# Compartmental models of infectious disease dynamics

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# Overview

• Disease outbreaks of acquired immunodeficiency syndrome, severe acute respiratory syndrome, pandemic H1N1, H7N9, H5N1, Ebola, Zika, Middle East respiratory syndrome, and recently COVID-19 have raised the attention of the public over the past half-century;

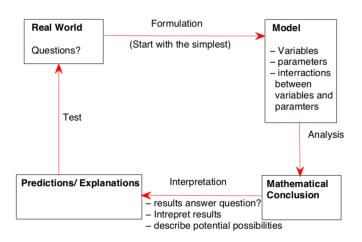
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- The emergence and reemergence of neglected tropical diseases continue to pose significant challenges to humanities and societies;
- Revealing the characteristics and epidemic trends are important parts of disease control;
- The biological scenarios including transmission characteristics can be constructed and translated into mathematical models, which can help to predict and gain a deeper understanding of diseases.

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# The interface between infectious diseases and mathematical modelling



• dynamics of infectious diseases;

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# Summary

understand the general principles, assumptions and basic techniques used in mathematical models for infectious diseases, appreciate the value and limits of mathematical models and explore the behavior of different structures.

#### Mathematical model

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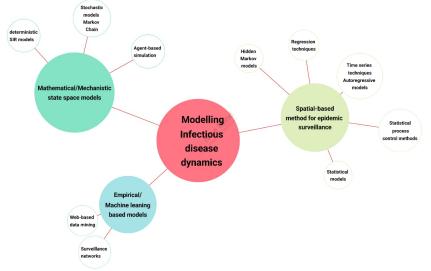
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- A. Einstein: Everything should be made as simple as possible, but not simpler;

# Model types

Influenced by the scientific question of concern - research question



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### What models can do?

#### Prediction

- Guiding difficult policy decisions where a trade-off between alternative control strategies exists;
- Predict epidemic thresholds;
- Estimate critical parameters;

### What models can do?

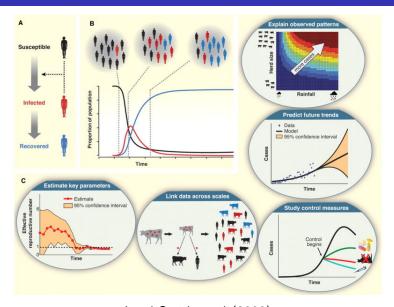
#### Prediction

- Guiding difficult policy decisions where a trade-off between alternative control strategies exists;
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### Understanding

- How various complexity affect the dynamics;
- The risks associated with the global spread of infectious diseases.
- A framework for examining disease features in a fairly robust and generic way;
- Understanding gained can help to build more sophisticated predictive models;

# What models can do? ...



# Modelling process

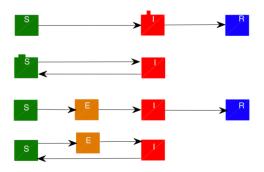
- Models are designed to address scientific questions Rule of thumb
  - Choose the simplest model that explains observed phenomena (data)
  - Choose a model that is able to answer the question of interest
  - Model development can be an iterative process based on new observations or omissions

# Formulating an model

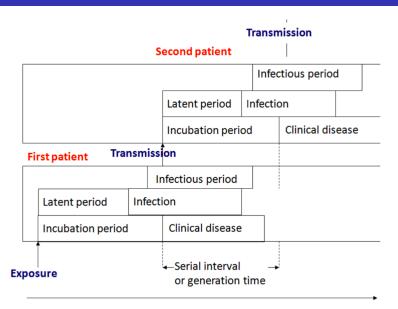
- Specify the <u>state variables;</u>
- Specify the *processes affecting* the state variables;
- Specify the process rates of the state variables;
- Produce the <u>dynamic equation</u> specifying the 'state variables' change over time.

# Specifying the state variables

- epidemiological compartmental structure:
  - SI, SIS, SEI, SEIS, SIR, SIRS, SEIR, SEIRS;
  - More classes can be added: P (passively immune), A (asymptomatic infectives), C (carriers), V (vaccinated), SS (Super Spreaders);



# Stages of infection according to time



# Specifying the **state variables**

- Susceptible no pathogen present;
- Exposed host encounters infected individuals, infected with the pathogen which grows over time but no obvious signs of infection low pathogen load;
- **Infectious** level of parasite grows and individual has high potential to transmit infection to other individuals;
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- Demographics birth, death, migration;
- Waiting times in compartment;
- recovery from infection immune/non-immune;

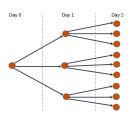
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### Sequence of cases

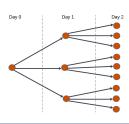
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### Geometric progression model

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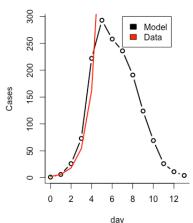
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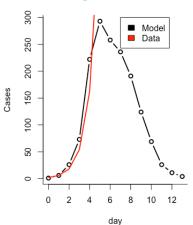
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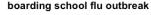


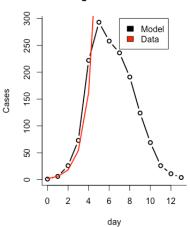
### Glory

It predicts the initial phase of the outbreak.

