

Simple Introduction to Mathematical Modelling of Infectious Diseases

Andree Valle Campos and Abdoelnaser M Degoot
Epiverse-TRACE Team @ LSHTM

November 21, 2024

1 Introduction

This practical aims to assess your understanding of the fundamental principles of mathematical modeling while guiding you in constructing models using a simple SEIR framework for infectious disease outbreaks.

Note: Please fill in the blanks.

2 SEIR Model

In the SEIR model, we have four compartments (S , E , I , R):

- S stands for _____, meaning _____.
The parameter that explains the transition from (S) compartment to (E) compartment is _____.
- E stands for _____, meaning that it can _____.
The rate that explains the transition from (E) to (I) is the rate of _____.
- I stands for _____, meaning that it can _____.
The rate that explains the transition from (I) to (R) is the rate of _____.
- R stands for _____. This compartment includes those who have ceased to be infectious and acquire immunity against infection, regardless of the clinical course.

3 R_0

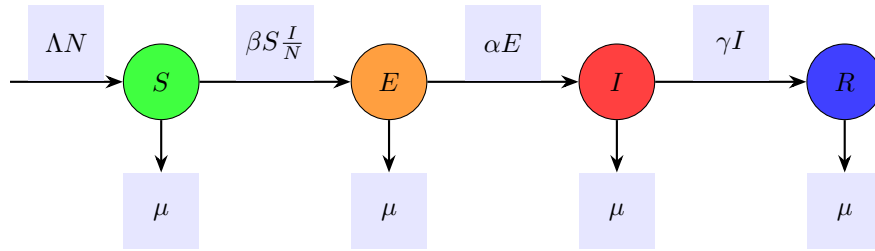
R_0 helps project the potential size of an epidemic and calculate the herd immunity threshold. It is defined as the average number of _____ secondary cases generated from a primary case in a completely _____ population.

4 R_t

R_t helps monitor the progress of the epidemic. When the population is no longer _____, the instantaneous reproduction number R_t is used. This is defined as the average number of s_____ in a population composed of _____ and non-_____ individuals at time t .

5 A Diagram for Measles outbreak

Below is a typical SEIR model with demography (births and deaths). This is a simple model applicable to person-to-person infections in a homogeneously mixing population. Please carefully observe the model and examine the interactions with the equations in section 6. Use color codes or arrows to relate the diagram to the equations.



Where:

- β : Transmission rate
- α : Infectiousness rate, or rate of progression from exposed to infectious
- γ : Recovery rate
- μ : Death rate (natural death rate)
- N : Total population size, $N = S + E + I + R$.

The parameter β , defined as the average rate at which infectious individuals can infect susceptibles, is derived from the multiplication of p and c , where p is the probability of transmission during contact, and c is the contact rate, defined as the average number of contacts per unit of time.

If a transmission rate β equals 3, it means each infectious individual causes 3 new infections per day in a fully susceptible population.

Model parameters are often (but not always) specified as rates. The rate at which an event occurs is the inverse of the average time until that event. For example, in the SEIR model, the recovery rate γ is the inverse of the average

infectious period.

Values of these rates can be determined from the natural history of the disease. For example, if people are on average infectious for 8 days, then in the model, $1/8$ of currently infectious people would recover each day (i.e. the rate of recovery, $\gamma = 1/8 = 0.125$).

6 Equations

Note that in the diagram, arrows entering compartments are expressed as positive terms in the equations, while arrows exiting compartments are represented with negative terms. Based on the above diagram, deduce the following equations that describe this system:

Compartment Equations

- **S compartment:**

$$\frac{dS}{dt} =$$

- **E compartment:**

$$\frac{dE}{dt} =$$

- **I compartment:**

$$\frac{dI}{dt} =$$

- **R compartment:**

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

7 Parameters for the Measles outbreak

A parameter within a transmission model corresponds to a biological or social property of a dynamic system for a specific context. In this section we will give the elements to feed the parameters of a SEIR model for a Measles outbreak in Burkina Faso.

- The average latent period (or pre-infectious) for measles is around 8 days (Masters et al., 2023).
- The average infectious period lasts for 5 days (Masters et al., 2023).
- For measles the basic reproduction number typically ranges from 12 to 18, or even more (Fiona et al., 2017).
- A single infectious case is introduced into the population.

- The entire population, except for this one case, is initially susceptible. This assumption simplifies the model and allows us to explore the spread of infection in the absence of immunity. Although real populations typically have some immunity due to vaccination or prior infection. Also, no individuals are exposed or recovered at this moment.
- The population of Burkina Faso is approximately $N \approx 22.67$ million.
- The age structure of Burkina Faso is characteristic of a young population, with a majority of the population being under 25 years old. According to recent estimates (United Nations, 2023; Central Intelligence Agency, 2023); World Bank, 2023), the age structure is broken down as follows:
 - $[0 \rightarrow 15)$ years: ~ 44 ($43 - 45$)% of the population
 - $[15 \rightarrow 25)$ years: ~ 19.5 ($19 - 20$)%
 - $[25 \rightarrow 55)$ years: ~ 29 ($28 - 30$)%
 - $[55 \rightarrow 65)$ years: ~ 5 ($3 - 5$)%
 - $65+$ years : ~ 2.5 ($2 - 3$)%

8 Table of parameters

Please fill in the table below with the parameters described above. Additionally, please note that we will do the simulation for 120 days.

Parameter	Value	Definition
bf_pop	_____	Population size
S/N	_____	Proportion of Susceptibles
E/N	_____	Proportion of Exposed
I/N	_____	Proportion of Infectious
R/N	_____	Proportion of Recovered
V/N	_____	Proportion of Vaccinated
r0	_____	Basic reproduction number
latent_period	_____	Time between becoming infected and the onset of infectiousness (in days)
infectious_period	_____	Time between the onset and end of infectious viral shedding (in days)
transmission_rate	_____	Rate at which infectious individuals can infect susceptibles ($r0/infectious_period$)
infectiousness_rate	_____	Rate of progression from exposed to infectious ($1/latent_period$)
recovery_rate	_____	Rate of progression from infectious to recovered ($1/infectious_period$)
time_end	_____	Maximum number of timesteps over which to run the model (in days)
increment	_____	The size of the time increment (in days)

9 Computing R_0

The expression for the basic reproduction number (R_0) in the above system is given by:

$$R_0 = \frac{\mu}{(\mu + \alpha)} \frac{\beta}{(\mu + \gamma)}.$$

To calculate the R_0 value for given parameter values, write an R object called `MeaslesR0` that implements this formula. The function will use the following parameter values:

- $\mu = \frac{1}{75}$ (natural mortality rate)
- $\alpha = \frac{1}{10}$ (rate of progression from the exposed to the infectious stage)
- $\gamma = 1/8$ (recovery rate)
- $\beta = 1.8$ (transmission rate)

Then compute the final size of such epidemic.

10 About this document

We adapted this material from "Practical: building a simple compartmental model for Zika" by Zulma Cucunubá, Pierre Nouvellet, and José M. Velasco-España, 2024-01-10 (V.1.0.3.). License: CC-BY 4.0 by the authors. For more details, visit: <https://epiverse-trace.github.io/tutorials-late/LICENSE.html>