Practical 2: Compartmental Models to Equations

Sam Abbott

# Learning Objectives

1. How to translate a simple model flow diagram into equations
2. Understand how changing parameter values can change model dynamics
3. Using a simple model scaffold to develop a more complex model

# Outline for Session

1. Set up (5 minutes)
2. Explore the dynamics of a simple SEIR model (10 minutes)
3. Add high and low risk latency to a SEIR model (10 minutes)
4. Explore SHLIR model dynamics and compare to the SEIR model (10 minutes)
5. Extension: Translate your Model Flow Diagram to Equations (20 minutes)
6. Extension: Explore the parameter space of multiple models (20 minutes)(If having trouble with the previous excercises then skip to this point for an R free exercise)
7. Session wrap up (10 minutes)

# Excercises

## A Simple SEIR Model of Tuberculosis (TB)

As a first excericse we are going to run the simple SEIR model, as seen in the design a model practical, in R. As a first step you will need to load the following packages.

library(biddmodellingcourse)  
library(tidyverse)  
library(knitr)  
library(prettypublisher)

### Populations and Initialisation

We first set up the initial populations for the Susceptible (), Latent (), Infected (), and Recovered () compartments. We have initialised the model as an early stage epidemic with a single case of TB.

inits = c(  
 S = 999,  
 E = 0,  
 I = 1,  
 R = 0  
)

### Parameters

We then specify the model parameters (with the units being years), varying these paremeters will impact the model dynamics.

parameters <- c(  
 beta = 3, # Rate of transmission  
 gamma = 2, # Rate of progression to active symptoms   
 tau = 1/2, # Rate of recovery  
 mu = 1/81 # Rate of natural mortality  
)

### Equations

Finally we specify the model equations for each population compartment. This is model incorperates simple demographic processes with a constant natural death rate from all compartments which is equal to the birth rate into the susceptible compartment.

SEIR\_demo\_ode <- function(t, x, params) {  
  
 ## Specify model compartments  
 S <- x[1]  
 E <- x[2]  
 I <- x[3]  
 R <- x[4]  
  
 with(as.list(params),{  
  
 ## Specify total population  
 N = S + E + I + R  
  
 ## Derivative Expressions  
 dS = - beta \* S \* I / N - mu \* S + mu \* N  
 dE = beta \* S \* I / N - gamma \* E - mu \* E  
 dI = gamma \* E - tau \* I - mu \* I  
 dR = tau \* I - mu \* R  
  
 ## output  
 derivatives <- c(dS, dE, dI, dR)  
  
 list(derivatives)  
 })  
}

### Simulate and Summarise

To simulate the model we specify the starting year (begin\_time) and final year (end\_time) and define a sequence over all intervening years. The model is then solved using deSolve::lsoda which is used within a simple wrapper function (see ?solve\_ode for details). The resulting table summarises the simulation results for the first 5 years.

begin\_time <- 0  
end\_time <- 200  
times <- seq(begin\_time, end\_time, 1)  
  
## see ?solve\_ode for details  
SEIR\_sim <- biddmodellingcourse::solve\_ode(model = SEIR\_demo\_ode,   
 inits = inits,   
 params = parameters,  
 times = times,   
 as.data.frame = TRUE)  
SEIR\_sim %>%   
 head %>%   
 pretty\_table(caption = "First 5 years of model simulation",  
 label = "tab-1")

Table 1: First 5 years of model simulation

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| time | S | E | I | R |
| 0 | 999 | 0 | 1 | 0 |
| 1 | 994.8 | 2.123 | 2.372 | 0.7042 |
| 2 | 980.6 | 7.697 | 8.584 | 3.099 |
| 3 | 931.5 | 26.49 | 30.33 | 11.67 |
| 4 | 783.3 | 78.18 | 97.97 | 40.58 |
| 5 | 479.7 | 151.5 | 246.2 | 122.6 |

We then summarise the epidemic peak (epi\_peak) and epidemic duration (epi\_dur), along with population sizes at the end of the time period simulated.

biddmodellingcourse::summarise\_model(SEIR\_sim) %>%   
 pretty\_table(caption = "SEIR model summary statistics; The final size of each population at the end of the simulation, along with the time the epidemic peak was reached, the number of infected at the epidemic peak and the duration of the epidemic")

Table 3: SEIR model summary statistics; The final size of each population at the end of the simulation, along with the time the epidemic peak was reached, the number of infected at the epidemic peak and the duration of the epidemic

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| S | E | I | R | epi\_peak\_time | epi\_peak\_size | epi\_dur |
| 172 | 5 | 20 | 803 | 6 | 391 | Inf |

Finally we plot the population in each model compartment over time.

