

Topic 4: Epidemics

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How epidemics spread

The spread of a disease depends on the properties of the **pathogen** that carries it:

- how **contagious** it is,
- the length of its **infectious period**,
- its severity,

but also on the **network** structure of its affected population.

In the **contact network** of a population, nodes are joined whenever two people come into contact in a way that allows the disease to pass from one to the other.

Even within the same population, different pathogens can lead to different networks.

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Modelling Epidemics

Epidemics:

- Nodes do not make decisions.
- Complex process.
- Transmission from node to node is not observable.

We will therefore model epidemics as a **random** process. If two people are linked in a contact network and one is infected, then there is a certain **probability** that they will infect the other.

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A simple model: Branching Process

First wave

- A person carrying a disease **transmits** it to each person he meets with probability p .
- He meets k people while he is **contagious**.

Second wave

- Each person carrying the disease in the first wave **transmits** it to each person he meets with probability p .
- And they each meets k different people while **contagious** (creating a second wave of k^2 people).

and so on

For which values of p and k does the epidemic die out after a finite number of waves. When will it run forever?

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Basic Reproductive Number

- The **basic reproductive number** R_0 is the expected number of new cases of a disease caused by one individual.
- So $R_0 = pk$ for the branching process.

Theorem

If $R_0 < 1$, then with probability 1, the disease dies out after a **finite** number of waves.

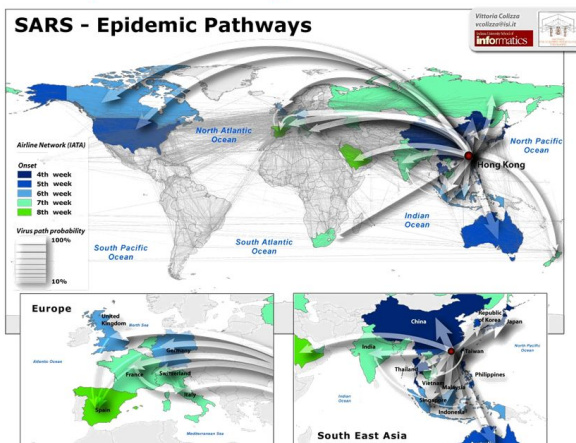
If $R_0 > 1$, then with probability greater than 0, the disease persists by infecting at least one person in each wave.

This suggests that if R_0 is close to 1, public health measures can have significant impact. Possible measures:

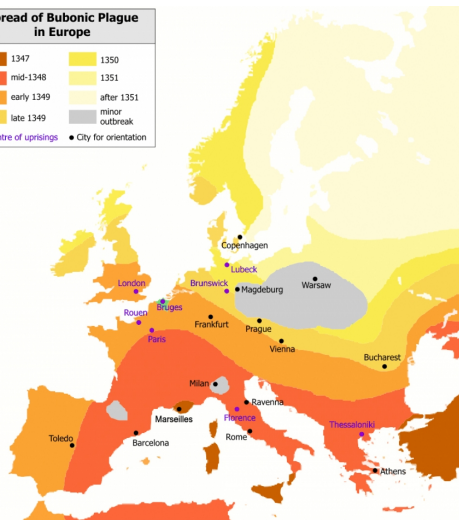
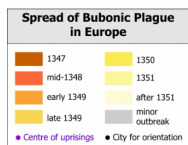
- quarantine (reduce k),
- change behaviour (reduce p).

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Worldwide spread of SARS through international airline network



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SIR Epidemic Model

This model can be applied to any **contact network**: that is any directed graph where the an edge from u to v indicates that if u becomes infected, the disease has the potential to spread to v .

An individual node passes through three states

- **Susceptible (S)**: before a node has caught the disease, it is susceptible to infection from its neighbours.
- **Infected (I)**: once the node has caught the disease it is infectious and has some probability of infecting each of its susceptible neighbours.
- **Removed (R)**: once a node has reached the end of the infectious period it can be considered to be no longer part of the network as it has no further effect on the spread of the disease since it can no longer infect its neighbours but nor is it susceptible to infection.

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SIR Model

Progress of the epidemic is influenced by

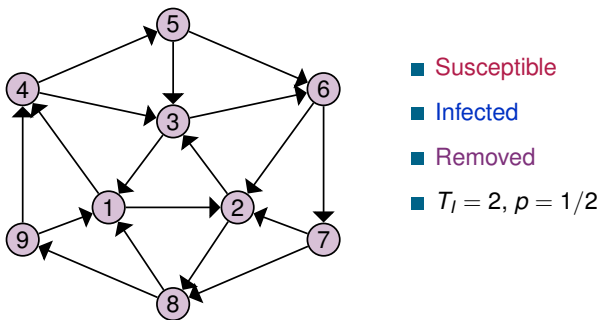
- the **structure** of the network,
- two parameters:
 - the **probability** of transmission, p ,
 - the **length** of infection, t_i .

