How can Mathematical Models be used to Exchange Information about a Disease Outbreak?
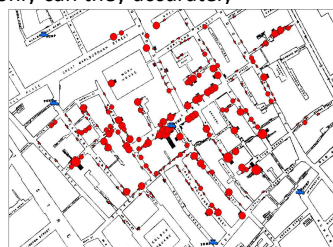
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- Public health is a relatively new area of study within medicine, as its importance was brought into light during the mid-nineteenth century cholera epidemics.
- Nowadays, public health and epidemiology are considered an essential part of modern medicine.
- The idea of tracking and modelling a disease's spread is also recent. John Snow's 'disease mapping' was a simple geographical technique of identifying an outbreak's source and journey, and was the first example of this.
- Today, intricate mathematical systems are used to model a disease's spread instead. Not only can they accurately predict a disease's trajectory, but they also allow for information about the disease's activity to be exchanged to health authorities – allowing for informed control decisions to be made.

John Snow's 'disease map' of cholera cases around Broad Street, London, 1854

Basic Model:
- Let's first imagine that a single person in a population is infected with the disease we are analysing. Assuming the rate of transmission from one person to another is constant, it will take a certain time t for the person to infect another.
- This means after time t, the total number of infected people will have doubled. This pattern is followed constantly, meaning the number of people infected will double every unit time t.
- The total number of infected people in the population can therefore be modelled with the function:

Which can be re-written as: $N = 2^t$

This means its derivative can be calculated: $N = e^{\ln(2)t}$

$$dN/dt = \ln(2)e^{\ln(2)t} = \ln(2)2^t$$

This allows the disease's rate of transmission to be calculated for each given time t – allowing for data about the spread of the disease to be exchanged to authorities.

However, this model is only valid if we assume:
- Everybody in the population is susceptible to the disease.
- Nobody who becomes infected makes a recovery or dies.
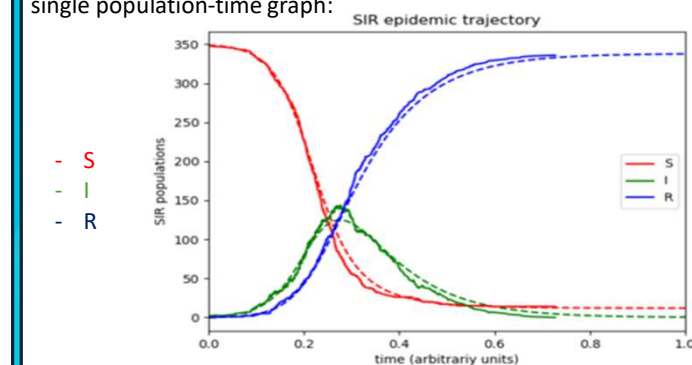- The rate of transmission from one person to another is constant.

Realistically, these three assumptions are false for all epidemics, meaning a more complex model that is not based on these assumptions must be constructed.

SIR Model
- The basic form of this mathematical model forms the basis of all epidemic models used today. It functions by splitting a given population (N) into three different categories: susceptible (S), infected (I), and removed (R) – so that S + I + R = N.
- A system of three nonlinear ordinary differential equations is then constructed, with each category having its separate one.
- Like the previous one, this model follows assumptions about the population and rates of disease transfer. However, these assumptions are much more realistic.

$$S \xrightarrow{\beta} I \xrightarrow{\gamma} R$$

1. The first differential equation is for the rate of change of susceptibles:

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

S = total susceptible
I = total infected
β = rate of contact between S and I
t = time

- It follows the assumption that the disease's transmission rate remains proportional to the contact time between the susceptibles and infectives – so the product of S and I is used.
- The equation is negative because the number of susceptibles decreases with time as they become infected with the disease as the epidemic grows.

2. The second differential equation is for the rate of change of infectives:

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

γ = removal rate of infectives

- This equation follows the assumption that the removal rate of infectives (recoveries and deaths) remains constant.
- The 'βSI' term is just a follow up from the previous equation – the rate of decrease of susceptibles is the same as the rate of increase of infectives.
- The '- γI' term is the rate of decrease of infectives as they move to the recovered category. Following the previously stated assumption, 'b' is the constant representing the rate of this.

3. The third differential equation is the rate of change of removals:

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

Much like 'βSI', 'γI' is a follow up of the rate of decrease of infectives, as they move to the recovered category at the same rate they leave the infected category.

The entire differential equation system can be visualised on a single population-time graph:

- S
- I
- R

How can this model exchange data?
- The value of the rate of change of infectives can be used to draw conclusions about the disease's activity: if 'βSI – γI' is greater than zero, the number of infections will increase with time and the disease will spread. The ideal scenario is for 'βSI – γI' to be less than zero, which means the number of infections will decrease with time and the epidemic will eventually end.
- If we eliminate the constant 'I', we are left with with 'βS – γ < 0'. If the 'γ' term is moved to the right side and both sides are then divided by 'γ', we are left with 'βS/γ < 1'. The value of this inequality determines whether a disease spreads or dies out – and this can be used exchange information about the future of the epidemic.
- If the inequality holds, the disease will die out. So, health authorities such as the NHS will take measures to minimise the value of 'βS/b'. This is done by:
  - Minimising the rate of contact between susceptibles and infectives (β). Methods include: isolating, wearing face coverings, and washing hands – all of which was encouraged by the UK Government and NHS during the Covid-19 Pandemic.
  - Minimising the number of people susceptible to the disease by providing vaccinations to the population, starting with the most vulnerable people (e.g. people over the age of 70). Being vaccinated against a disease eliminates your susceptibility to it.
  - Maximising the removal rate of infectives (γ) by speeding up recovery from the disease. For example, giving infectants ventilators to maximise their respiratory air flow encourages their recovery to diseases.