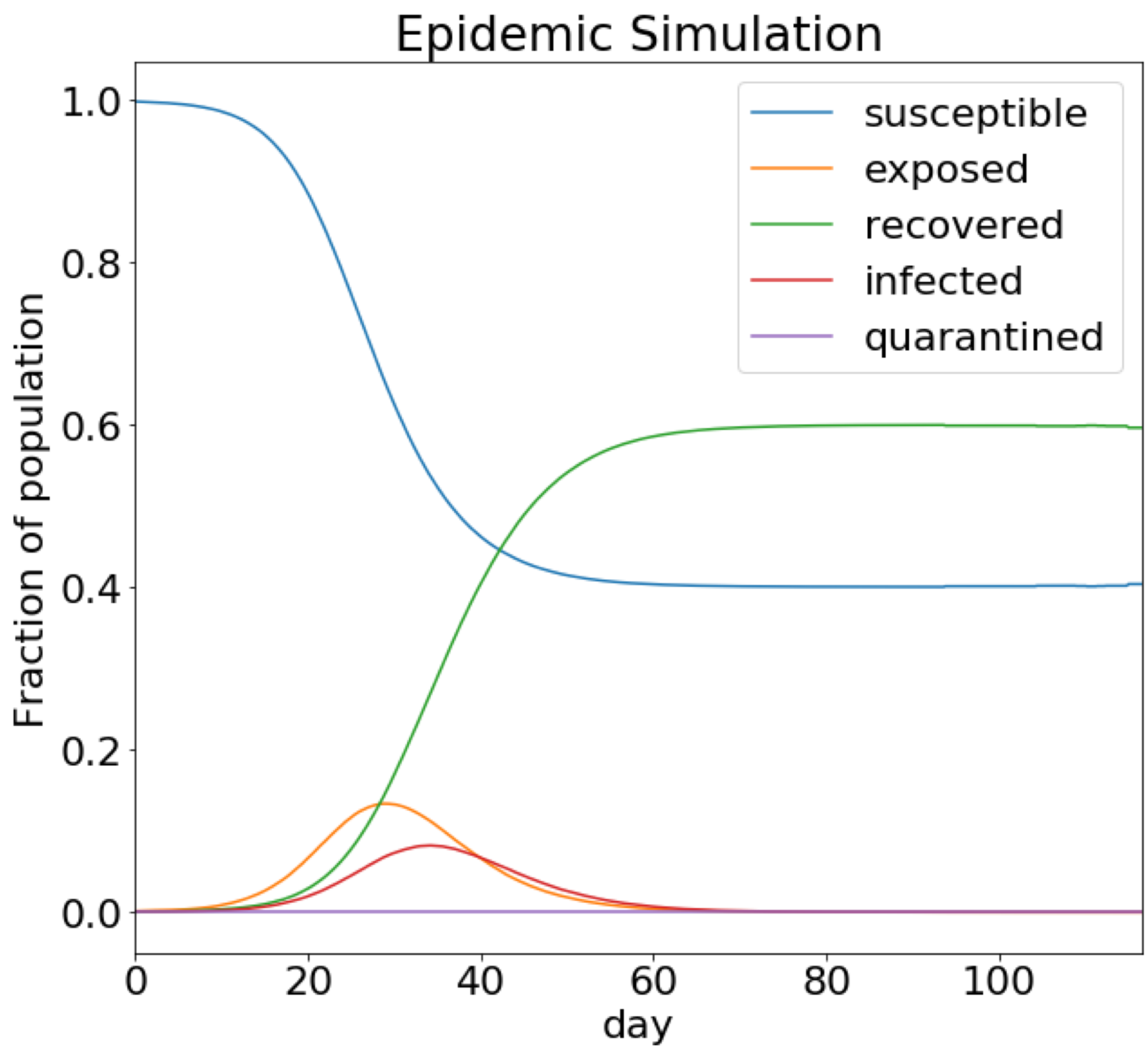
Let r be the average of r_j over the network. For a homogeneous population (in which all nodes have the same degree), $r = R_0$, the basic reproduction number.

Some fraction of nodes randomly chosen as Infected. A slightly larger fraction is selected as Exposed.

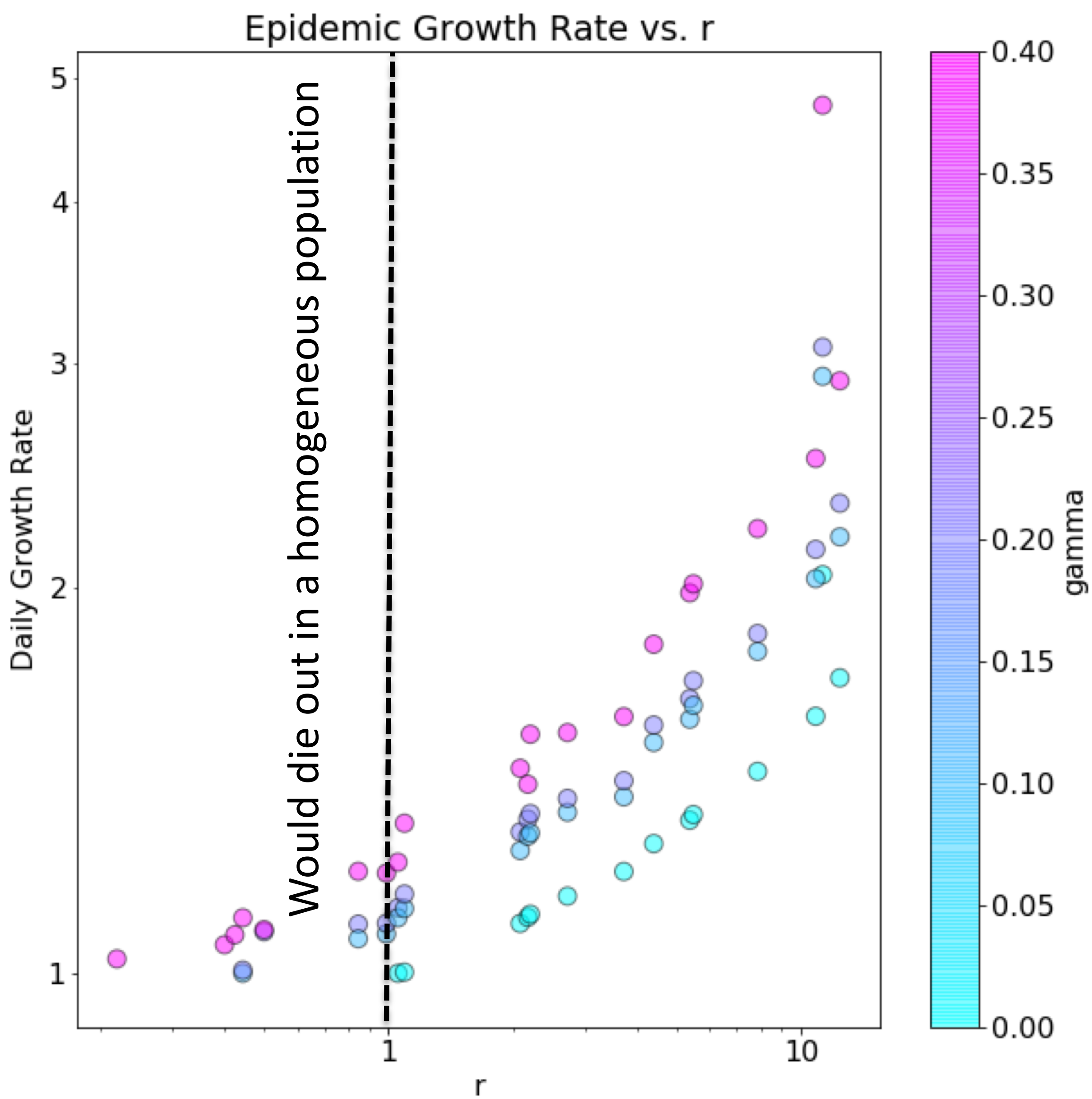
Define the **daily growth rate** as the factor in which the number of infected people grows each day. If this is greater than 1, then the epidemic grows.

