Epidemics

CMPS 17

Theresa Migler-VonDollen

Epidemics

Epidemics

We will only be discussing contagious diseases caused by biological pathogens:

- Flu
- Measles
- HIV
- Ebola
- Bubonic plague
- The common cold

Epidemics

What determines how devastating a disease will be?

- contagiousness
- length of infectious period
- severity

Suppose a disease existed on an island with no connection to the outside world.

- We must also consider the underlying social network.

Definition

In a *contact network*, there is a vertex for each person and an edge between two people if they come in contact with one another in a way that makes it possible for the disease to spread between them.

Epidemics

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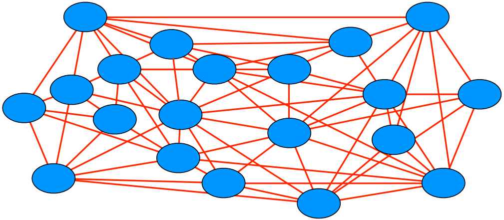
Consider the subnetwork of the contact network involving the common cold and the people in a dormitory.

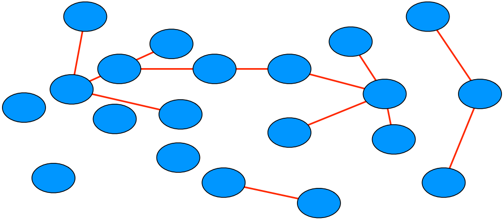


Epidemics

Definition

In a *contact network*, there is a vertex for each person and an edge between two people if they come in contact with one another in a way that makes it possible for the disease to spread between them.

Consider the subnetwork of the contact network involving an STD and the people in a dormitory.



Epidemics

The diffusion of ideas is similar to the spread of disease.
The process of spreading ideas is referred to as “social contagion”.
Most of the discussion that we have for epidemics applies immediately the diffusion of ideas.

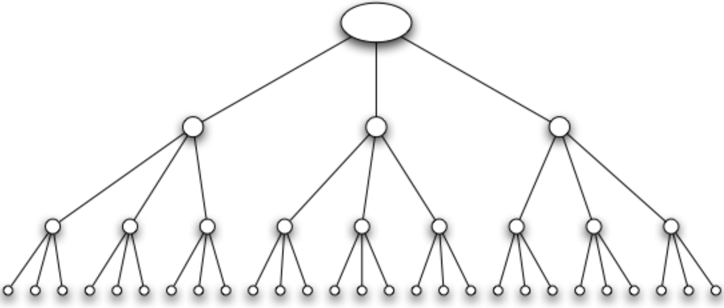
Branching processes

Most simple model of contagion.

- A person carrying a new disease enters a population and transmits it to each of the k people he meets with probability p. Call these k people the *first wave*.
  Some of the people in the first wave get infected, some don't.
- Suppose each person in the first wave goes into the population and meets k different people. These k^2 people are the *second wave*.
  Each infected person in the first wave passes the disease on to each person they encounter with probability p.
- Continue in this manner.

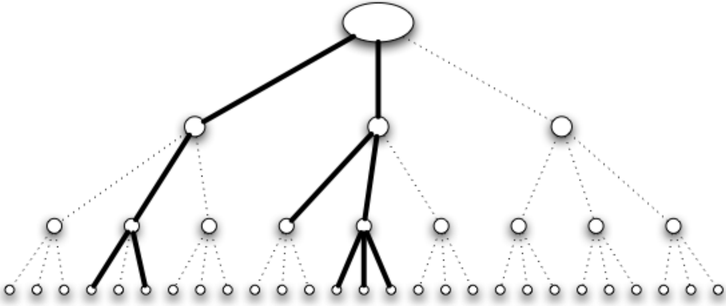
Branching processes

For example, if $k = 3$, our contact network has the form:



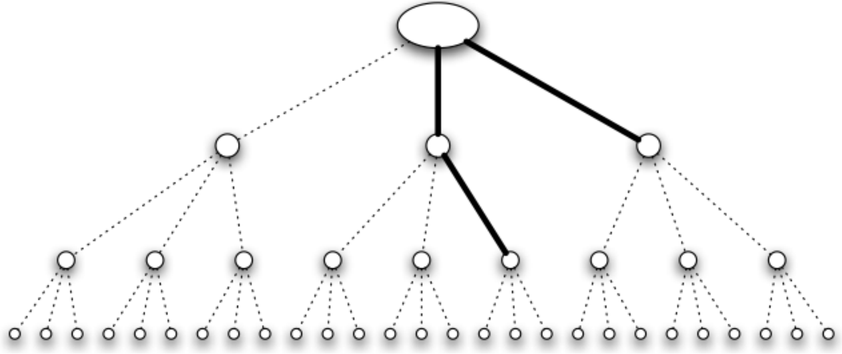
Branching processes

Suppose that the disease modelled in our contact network is highly aggressive:



Branching processes

If the disease modelled in our contact network is milder. It might die out:



Basic reproductive number

There are only two possibilities for a disease in the branching process model:

- It reaches a wave where it infects no one.
    - It dies out over a finite number of steps.
- It continues to infect people at every wave.
    - It continues indefinitely through the contact network.

