

Lesson 4: Building up a contact-based marine disease transmission model

Learning objective: The learning goal of this lesson is to gain substantial knowledge for modeling contact-based disease models using Matlab and ordinary differential equation systems.

Self-learning steps: The learner will understand the pathogen transmission concepts and models through two contact-based disease models. Following the sections of this lecture, first, the student will understand to build the conceptual model using compartments for each variable (S, Susceptible; I, Infected; D, Dead) of the disease model. Second, the student will learn to build differential equations for each variable using parameters defining the processes and mechanisms modulating each variable or population dynamics. Third, the student will try to understand the association of equations, parameters and the matlab code for these equations. For this, the student will go through the matlab code defining the two disease models described in the equations. Once the code structure and scripts are understood, the student can run simulations changing initial conditions and parameter values and obtaining different plots. The student will be able to construct other more sophisticated models in the following exercise section. The student will need to spend 7 hours to learn the modeling structure in matlab and how to construct and run new models including creating scripts, running different scenarios and making plots.

Additional resources for the lecture: Additional learning resources about building a contact based disease model using MATLAB or the alternative open source software GNU Octave can be found on links 7 and 8 in section “Readings and other resources”.

4.1. Contact-based marine disease models

Examples of marine host-pathogen systems associated with the models in this lesson (SI and SID models) are described in Table 1.

Model	Transmission	Applicable systems
SI	Contact with infected individuals	Diseases in fish (e.g. salmon) and mammals such as seals where the disease is transmitted through rubbing. In corals, contact between sea fans when growing close together.
SID	Contact with dead infected individuals	Polar bears, fish, shrimps, and amphipods get infected by contacting or feeding on dead carcasses.

Table 1: Models, model characteristics, and example disease potentially applicable. The disease list is not meant to be comprehensive, nor does a unique mention of a disease imply restriction of the disease to that particular model.

For each model the basic reproduction number R_0 is formulated. R_0 represents the number of new cases of infection caused by one infected individual in a population of only susceptible individuals. Usually, the definition of R_0 in an epidemiological context includes the threshold value of 1, wherein, if $R_0 > 1$, the disease can invade and an epidemic can occur and if $R_0 < 1$, the disease cannot invade and an outbreak is not expected.

Lessons 4 and 5 will describe in detail the calculations for getting the formulation of R_0 for each model. The student will learn to get R_0 by applying the next-generation matrix (NGM) method for each model.

4.2. SI model

The most simple model is the standard SI model (Susceptibles-Infecteds) in which contact with an infected individual spreads the infection (Figure 1). Transmission of the disease is controlled by the transmission rate $\beta_{contact}$ (Equations 1 and 2). The number of infected individuals, $\beta_{contact}IS$, is linearly proportional to the product of the spatial densities of S and I .

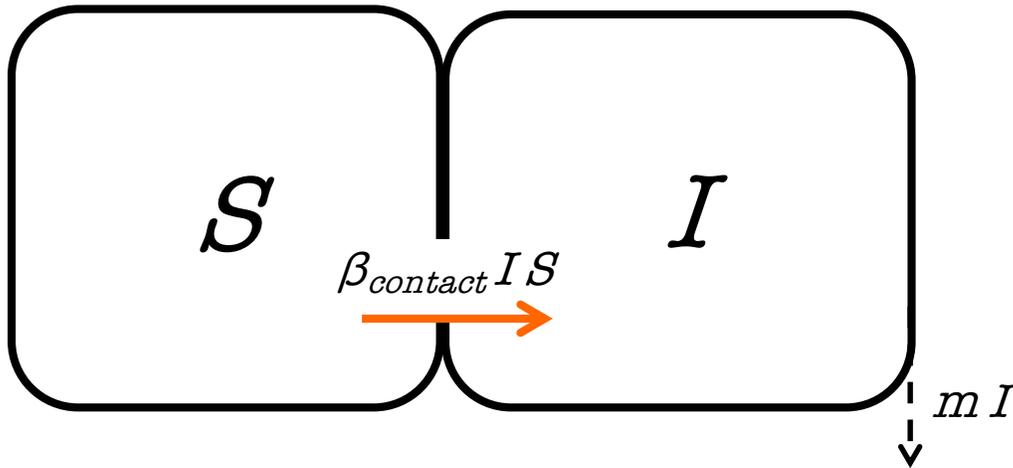


Figure 1: Flow diagram for the SI model. The variables (compartments) for each model are represented by upper letters (susceptible animals S), infected animals I . The model parameters are represented by lower letters described in Table 2. Orange solid arrows represent the transmission processes and dashed black arrows represent the other main processes.