They took as many parameters values as they could find from the COVID-19 epidemic in the U.S. In particular, from March 4, 2020 until March 28th, the number of deaths increased from 11 to 2220.

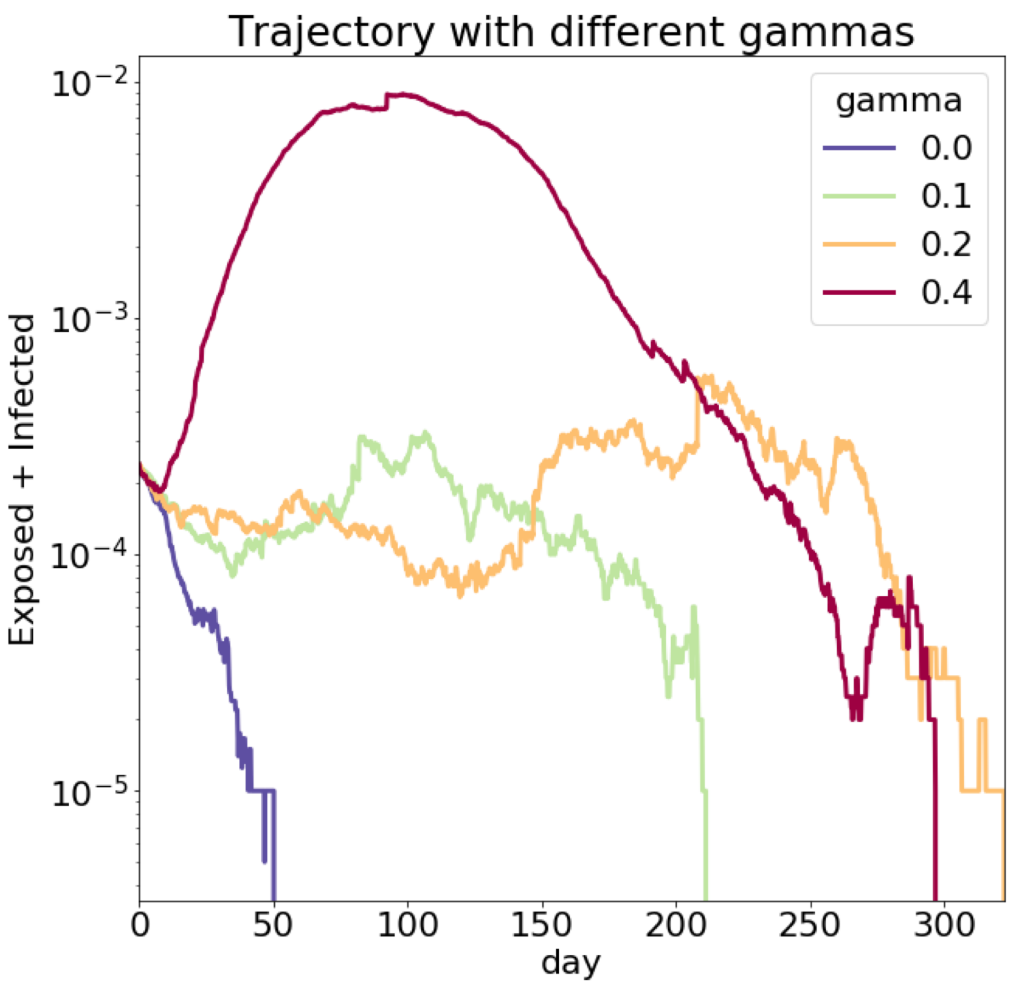
Time Dynamics of One Simulation



Daily Growth Rate in Multiple Simulations



Epidemics are Worse With Larger γ



r=0.5

$\gamma = 0$ is a homogeneous population

Why Does Exponential Spread Occur Even Though $r < 1$?

This occurs because *R*=average number of nodes infected by an infectious individual in a simulation is greater than *r*. Why is this true?

Recall that *r* is the expected number of individuals infected by a single random person if that person is infectious and some neighbors are susceptible.

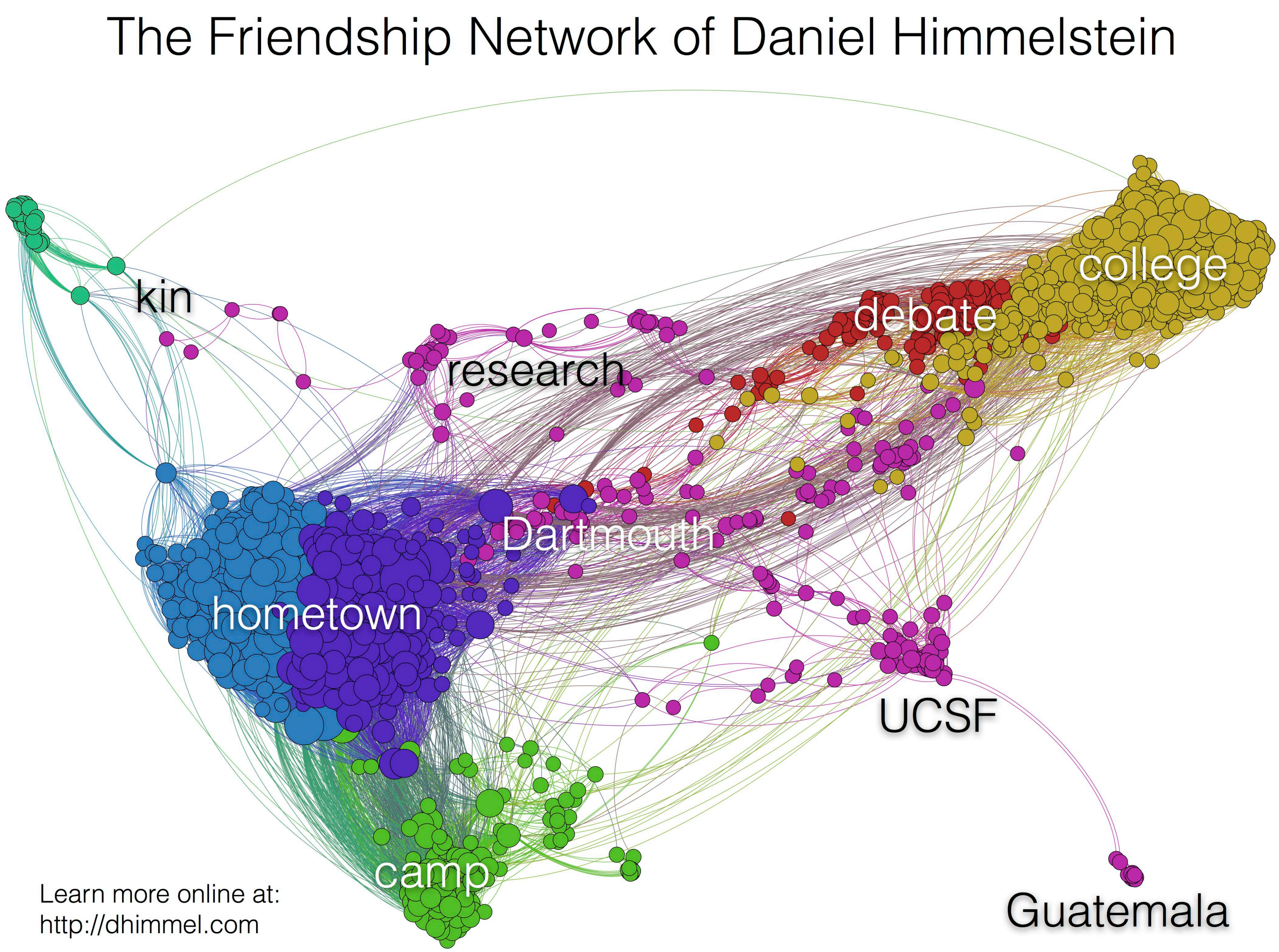
After the first step, individuals with larger degrees are more likely to be infected, so the degree distribution of the infected nodes skews higher than the degree distribution of all nodes. These higher-degree individuals will infect more than *r* individuals, that is, $R > r$.

