

## Lesson 6. Sensitivity analysis of $R_0$ models

**Learning objective:** The learning goal of this lesson is to analyze the sensitivity of disease models to the parameters describing disease dynamic processes.

**Self-learning steps:** Following the sections of this lesson, first, the student will learn the application of the normalized sensitivity index. For this, the student will go through two examples of sensitivity analyses: SI and SID models. These examples use baseline parameter values uniformly distributed (i.e. at increments of 10%) over the parameter's full range of feasible values. Once the concept and formulations for the sensitivity analysis of these models are understood, the student can analyze the sensitivity of other more complex models to parameters. The student will need to spend 1 hour to learn how to get the normalized sensitivity index for disease models.

**Additional resources for the lecture:** Additional and advanced learning resources about sensitivity analysis of infectious disease models can be found on link 10 in section “Readings and other resources”.

### Sensitivity analysis

$R_0$  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. The formulations for  $R_0$  for the series of models presented

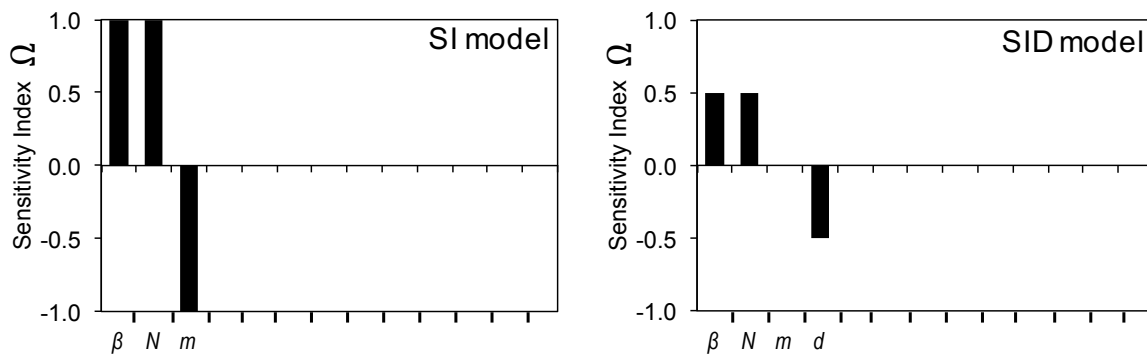
here are obtained using the next-generation matrix (NGM) method (see Lesson 5).

The local sensitivity of  $R_0$  for each model is analyzed through the sensitivity index  $\Omega$ . The normalized sensitivity index of  $R_0$  with respect to any parameter  $p_i$  at a fixed value  $p^0$  is

$$\Omega_{p_i}^{R_0} = \frac{\partial R_0}{\partial p_i} \times \frac{p_i}{R_0} \Big|_{p_i=p^0} \quad (1)$$

The baseline parameter values were selected using as examples marine diseases described in each model. The parameter values are selected uniformly distributed (i.e. at increments of 10%) over the parameter's full or at least wide range of feasible values.

In other words, the idea is to get  $R_0$  values for each of the values of the parameter along the range. For example, if you give the parameter values from 0.01 to 1 at intervals of 0.01, you calculate  $R_0$  values for each value of the parameter. Then, you look at the differences between consecutive values both for the parameter and for  $R_0$  along the parameter values range. You standardize these differences for both the parameter and  $R_0$ , by dividing each of them by the lower value in this difference equation. Finally, you get the sensitivity index  $\Omega$  by dividing the standardized difference of  $R_0$  by the standardized difference of the parameter for each of the steps along the range of the parameter value. You can do it easily using the software Excel.  $\Omega$  can be constant or variable. For SI and SID models the  $\Omega$  is constant for each of the parameter in the  $R_0$  equation.



**Figure 1:** Sensitivity analysis (SA) of  $R_0$  to the parameters for the SI and SID models. The sensitivity index represents the unit  $R_0$  change per unit change in the given parameter. The analysis for each parameter was computed at a 0-1 parameter range for all parameters and  $N$  (0-200), while the rest of the parameters were held constant with these baseline values:  $\beta = 0.001$ ,  $m = 0.1$ ,  $d = 0.1$ ,  $N = 100$ . The asterisks mark parameters for which the sensitivity index was not constant over the evaluated range. For these parameters, the sensitivity index obtained for the baseline value of the parameter is shown.