The process:

- Initially some nodes are in state **I** and others are in state **S**.
- Each node v that enters **I** remains infectious for a fixed number of time steps t_i .
- During each of the t_i steps, v has probability p of passing the disease to each of neighbours in **S**.
- After t_i steps, v enters state **R**.

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Example



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Basic Reproductive Number Revisited

- The **basic reproductive number** $R_0 = pk$ is the expected number of new cases of a disease caused by one individual.
- For the branching process we saw that whether or not the disease persists depends on whether or not $R_0 > 1$.
- Are there networks where $R_0 > 1$ but the disease will **not** propagate through the network?

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SIR Epidemics and Percolation

In the $t_I = 1$ case, epidemics can be viewed as a **static** process!

- In this case, each node has one chance to infect a neighbour.
- This event happens with probability p — so we can determine whether it happens with the flip of a (biased) coin.
- But we can flip the coin for each edge at the start. Then we divide the edges into **open** and **closed**.
- To see how the epidemic spreads we just look at which nodes can be reached along open edges.

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An Epidemic Model with Vaccinations

An extension of the SIR model. A first attempt.
There is one additional state.

- **Vaccinated (V)**: a node that is susceptible can become vaccinated and is considered to be no longer part of the network.

This assumes that vaccinations are perfect. If this is the case, then it is not necessary to define a new state.

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An Epidemic Model with Vaccinations

We need **two** new states:

- **Vaccinated (V)**: a node that is susceptible can become vaccinated and remains susceptible to infection.
- **Vaccinated and Infected (VI)**: a vaccinated node can catch the disease and become infectious and has some probability of infecting each of its neighbours in **S** and **V**.

and to update the parameters:

- the probability $p(I, S)$ of transmission from a node in **I** to a node in **S**,
- the probability $p(I, V)$ of transmission from a node in **I** to a node in **V**,
- the probability $p(VI, S)$ of transmission from a node in **VI** to a node in **S**,
- the probability $p(VI, V)$ of transmission from a node in **VI** to a node in **V**,
- the length of infection, t_I .

How do vaccinations affect infection rate?

- Depends on the different probability parameters?
- Does the network structure matter?
- Does it matter which nodes are vaccinated?

See the coursework ...

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SIS Epidemic Model

This model can also be applied to any **contact network**. Nodes can now be infected **multiple** times.

An individual node alternates between two states

- **Susceptible (S)**: a node is susceptible to infection from its neighbours.
- **Infected (I)**: once the node has caught the disease it is infectious and has some probability of infecting each of its susceptible neighbours.

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SIS Model

Progress of the epidemic is influenced by

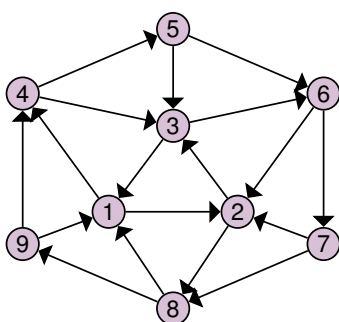
- the **structure** of the network,
- two parameters:
 - the **probability** of transmission, p ,
 - the **length** of infection, t_I .

The process:

- Initially some nodes are in state **I** and others are in state **S**.
- Each node v that enters **I** remains infectious for a fixed number of time steps t_I .
- During each of the t_I steps, v has probability p of passing the disease to each of neighbours in **S**.
- After t_I steps, v reenters state **S**.

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Example



- **Susceptible**
- **Infected**
- $T_I = 2, p = 1/2$

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SIR vs SIS

- An SIR epidemic on a finite graph must come to an end. There is a **limited** supply of nodes that can be infected.
- An SIS epidemic can run for a long time as the disease cycles through nodes **multiple** times.
- But an SIS epidemic cannot run **forever** if $p < 1$. Eventually there will be t_I consecutive steps when the contagion is not passed to a susceptible node.
- Whether an SIS epidemic persists or dies out quickly can depend critically on p .

Can we represent an SIS epidemic with an SIR network?

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A further refinement: SIRS Epidemic Model

An individual node is in one of three states

- **Susceptible (S)**: susceptible to infection
- **Infected (I)**: can infect neighbours
- **Recovered (R)**: can not be infected

There are three parameters:

- the probability of **transmission**, p , the length of **infection**, t_I , and the length of **recovery**, t_R .

The process:

- Initially some nodes are in state **I** and others are in state **S**.
- Each node v that enters **I** remains infectious for t_I steps.
- During each of the t_I steps, v has probability p of passing the disease to each of neighbours in **S**.
- After t_I steps, v enters state **R**.
- After a further t_R steps, v reenters state **S**.

In the SIRS model, what is the rate of infection over time?