Public Health Takeaways

Most contact networks are approximately scale-free

Epidemics spread more effectively on scale-free networks, particularly with larger values of the exponent γ where there are more superspreaders.

Bond Percolation Model for Disease Spread on a Contact Network



Transmission Rate and Probability

In a contact network, if two individuals have substantial contact with one another, then they are connected by an edge.

Let β be the probability per unit time that an infection is transmitted from an infected individual to a susceptible neighbor. This is the transmission rate or infection rate.

The probability that a neighbor gets infected over a time interval $\delta\tau$ is then $\beta\delta\tau$. The probability the neighbor is not infected over that time interval is $1 - \beta\delta\tau$.

The probability the individual is still uninfected after a total time of $\tau = n\delta\tau$ is then

$$\lim_{\delta\tau\to 0}(1 - \beta\delta\tau)^n = \lim_{\delta\tau\to 0}(1 - \beta\delta\tau)^{\tau/\delta\tau} = e^{-\beta\tau}$$

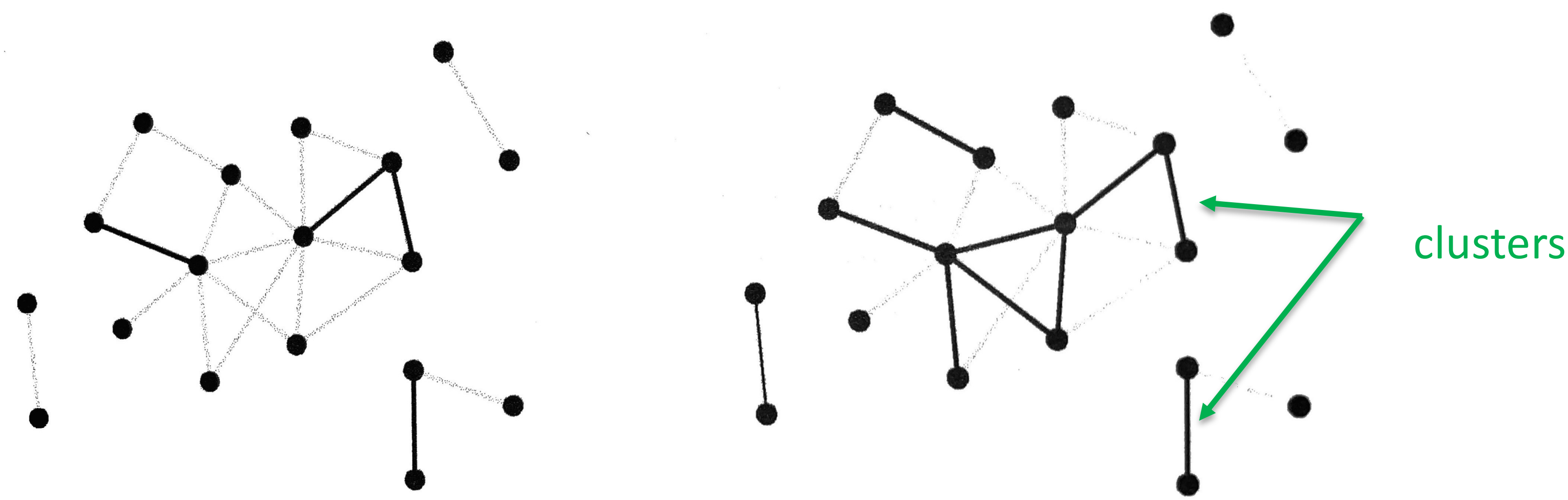
The probability that the individual is infected over time period τ is then

$$\boxed{\phi = 1 - e^{-\beta\tau}}$$ Transmission probability

A Method for Disease Spread

This approach does not consider the time dynamics of disease spread, only the possible population outcomes that can occur over a given time interval.

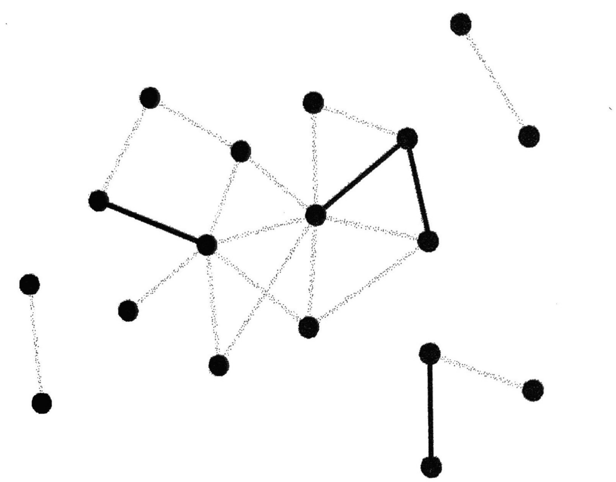
For each edge in the contact network, select it for transmission over a time interval τ with probability ϕ.



(a) $\phi = 0.2$ (b) $\phi = 0.5$

Bond Percolation

If any of the initial infected individuals land in a cluster, then everyone in the cluster will be infected by the end of the time interval.



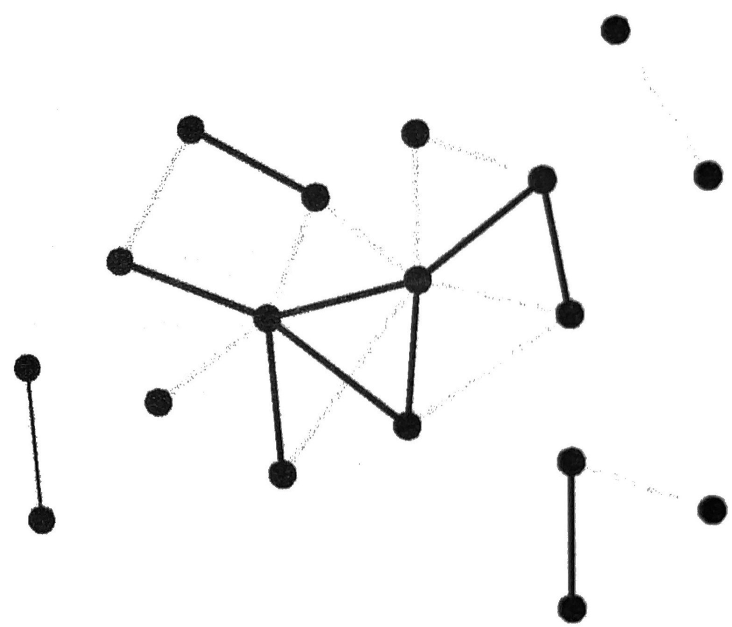
(a) $\phi = 0.2$

This approach is called bond percolation, since only a subset of the existing bonds are selected. The name refers to the flow of fluid through pipes. If you randomly add pipes between locations, which locations will receive water?

When ϕ is small, spread of the disease will be very limited, as long as the initial number of infected individuals is small.