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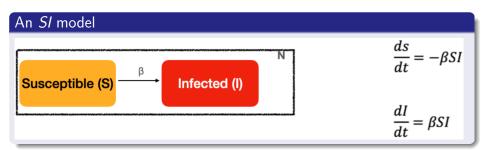


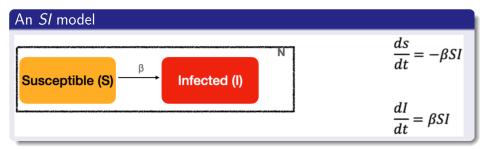
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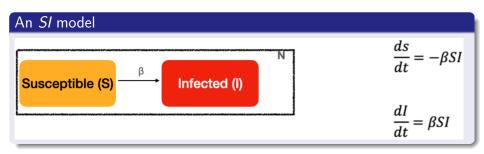
### Misery

- The model predicts exponential growth infinitely;
- It fails to capture the turn down;
- It missed the disease biology (what exactly?);





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- Separate total population in groups;
- Keep track of each individual in each group;
- Include epidemiological processes;
- Overall rate of new infections depend on S and I;

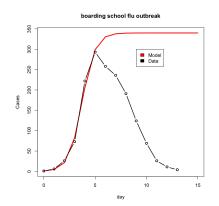


### SI model

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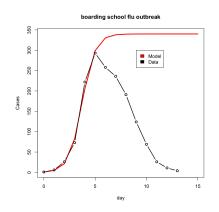
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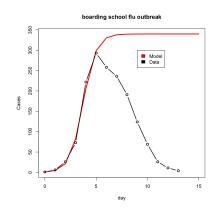


### Glory

- It predicts the initial phase of the outbreak;
- Epidemic no longer grows without bounds;

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- It fails to capture the turn down;
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# Building a simple SIR model

- Some model assumptions and simplifications;
  - The populations is well-mixed.
  - It is spatially homogeneous.
- This defines implicitly time and space scales;
- Then, we classify individuals in three compartments:
  - S susceptibles;
  - I infectious ( we will use 'infected' interchangeably);
  - R recovered (including immune and dead);
- From population biology point of view, we have a structured population;

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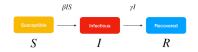
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- That is, we assume that the time scale of disease spread is sufficiently fast so as not to be affected by population births and deaths;
- If this is the case, we can take the population as a constant, *N*, (note that this case is valid for a wide range of both communicable and non-communicable diseases).

# The Kermack & McKendrick (1927) model



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$$\frac{dS}{dt} = -rSI \tag{1}$$

$$\frac{dl}{dt} = rSl - \gamma l \tag{2}$$

$$\frac{dR}{dt} = \gamma I \tag{3}$$

### Model description

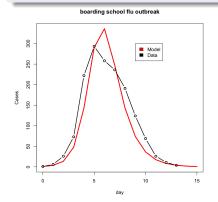
- The per capita rate of change of susceptibles is proportional to the number of infected, where *r* is the infection rate.
- The per capita rate of change of the infected is proportional to the number of susceptibles minus a factor accounting for the removal.
- The rate of change of the recovered is proportional to the number of infected.

### SI model

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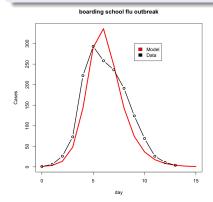
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# Glory

- It predicts the initial phase of the outbreak;
- It predicts the entire course of the outbreak with just parameters;
- Including recoveries allows to capture the overall "shape";

### SIR model extensions



### Coronavirus case

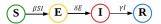
If you live with others and you are the first in the household to have symptoms of coronavirus, then you must stay home for **7 days**, but all other household members who remain well must stay home and not leave the house for **14 days**. why?

### SIR model extensions

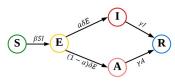


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- delay between infection and symptoms;
- delay between infections and infectiousness;



### Problem - tutorial sessions

Consider an SIR epidemic model and extend it by assuming that there a treatment for infection once a person has been infected. Model this by supposing that a fraction  $\gamma$  per unit time of infectives is selected for treatment, and that treatment reduces infectivity by a fraction  $\delta$ . Suppose that the rate of removal from the treated class is  $\eta$ .

### Problem - tutorial sessions

Formulate a model to describe the course of an epidemic when control measures are begun under the assumptions:

- **①** Exposed members may be infective with infectivity reduced by a factor  $\epsilon_E$ ,  $0 \le \epsilon_E < 1$ .
- **②** Exposed members who are not isolated become infective at rate  $\kappa_1$ .
- We introduce a class Q of quarantined members and a class J of isolated members.
- ① Exposed members are quarantined at a proportional rate  $\gamma_1$  in unit time (in practice, a quarantine will also be applied to many susceptibles, but we ignore this in the model). Quarantine is not perfect, but reduces the contact rate by a factor  $\epsilon_Q$ . The effect of this assumption is that some susceptibles make fewer contacts than the model assumes.
- ullet There may be transmission of disease by isolated members, with an in- fectivity factor of  $\epsilon_J$  .

### Problems - tutorial session . . .

- **1** Infectives are diagnosed at a proportional rate  $\gamma_2$  per unit time and isolated. In addition, quarantined members are monitored and when they develop symptoms at rate  $\kappa_2$  they are isolated immediately.
- ② Infectives leave the infective class at rate  $\alpha_1$  and a fraction  $f_1$  of these recover, and isolated members leave the isolated class at rate  $\alpha_2$  with a fraction  $f_2$  recovering.

End Lecturer One!

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# The End