The *basic reproductive number* can predict which case a disease will fall in.

Basic reproductive number

Definition

The *basic reproductive number*, R_0, is the expected number of new cases of the disease caused by a single individual.

For the branching model described above, $R_0 = pk$.

Theorem

If $R_0 < 1$, then with probability 1, the disease dies out after a finite number of waves.
If $R_0 > 1$, then with probability greater than 0 the disease persists by infecting at least one person in each wave.

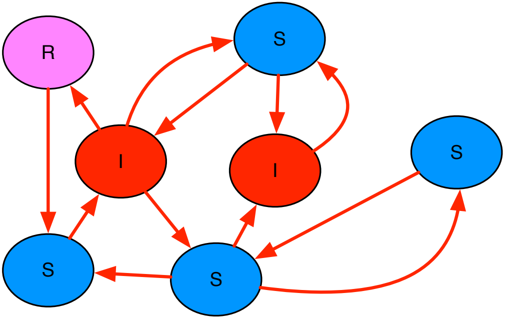
The interesting case is when $R_0 \approxeq 1$
When $R_0 \approxeq 1$ governments spend a lot of money and resources to bring p down.

SIR epidemic model

This is a more general model for epidemics.
It can be applied to any contact network.
Three possible stages for each individual:

- *Susceptible*: Before the individual has caught the disease it is susceptible to infection.
- *Infectious*: Once the individual has caught the disease, it is infectious and has some probability of passing the disease on to its susceptible neighbors.
- *Removed*: Once an individual has experienced the full infectious period, this individual is removed (no longer poses a threat).

SIR epidemic model



SIR epidemic model

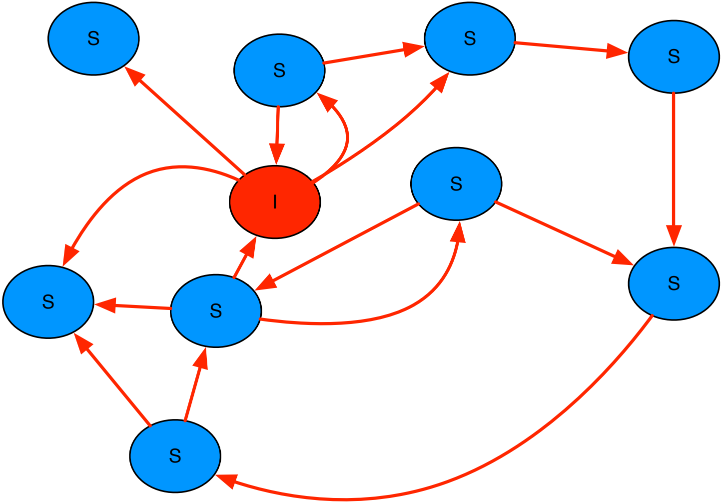
Let p be the probability of infection and t be the length of the infection.

The epidemic progresses as follows:

- Initially some individuals are in the infectious state and all others are in the susceptible state.
- Each individual, v, that enters the infectious state remains infectious for t steps.
- During each of these t steps, v has a probability p of passing the disease to each of its susceptible neighbors.
- After t steps, v is no longer infectious or susceptible, so it is removed.

SIR epidemic model

Suppose $p = .3$ and $t = 2$.