Epidemics are Possible Past the Percolation Threshold

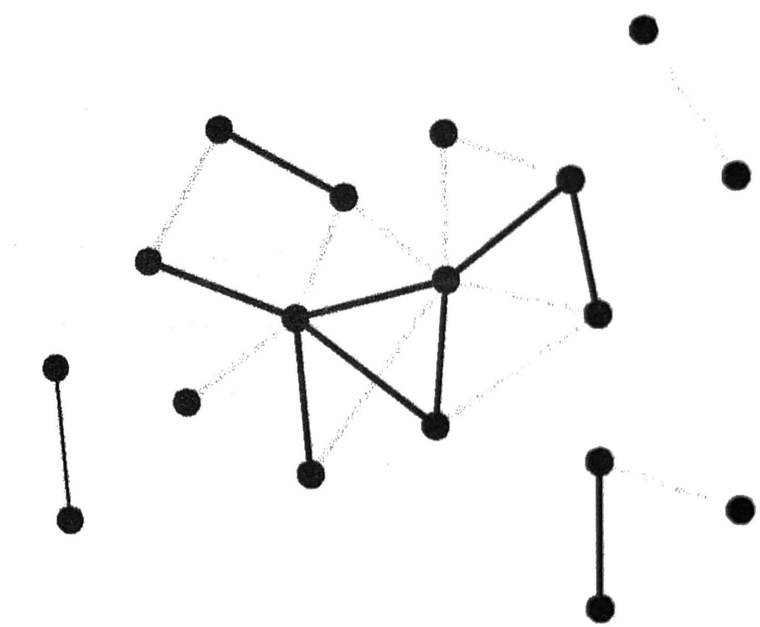
If the transmission probability is high enough, then a giant cluster can form. That is, the infection network could percolate. At his point, an epidemic is likely to emerge over time interval τ, but not guaranteed, depending on whether an initially infected individual is in the giant cluster.



(b) $\phi = 0.5$

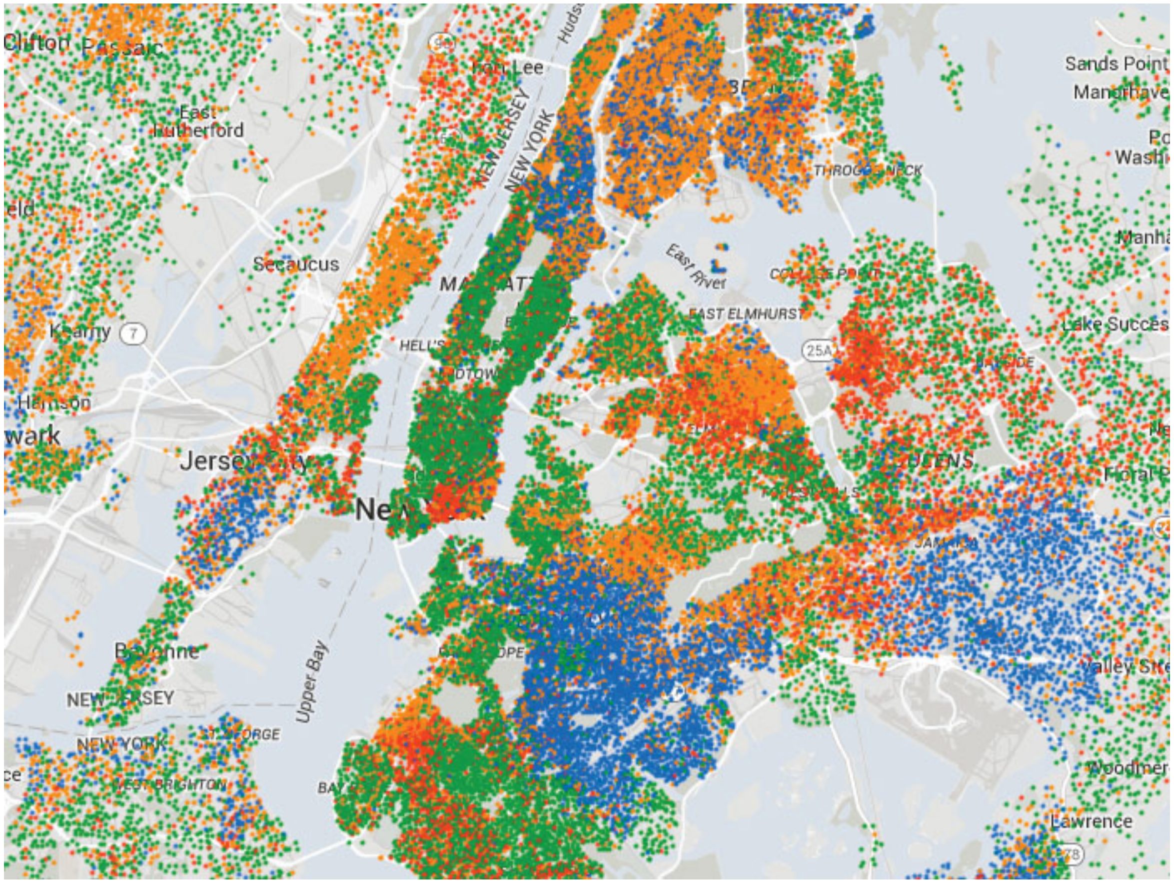
Can the Disease Just Die Out?

Yes, with probability $1 - S$, where S is the size of the giant cluster of the infection network. Goal of public health is to keep S as small as possible. The best way to do this is to reduce the size of the giant component in contact networks, through social distancing.



(b) $\phi = 0.5$

Spatial Segregation in Social Networks



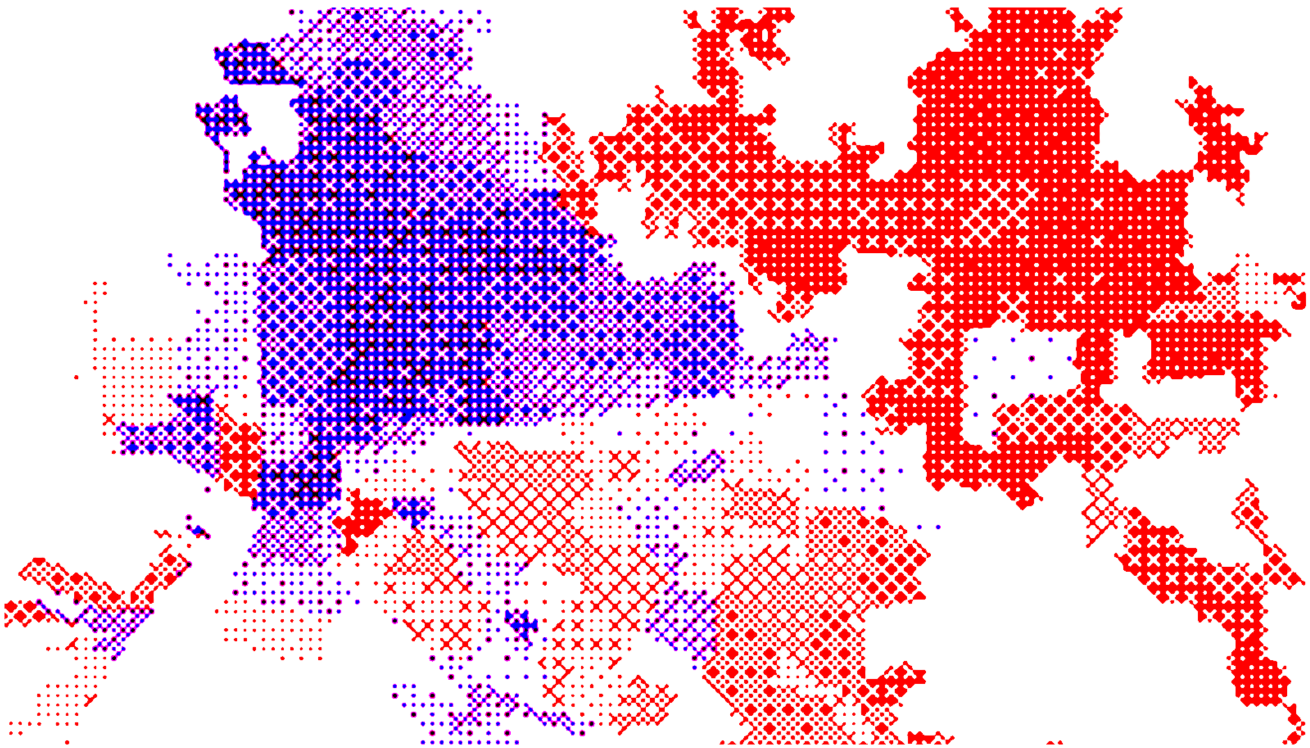
Segregation in Society

The concept of homophily states that people tend to form links with those that share common characteristics (race, ethnicity) or beliefs (political or religious). For example,

Most neighborhoods were once filled with Biden signs, or filled with Trump signs. Few neighborhood had a mix of the two.