## For an interactive graph change interactive to TRUE  
biddmodellingcourse::plot\_model(SEIR\_sim, interactive = FALSE)

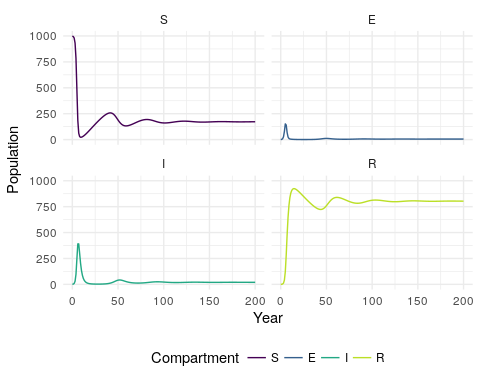


Figure 1: Plot of population over time in each SEIR model compartment

### Explore

Model dynamics are parameter dependent. Even in a simplistic model like the one outlined above parameter values can greatly alter the dynamics. Answer the following questions by varying the parameters above and rerunning the model.

1. What is the impact of adding demographic processes (births and deaths)?
2. What happens when the transmission rate (beta) is reduced below 1?
3. What happens as the rate of recovery is increased?

## Add High and Low Risk Compartments

We are now going to make the model slightly more realistic, and therefore better able to capture the observed dynamics of TB. We are going to do this by adding a second latent population. Go back to [practical 1](https://bristolmathmodellers.github.io/biddmodellingcourse/articles/practical_1.html) if you need a refresher for the motivation behind this.

### Populations and Initialisation

As in the previous model the first step is to define the model populations. There are now two new compartments, high risk latents (H), and low risk latents (L). These replace the orginal latent population (E) used in the previous model.

SHILR\_inits = c(  
 S = 999,  
 H = 0,  
 L = 0,  
 I = 1,  
 R = 0  
)

### Parameters

We add two additional parameters for the rate of progression from high to low risk latents (nu) and the rate of progression from low risk latent to active disease.

SHILR\_parameters <- c(  
 beta = 3, # Rate of transmission  
 gamma\_H = 2, # Rate of progression to active symptoms from high risk latent  
 nu = 1/2, #Rate of progression from high to low risk latent  
 gamme\_L = 1/100, # Rate of progression to active symptoms for low risk latent  
 tau = 1/2, # Rate of recovery  
 mu = 1/81 # Rate of natural mortality  
)

### Equations

The code below is a starting point, fill in the missing model terms using the following model flow diagram and the code for the previous SEIR model as reference points.

SHLIR\_demo\_ode <- function(t, x, params) {  
  
 ## Specify model compartments  
 S <- x[1]  
 H <- x[2]  
 L <- x[3]  
 I <- x[4]  
 R <- x[5]  
  
 with(as.list(params),{  
  
 ## Specify total population  
 N = S + H + L + I + R  
  
 ## Derivative Expressions  
 dS = - beta \* S \* I / N - mu \* S + mu \* N  
 ## These are the new equations - fill in the remaining terms  
 dH = beta \* (S + L) \* I / N   
 dL = - beta \* L \* I / N  
 ## Hint terms are missing from this equation as well  
 dI = - tau \* I - mu \* I  
 dR = tau \* I - mu \* R  
  
 ## output  
 derivatives <- c(dS, dH, dL, dI, dR)  
  
 list(derivatives)  
 })  
}

### Simulate and Summarise

Simulation is the same as for the previous model. Does the simulation of your improved model make sense? Evaluate the summary tables and plot of model populations over time.

begin\_time <- 0  
end\_time <- 200  
SHILR\_times <- seq(begin\_time, end\_time, 1)  
  
## see ?solve\_ode for details  
SEIR\_sim <- biddmodellingcourse::solve\_ode(model = SHLIR\_demo\_ode,   
 inits = SHLIR\_inits,   
 params = SHLIR\_parameters,  
 times = SHILR\_times,   
 as.data.frame = TRUE)  
SHLIR\_sim %>%   
 head %>%   
 pretty\_table(caption = "First 5 years of SHLIR model simulation",  
 label = "tab-1")

biddmodellingcourse::summarise\_model(SEIR\_sim) %>%   
 pretty\_table(caption = "SHLIR model summary statistics; The final size of each population at the end of the simulation, along with the time the epidemic peak was reached, the number of infected at the epidemic peak and the duration of the epidemic")

## For an interactive graph change interactive to TRUE  
biddmodellingcourse::plot\_model(SEIR\_sim, interactive = FALSE)

## Explore

1. How do the model dynamics for this model differ for different parameter values?
2. What has the impact of adding the second latent population been?

## Extension: Translate your Model Flow Diagram to Equations

* basic model outline
* suggestions for order in which to add complexity

## Extension: Explore the Parameter Space of Multiple Models

* link to shiny app
* help with shiny app
* question ideas

# References