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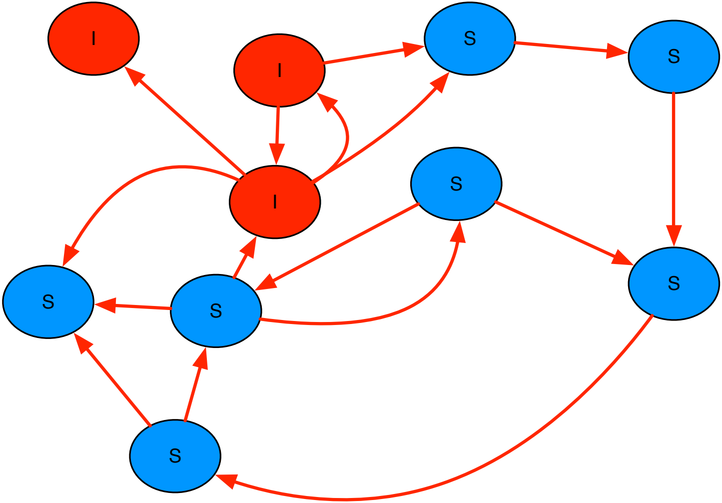

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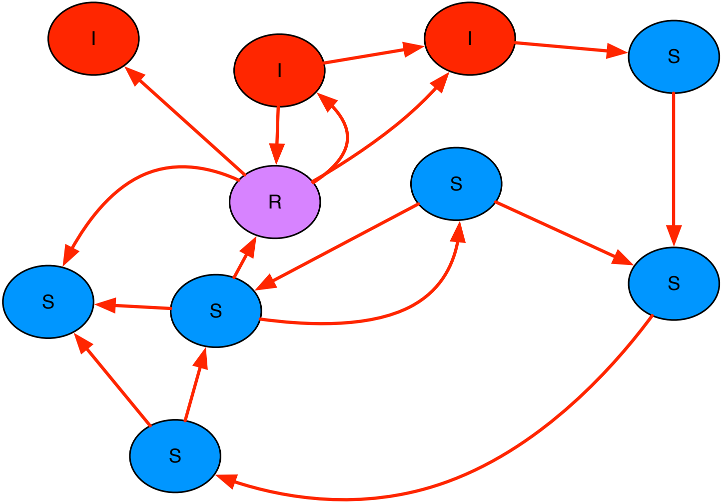

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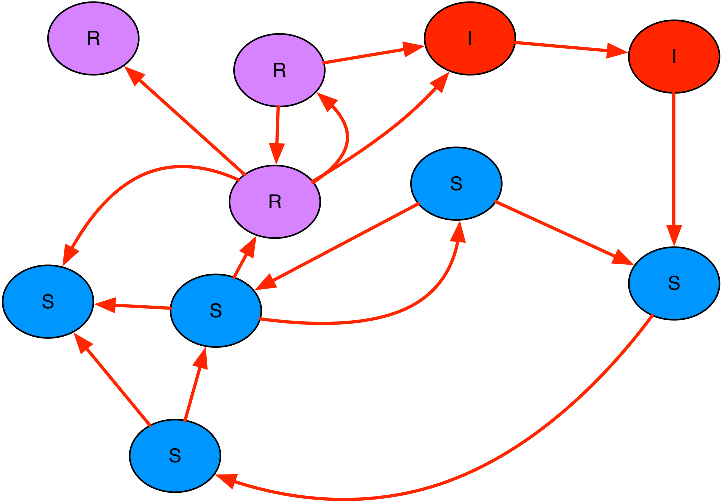

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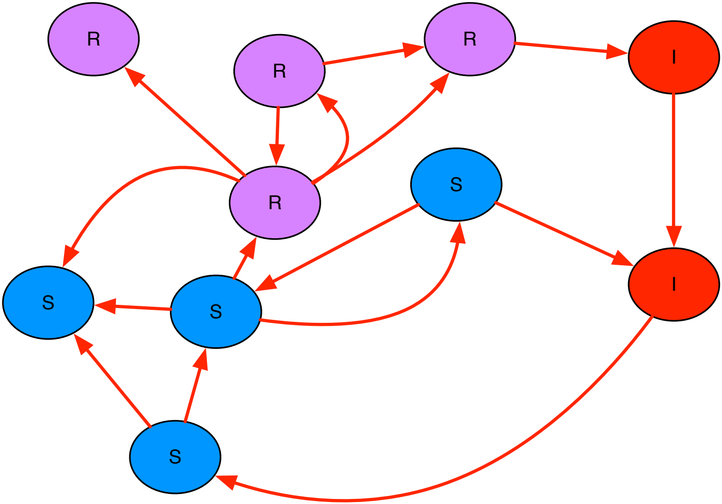