Segregation in Society

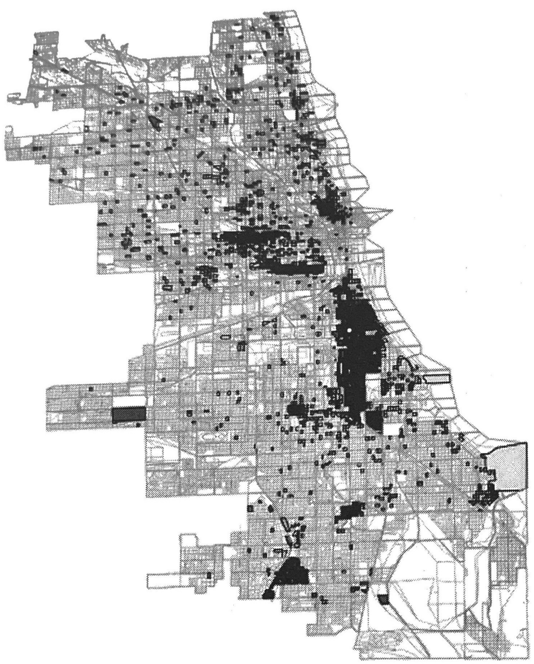
Segregation in Democratic (blue) and Republican (red) households in a community.

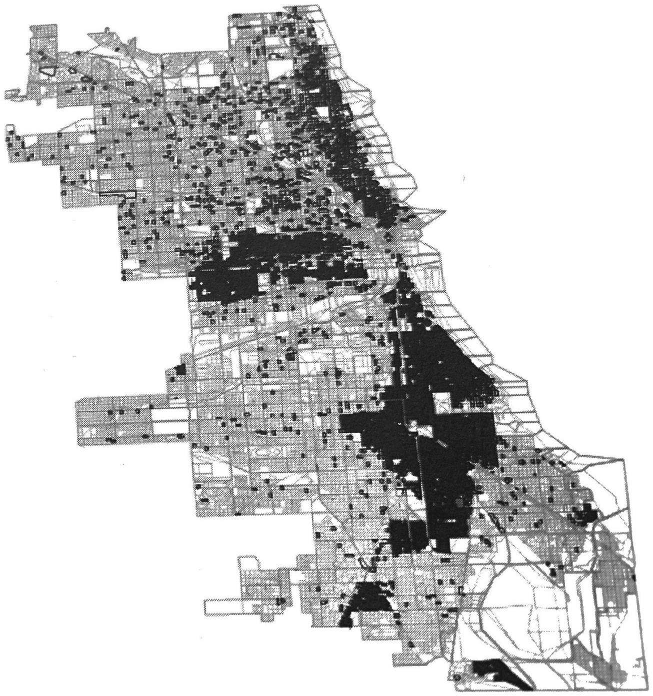


Segregation in Society

Segregation in housing in Chicago. Blocks with lighter colors have the smallest percentages of African-Americans. Left=1940, Right=1960

Easley and Kleinberg 2010





Is Segregated Housing Intentional?

This question was addressed indirectly using computer simulations with the Schelling model (1972). This is a simple model that tests how small individual choices can lead to segregated housing.

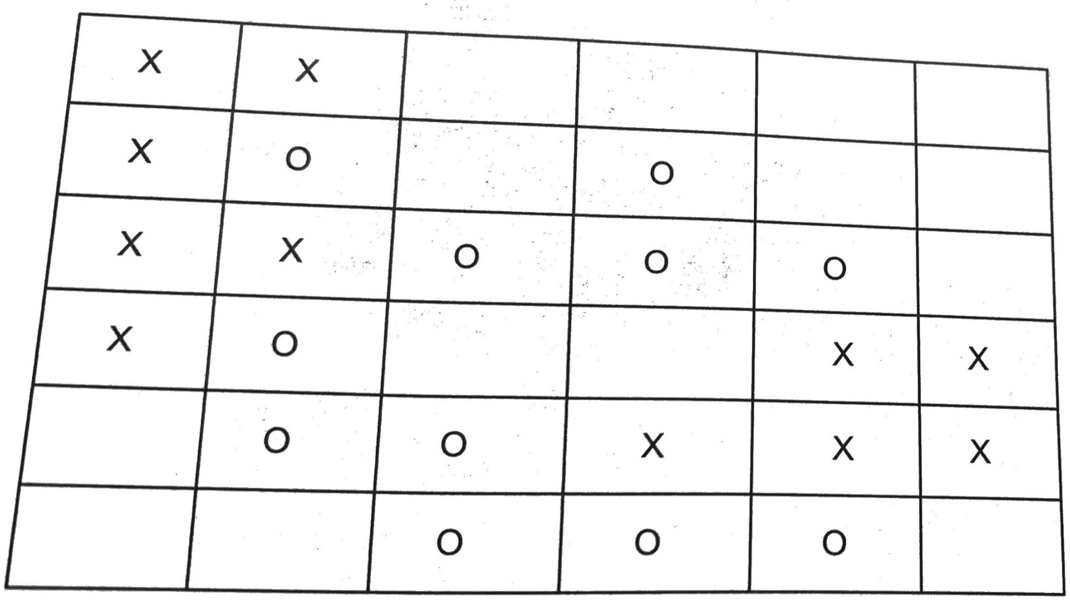
Assume a population of individuals (“agents”) of type X or O. These agents live on a grid of cells representing the two-dimensional geography of a city.

“Neighbors” of a cell are those that touch it (up to 8 neighbors).

Some fraction of the cells are empty.

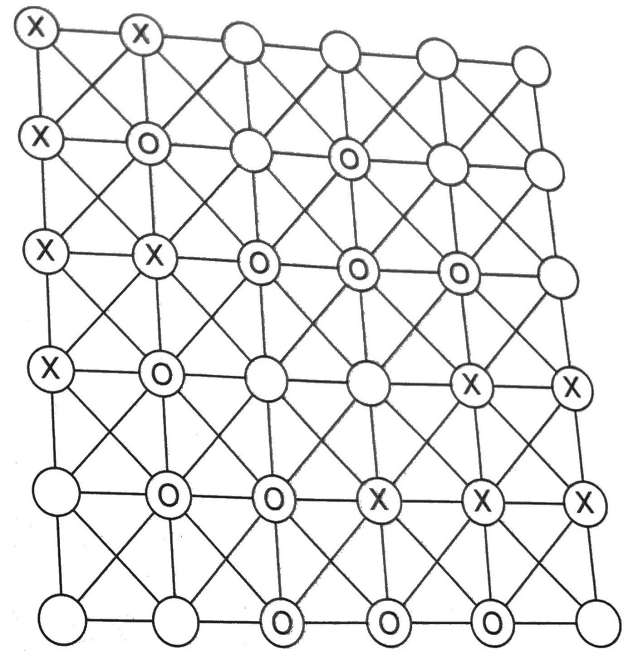
This grid can also be thought of as a network, with agents as nodes and physical neighbors as edges.