Besides transmission, the dynamics of the infected subpopulation I is controlled by disease mortality (mI), where m is the mortality rate (Equation 2):

$$\frac{dS}{dt} = -\beta_{contact} I S, \quad (1)$$

$$\frac{dI}{dt} = \beta_{contact} I S - m I. \quad (2)$$

The basic reproduction number is:

$$R_0 = \frac{\beta_{contact} N}{m}, \quad (3)$$

where N is the initial population of susceptible individuals S .

R_0 increases linearly with respect to N (Figure 2). Relatively large populations are more likely to inhibit epizootics if disease mortality rate m is high (i.e. infected hosts remain in the system for a shorter time and are less likely to spread the disease) and transmission rate is relatively low (i.e. susceptible hosts are less easily infected).

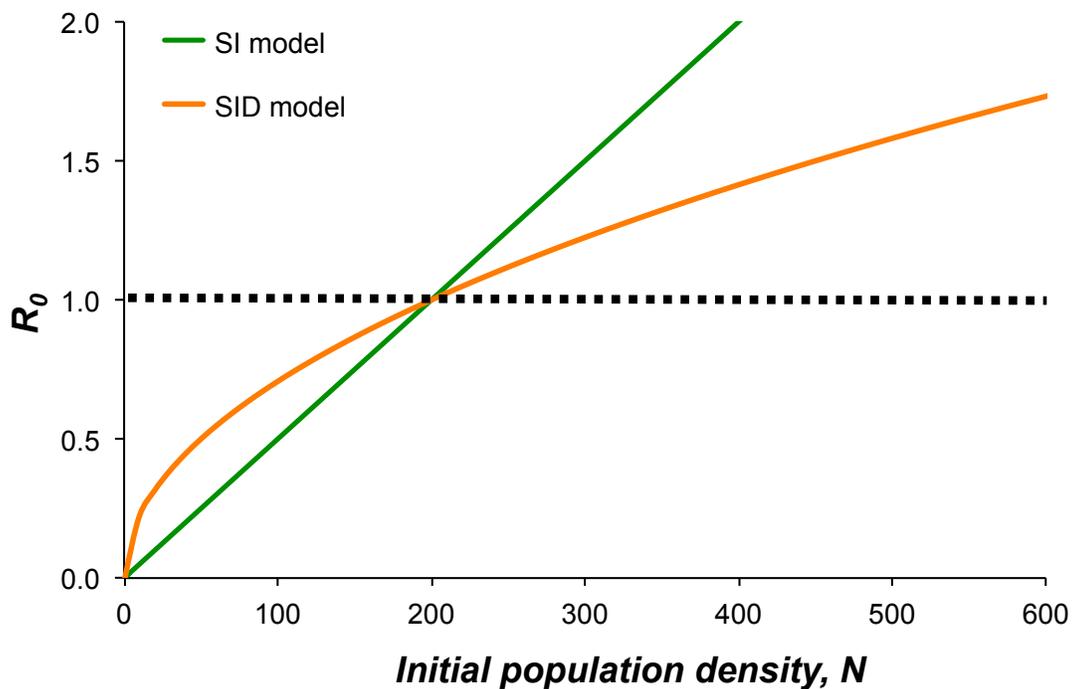


Figure 2: Theoretical estimations of R_0 for SI and SID models, for increasing population density N . Using as examples marine host-pathogen systems described in Table 1, the following values of the parameters were used: ($\beta_{contact} = 1 \times 10^{-3}$, $m = d = 1 \times 10^{-1}$)

4.3. SID model

In addition to susceptible S and infected animals I , the SID model incorporates the dead infected individuals (D). In this model contact with a dead infected individual spreads the infection (Figure 3). SD (Susceptibles-Deads) models arguably are less

common in terrestrial habitats (Figure 3). The infection rate of the S population is controlled again by the transmission rate $\beta_{contact}$, and is linearly proportional to the spatial density of S and, in this case, D instead of I (equations 4 and 5).