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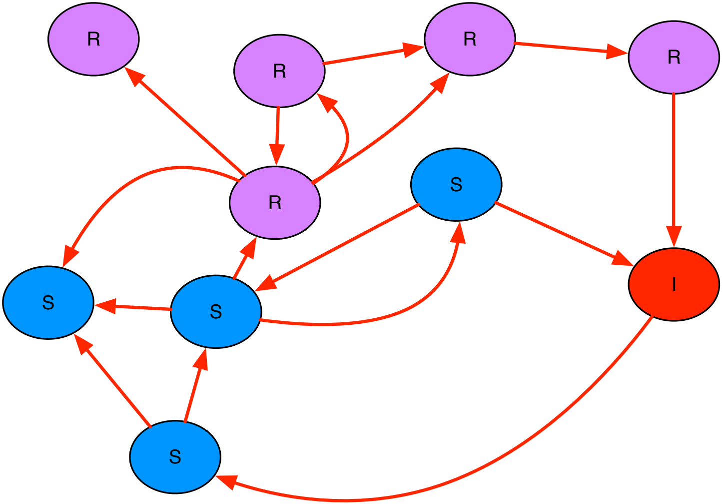

SIR epidemic model

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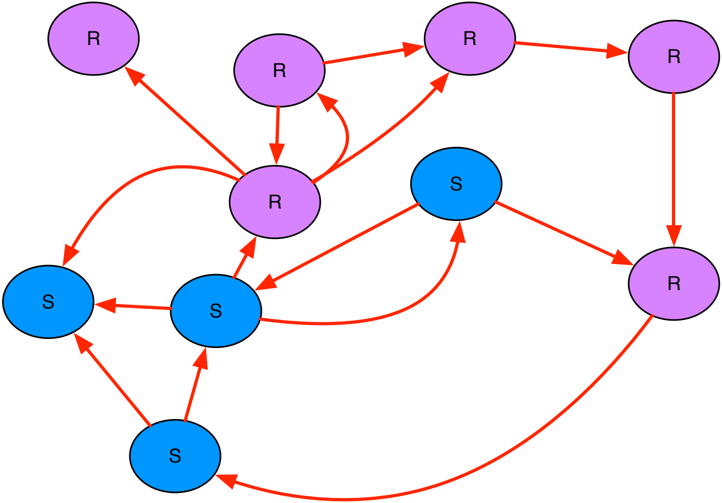


SIR epidemic model

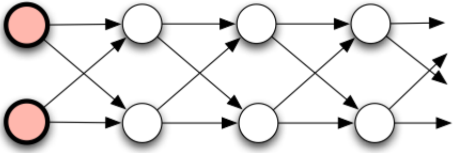
Extensions:

- You are more likely to spread a disease to someone who you are in close contact with, like a roommate, rather than a store clerk.
  Let $p_{u,v}$ be the probability that individual u infects individual v.
- Can also vary the length of infectiousness for each individual.
- Could also break the infectious state into substates: early, middle, and late and vary the probability of infecting for each stage.

R_0 in the SIR epidemic model

Recall that R_0 is the expected number of new cases of a disease caused by a single individual.

Suppose, in the following network, that $t = 1$ and $p = 2/3$.



Here, the expected number of new cases caused by each individual is $4/3$. So $R_0 > 1$.

But it is very likely that this disease will die out after a finite number of steps.

SIS epidemic model

Suppose that there is a disease where one can be infected multiple times.

In this model there is no removed state, just infectious and susceptible.

The models progresses very similarly to the SIR model:

- Initially some individuals are in the infectious state and all others are in the susceptible state.
- Each individual, v, that enters the infectious state remains infectious for t steps.
- During each of these t steps, v has a probability p of passing the disease to each of its susceptible neighbors.
- After t steps, v is no longer infectious, instead of being removed v goes back to the susceptible state.

There are ways represent a SIS epidemic as a SIR epidemic.

Synchronization

Sometime types of diseases lend themselves to large outbreaks, or strong oscillations in the number of infected individuals over time. These strong oscillations happen often for diseases such as measles and syphilis.
The synchronization of a disease occurs because of:

- Temporary immunity.
- Long range connections

Synchronization - the SIRS model

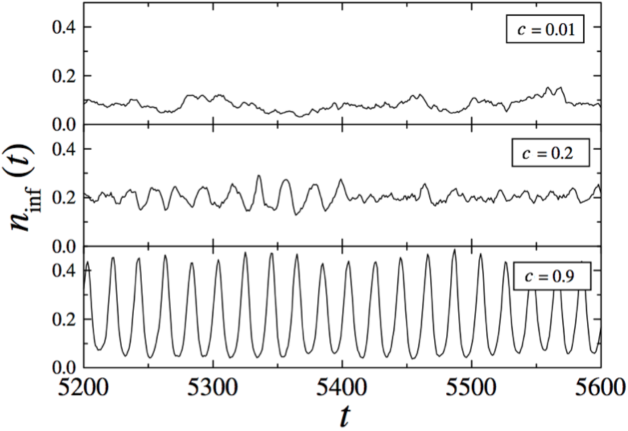
In the SIRS model an epidemic proceeds as follows:

- Initially some individuals are in the infectious state and all others are in the susceptible state.
- Each individual, v, that enters the infectious state remains infectious for t steps.
- During each of these t steps, v has a probability p of passing the disease to each of its susceptible neighbors.
- After t steps, v is no longer infectious, it enters the removed (recovered) state for t_R steps. During this time, v cannot be infected nor can it infect. After t_R steps it goes back to the susceptible state.