The Schelling Model



(a)

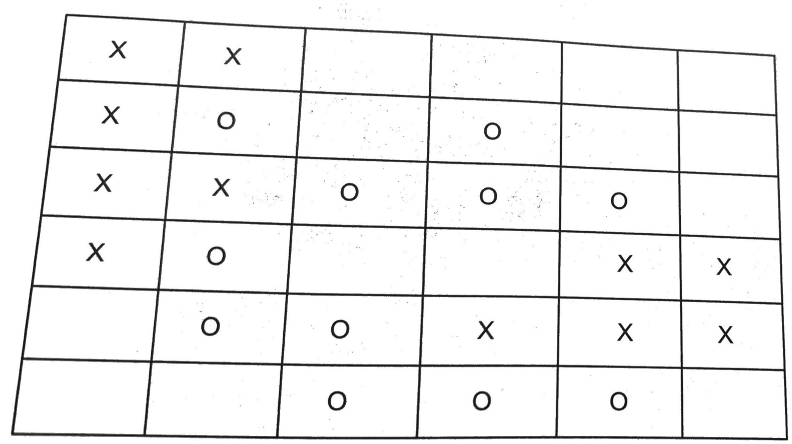
As a grid



(b)

As a network

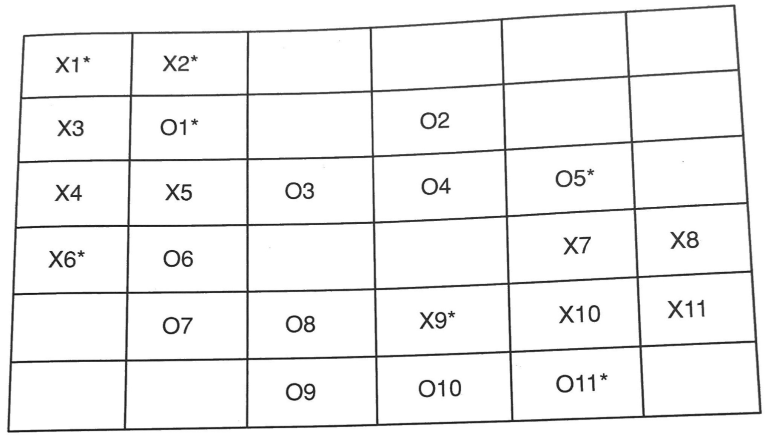
The Schelling Model



(a)

Movement: An agent is "unsatisfied" if fewer than T neighbors are of its type. In each round, each unsatisfied agent has the opportunity to move into a new location where it will be satisfied. The order in which this is done varies with different implementations.

The Schelling Model



(a)

T=3

Agents labeled according to starting location. Unsatisfied agents indicated with a * superscript.

The Schelling Model

X1*	X2*				
X3	O1*		O2		
X4	X5	O3	O4	O5*	
X6*	O6			X7	X8
	O7	O8	X9*	X10	X11
		O9	O10	O11*	

(a)

One round
(with T=3)

X3	X6	O1	O2		
X4	X5	O3	O4		
	O6	X2	X1	X7	X8
O11	O7	O8	X9	X10	X11
	O5	O9	O10*		

(b)

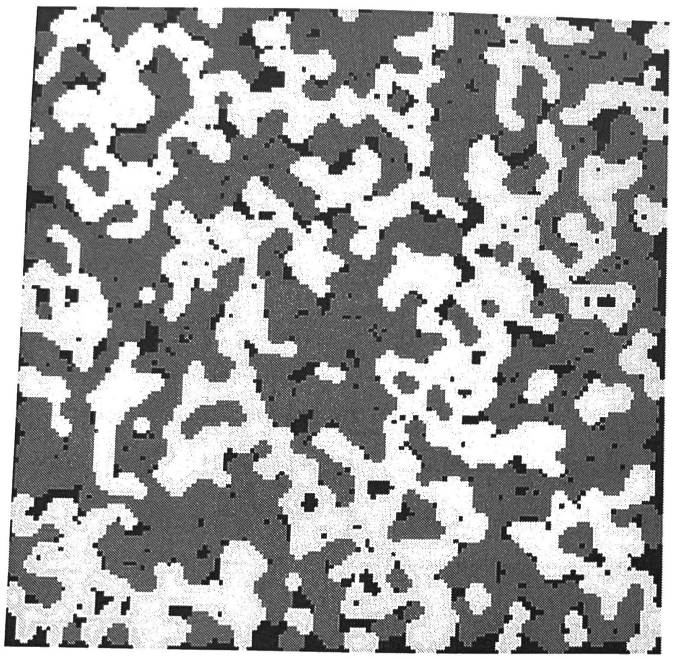
Unsatisfied agents (* superscript) moved to locations in which they were satisfied. This left other agents unsatisfied.

Computer Simulation with the Schelling Model

In this example, 10,000 agents are used and the grid is 150 X 150. The threshold for satisfaction is T=3. Start with random location of agents.

After many iterations:

Easley and Kleinberg 2010



(a)

Light dots=type O, gray dot=type X, black dot=empty

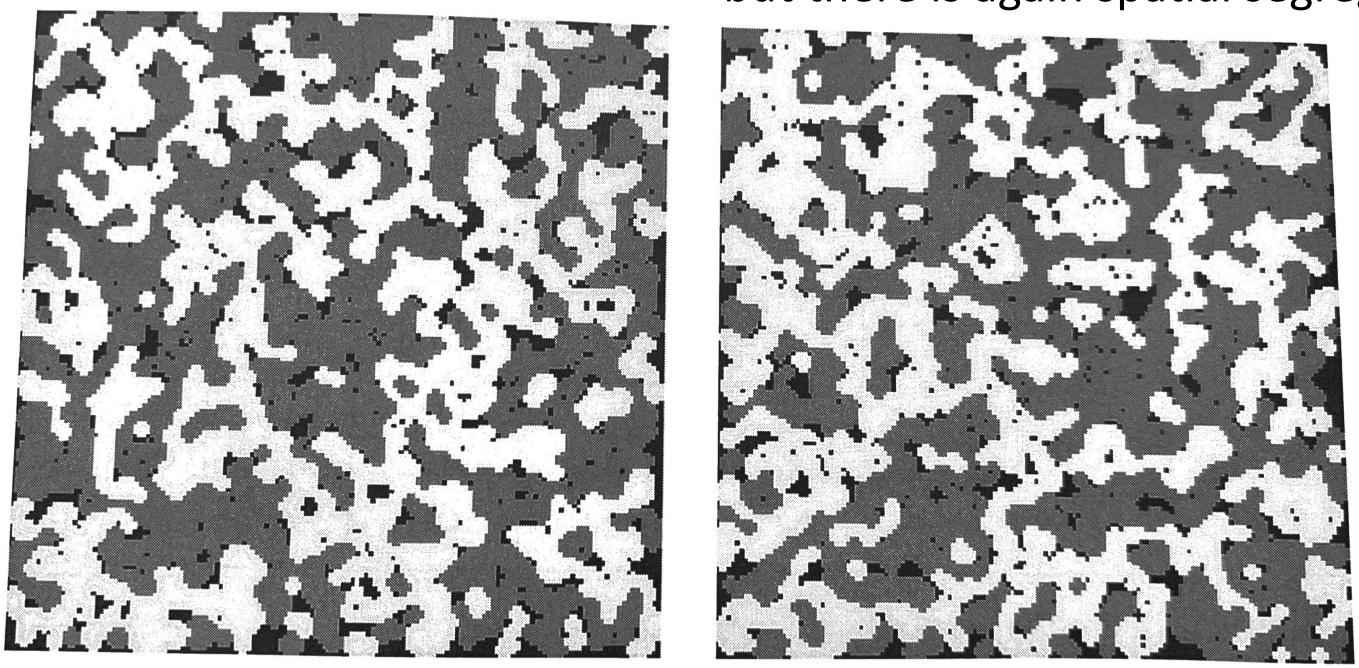
Patterns have formed, reflecting spatial segregation into types.

Computer Simulation with the Schelling Model

Do it again, but with a different set of random initial conditions.