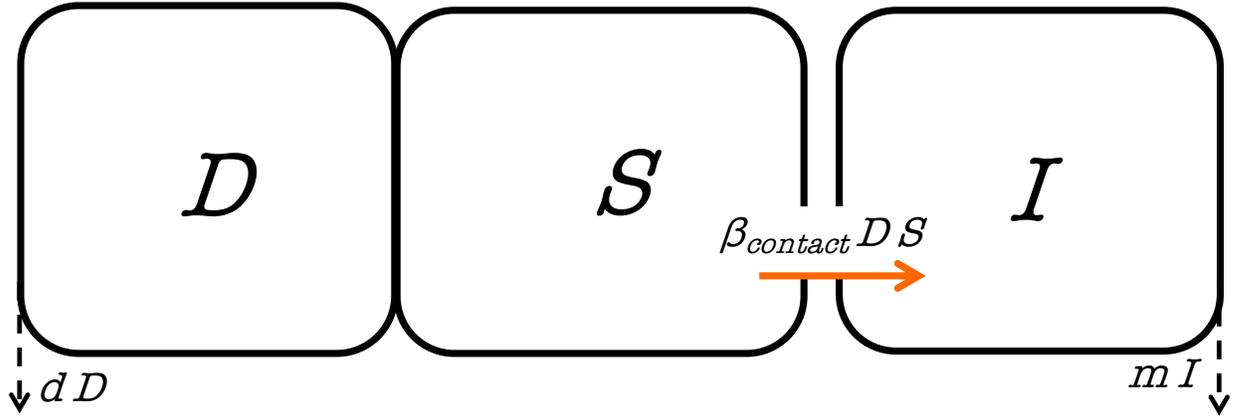


Figure 3: Flow diagram for the SID model (Table 1, section 3). The variables (compartments) for each model are represented by upper letters (susceptible animals S), infected animals I , dead animals D . The model parameters are represented by lower letters described in Table 2. Orange solid arrows represent the transmission processes and dashed black arrows represent the other main processes.

Equation 6 describes the introduction of dead animals to the system after infected individuals die from infection (mI) and their disappearance by natural decay or consumption by scavengers (i.e. an organism that mostly consumes decaying biomass) including conspecifics (dD), where d represents the removal rate. Thus,

$$\frac{dS}{dt} = -\beta_{contact} D S, \quad (4)$$

$$\frac{dI}{dt} = \beta_{contact} D S - m I, \quad (5)$$

$$\frac{dD}{dt} = m I - d D, \quad (6)$$

which yields a basic reproduction number:

$$R_0 = \sqrt{\frac{\beta_{contact} N}{d}}. \quad (7)$$

In this system, the generation of an epizootic, in addition to the initial population size and the disease transmission rate, is regulated by the removal or decay rate of dead animals d , not the mortality rate of infected animals m . The probability of an outbreak ($R_0 > 1$) is lower for the SID model at a given N than for the SI model (Figure 2) due to the extra step in the transmission process (i.e. infection via dead animals).

In nature, scavenging rates or decay rates of dead infected animals are markedly higher than disease mortality rates. This, together with the fact that the process is inherently slower, makes a susceptible population less vulnerable to an epizootic if transmission occurs via direct contact with dead infected individuals, assuming of course that the scavengers are not infected by the pathogen and become reservoirs for the disease.

Variables, Parameters	Definition	Units
S	Susceptible hosts in the population	Number of individuals
I	Infected hosts in the population	Number of individuals
D	Dead infected hosts in the population	Number of individuals
N	Susceptible hosts in the initial population	Number of individuals
R_0	Basic reproduction number	Nondimensional
$\beta_{contact}$	Disease transmission rate by direct contact between susceptible and infected individuals.	Individual ⁻¹ day ⁻¹
m	Disease mortality rate	day ⁻¹
d	Removal rate of dead individuals by scavengers or bacteria (decay)	day ⁻¹

Table 2: Description of variables and parameters. The last column identifies the models in which the variable or parameter is used. An asterisk identifies the use of the variable in the R_0 formulation for that model. Note that all models have an implicit surface area (m^{-2}) or volume (m^{-3}) for individuals and waterborne pathogens respectively.