Synchronization - small-world contact networks

Watts and Strogatz created a small world network as we discussed before.

Let c be the probability of rewiring an edge.



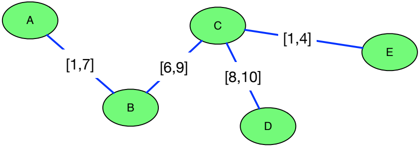
Transient contacts

For diseases that spread quickly through populations we can (and did) consider contact networks to be static.
However for many diseases that spread slowly through populations, we need to consider dynamic contact networks.

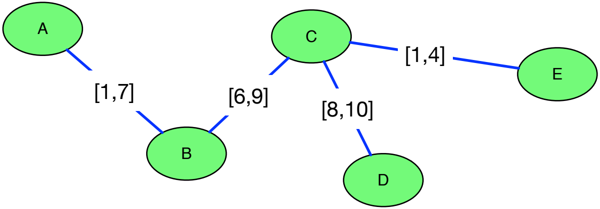
Definition

In a contact network a contact (an edge) is *transient* if it only exists for a particular window of time.

Now we annotate our contact network with the period of time which two individuals are in contact.



Transient contacts

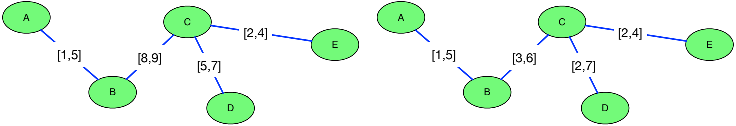


Can *D* infect *A*? Can *D* infect *B*?

Concurrency

Definition

An individual is involved in a *concurrent* partnership if he or she is involved in two or more active partnerships that overlap in time.



Same underlying contact network.
But a disease may spread to everybody in the second network at time $t = 3$.

Genetic inheritance

- In 1987 Cann, Stoneking, and Wilson published some interesting results in *Nature*.
- If we consider our maternal *lineage* we find that all lineages meet at a single woman.
- We call this woman our *Mitochondrial Eve*.
- She probably existed between 100,000 and 200,000 years ago, probably in Africa.

Genetic inheritance

What does this mean?

- It does not mean that when our Mitochondrial Eve was around that she was the only woman at that time, there were likely many other women.
- Although the mitochondrial DNA of other women wasn't passed down, their other genetic traits likely were.
- We find in fact that this isn't surprising.

Wright-Fisher model

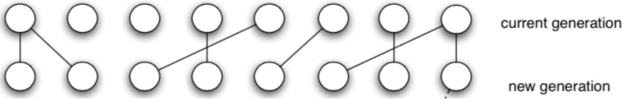
This is a model of single parent ancestry:

- It can model species that engage in asexual reproduction.
- It can model the inheritance of certain properties in sexual reproducing populations.
- It can be used to model “social” inheritance.

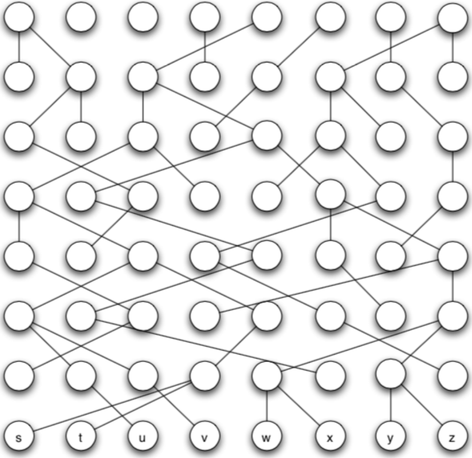
Wright-Fisher model

Simplifying assumptions:

- Suppose that the population is constrained to have a fixed size, N, for each generation.
- Each new generation is formed by having the current set of individuals produce N offspring in total.
- Each offspring in the new generation is produced by a single parent, and this parent is selected independently and uniformly at random from among those in the current generation.



Mitochondrial Eve



Is there a common ancestor?

Mitochondrial Eve