A different pattern is formed,
but there is again spatial segregation

Easley and
Kleinberg 2010



(a) (b)

Light dots=type O, gray dot=type X, black dot=empty

Computer Simulation with the Schelling Model

This did not have to happen! With T=3 it is possible to arrange agents into an integrated pattern:

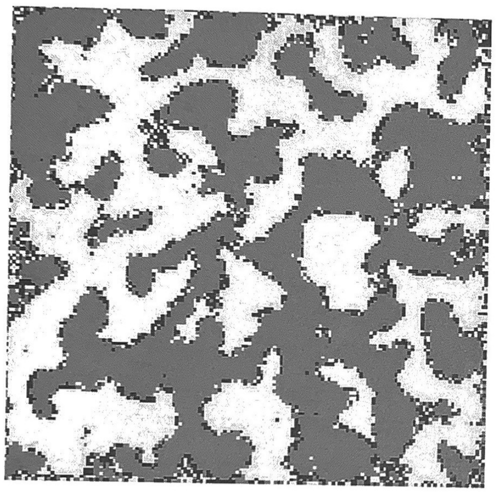
X	X	O	O	X	X
X	X	O	O	X	X
O	O	X	X	O	O
O	O	X	X	O	O
X	X	O	O	X	X
X	X	O	O	X	X

Everyone is satisfied, and there are no large clusters of agents of the same type. However, reaching this integrated distribution is very difficult from initial random placement of agents.

Computer Simulation with the Schelling Model

With threshold T=4 the segregation gets much worse.

20 rounds



Computer Simulation with the Schelling Model

With threshold T=4 the segregation gets much worse.

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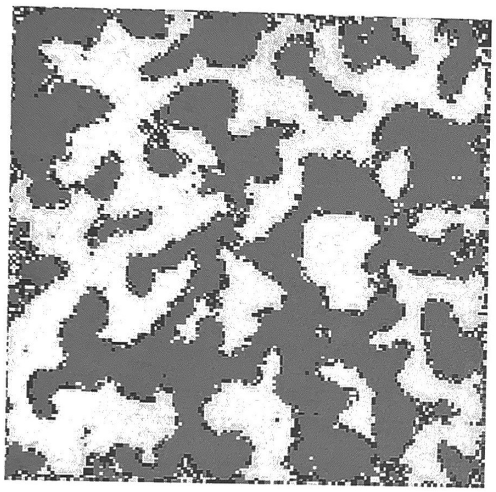
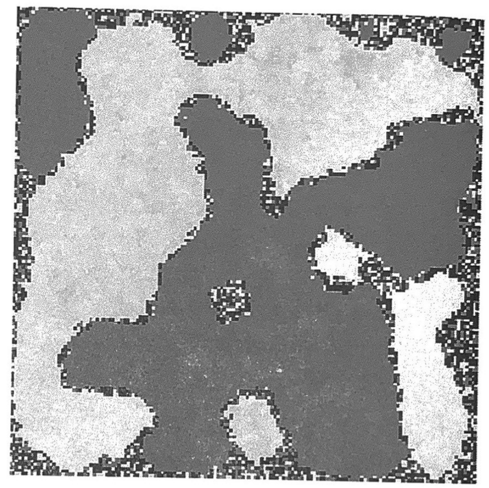


(a)



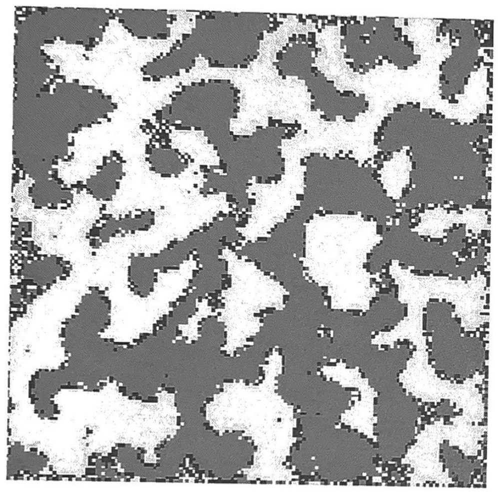
(b)

150 rounds

Computer Simulation with the Schelling Model

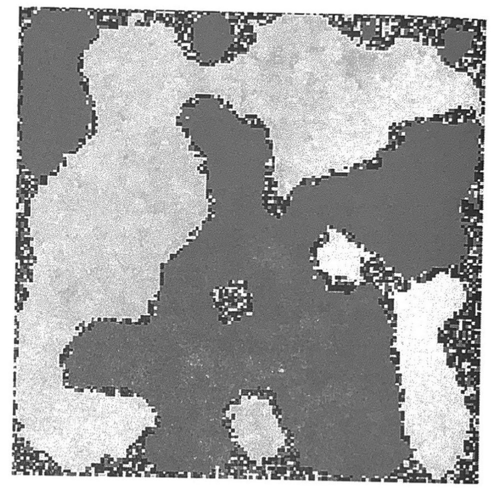
With threshold T=4 the segregation gets much worse.

20 rounds



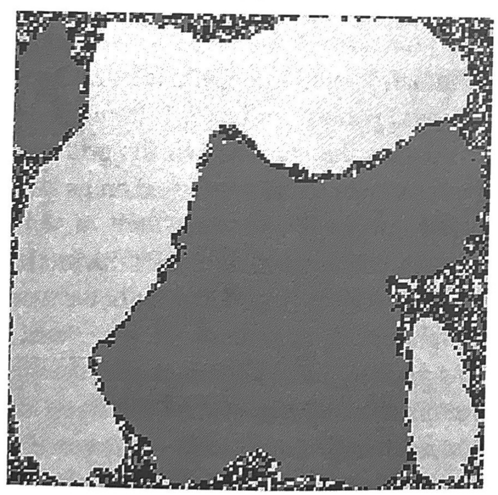
(a)

150 rounds



(b)

350 rounds



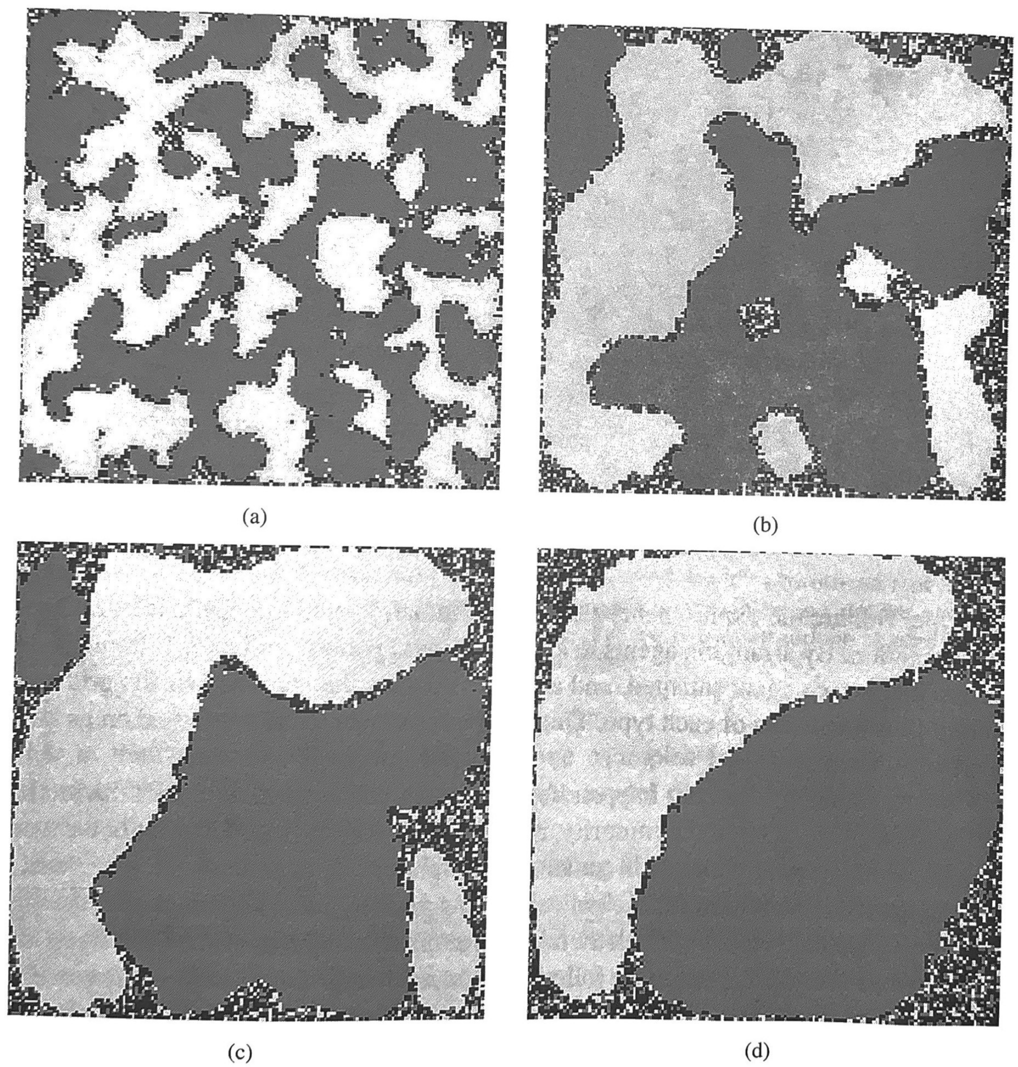
(c)

Computer Simulation with the Schelling Model

With threshold T=4 the segregation gets much worse.

20 rounds

150 rounds



350 rounds

800 rounds

Easley and
Kleinberg 2010

Important Observations from the Schelling Model

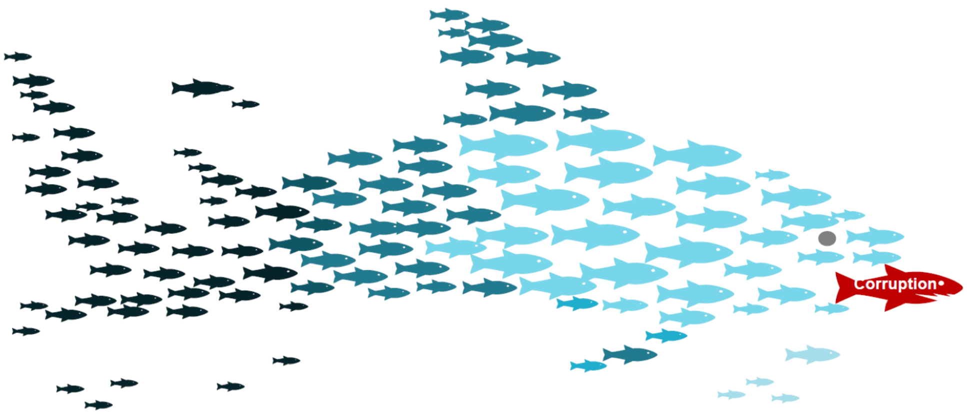
(1) With T=3 or 4, none of the agents minded being in the minority. For example, with T=3, an agent would be satisfied with having 3 neighbors of its type and 5 neighbors of the other type.

(2) The agents **did not plan to move into segregated clusters**, these just emerged over time in response to many individual moves to satisfy local preferences. It is an example of an emergent property of the system.

(3) Computer simulations with this model show that the underpinnings of segregation are present in a system where individuals simply want to avoid being in too extreme a minority in their own local area.

Collective Action

When we work together…



4

If we don't do anything…

3

The Collective Action Problem

Consider the following scenario:

A country is ruled by a ruthless and unpopular dictator.

A large number of people would like to see the dictator removed, and are willing to take part in public protests if they thought such protests would work.

These individuals know that a protest will successfully remove the dictator only if the number of protestors is very large.

If the protest is too small, most protestors will be arrested and maybe never heard from again.

A protest is arranged. Should a potential protestor attend?

The Collective Action Problem

Whether an individual attends the protest is largely determined by whether they know that large numbers of others will attend.

If they don't know this, then they probably won't risk attending.

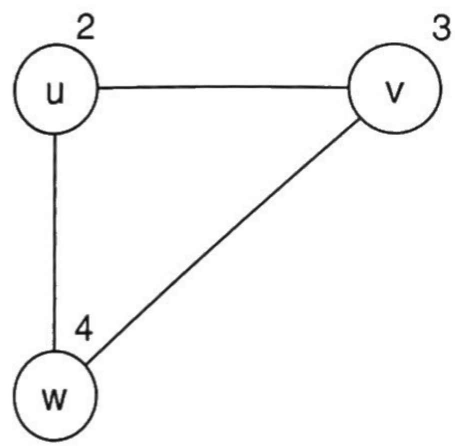
This is why dictatorial governments try to limit communication among the citizens. If citizens don't know that they are in the majority with their views of the dictator and that many others will join a protest, they won't risk joining it themselves.

This is called pluralistic ignorance (thinking you are in the minority but actually being in the majority), and it occurs because of lack of communication.

This is a network problem.

A Model for Collective Action

Suppose that 3 members of a board of directors are thinking about confronting a CEO of a company about some potentially unethical behavior that they believe the CEO is engaged in.

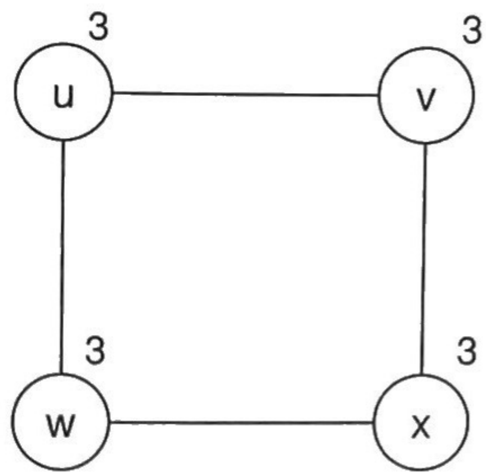


Individual *u* will only confront the CEO if 2 board members (including *u* itself) will go. For individuals *v* and *w* the thresholds are higher, 3 and 4. They each know a neighbor's threshold.

Do they go? No. Node *w* won't go, neither will *v* since it knows w won't go, and therefore *u* won't go since it knows that neither *v* nor *w* will go.

A Model for Collective Action

Same scenario, but with different board members.



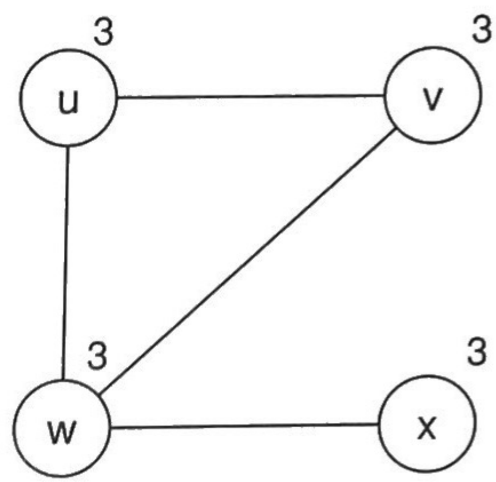
Will they confront the evil CEO?

No. Node *w* knows that its threshold, as well as those of *x* and *u* are 3, so there are enough for it to feel confident. However, *w* doesn't know *v*'s threshold, which could be something like 5. So it can't be sure that either *u* or *x* will feel confident enough to go. So *w* won't go. Due to symmetry, neither will the other nodes.

This attempt at collective action failed even though there were more willing participants than any node required. They just did not know it.

A Model for Collective Action

In the final scenario, let's make a change in one edge.



Will they confront the evil CEO?

Yes! Now *u*, *v*, and *w* know that there are enough willing participants, and they know that those participants know that. So these three will confront the CEO.

The Advantage of Common Knowledge

This example points out the advantage of common knowledge. The deciding factor in the collective action was the fact that the participants *knew that the other participants would act*. This knowledge required the right social network structure.

The example also points out that there are advantages to having strong ties in a social network. Weak ties are good for passing information, but not for supporting collective action.

The End