

# Two-Group Compartmental Models

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# Modeling Heterogeneity

- The modified SIR model we used previously assume a homogenous population – each infectious person is equally likely to infect each susceptible person in a given time period.
- A more accurate model should take into account differences in people's contacts and behavior, to the extent that these differences can be reasonably quantified. Models that go furthest in this direction are called “agent-based”: each person's health is accounted for individually and each person's behavior is described by different parameter values.
- We will instead look at the simplest way to add heterogeneity to the model, by dividing the modeled population into two homogeneous groups.

## Two-Group Model

- Divide the modeled population into a “Group 1” and “Group 2”, and let  $S_k$ ,  $I_k$ , and  $R_k$  be the number of susceptible, infectious, and removed people in group  $k$ . Assuming that people remain in the same group over time, the two-group version of our modified SIR model is:

$$dS_1/dt = q_1 - p_{11}S_1I_1 - p_{12}S_1I_2$$

$$dS_2/dt = q_2 - p_{21}S_2I_1 - p_{22}S_2I_2$$

$$dI_1/dt = p_{11}S_1I_1 + p_{12}S_1I_2 - r_1I_1$$

$$dI_2/dt = p_{21}S_2I_1 + p_{22}S_2I_2 - r_2I_2$$

$$dR_1/dt = r_1I_1$$

$$dR_2/dt = r_2I_2.$$

## Comments on Two-Group Model

- We can, for example, think of Group 1 as representing a “high-risk” population and Group 2 being a relatively “low-risk” population.
- The number of parameters is getting large, but still plausible to estimate from a large enough data set.
- This model should fit a given data set (that is not broken down into groups) at least as well as the one-group model, because it “includes” the one-group model in the following sense. If  $q_1 = q_2 = q/2$ ,  $p_{11} = p_{12} = p_{21} = p_{22} = p$ ,  $r_1 = r_2 = r$ , and the initial populations for each group are the same, then the model will do the same thing as if the two groups were combined into one with parameters  $p$ ,  $q$ ,  $r$ .

## More than Two Groups

- If there are  $n$  groups, we can write the equations more concisely as follows, where  $P$  is an  $n \times n$  matrix of parameters,  $\mathcal{I}$  is a column vector with entries  $\mathcal{I}_1, \dots, \mathcal{I}_n$ , and  $(P\mathcal{I})_k$  denotes the  $k$ th coordinate of the vector  $P\mathcal{I}$ :

$$dS_k/dt = q_k - (P\mathcal{I})_k S_k$$

$$d\mathcal{I}_k/dt = (P\mathcal{I})_k S_k - r_k \mathcal{I}_k$$

$$dR_k/dt = r_k \mathcal{I}_k,$$

for each  $k = 1, \dots, n$ .

# Normalized Parameters

- As before, we can replace the  $p$ 's,  $q$ 's, and  $r$ 's by parameters with simpler units and a more direct connection with the properties of the solutions to the model.
- To simplify matters, let's consider the case  $q_1 = q_2 = 0$ , so that the total population of each group is constant over time; then let  $N_k = S_k + I_k + R_k$  for each  $k$ .
- Recall that for the one-group model, we started by letting  $\lambda = Np$ . We can do something similar for the two-group model, but it's not clear which  $N_k$  to multiply each parameter by.

## Nondimensional Variables

- It can be helpful conceptually to write the equations in terms of the nondimensional variables  $s_k = S_k/N_k$  and  $i_k = I_k/N_k$ , which represent the fractions of people in group  $k$  that are susceptible and infectious (the fraction  $R_k/N_k$  that are removed is then  $1 - s_k - i_k$ ). Dividing the equations for group  $k$  by  $N_k$  yields:

$$ds_k/dt = -p_{k1}s_kI_1 - p_{k2}s_kI_2 = -N_1p_{k1}s_ki_1 - N_2p_{k2}s_ki_2$$

$$di_k/dt = N_1p_{k1}s_ki_1 + N_2p_{k2}s_ki_2 - r_ki_k$$

- Thus, it may be most reasonable to let  $\lambda_{k\ell} = N_\ell p_{k\ell}$  for each  $k$  and  $\ell$ , resulting in:

$$ds_k/dt = -\lambda_{k1}s_ki_1 - \lambda_{k2}s_ki_2$$

$$di_k/dt = \lambda_{k1}s_ki_1 + \lambda_{k2}s_ki_2 - r_ki_k$$

## Further Comments

- The  $\lambda$ 's and the  $r$ 's all have units of 1/time, and represent normalized rates of transmission and removal. We could introduce nondimensional parameters (like  $\nu = r/\lambda$  in the one-group model), or we can just keep in mind that it is only the ratios of these parameters that determine the shapes of the solutions to the model.
- Notice that if all the  $\lambda$ 's are equal (or even if just  $\lambda_{11} + \lambda_{12} = \lambda_{21} + \lambda_{22}$ ) and  $r_1 = r_2$ , then if  $s_1 = s_2$  and  $i_1 = i_2$  at some time,  $ds_1/dt = ds_2/dt$  and  $di_1/dt = di_2/dt$  as well, and the  $s$ 's and  $i$ 's will continue to be the same for each group. In this case, the two-group model behaves like the one-group model.



## Consequences for Data Fitting

- To make the last idea more precise, if  $\lambda_{11} + \lambda_{12} = \lambda_{21} + \lambda_{22} = \lambda$  and  $r_1 = r_2 = r$ , then if  $s_1(0) = s_2(0)$  and  $i_1(0) = i_2(0)$ , both groups follow the one-group model

$$ds/dt = -\lambda si$$

$$di/dt = \lambda si - ri.$$

- Consequently, if you have previously found the values of  $N$ ,  $\lambda$ , and  $r$  for which the one-group SIR model best fits a given data set, it may be reasonable, when fitting the two-group model to the data, to use an initial guess of  $\lambda_{11} = \lambda_{12} = \lambda_{21} = \lambda_{22} = \lambda/2$  and  $r_1 = r_2 = r$ . Alternatively, you can start with  $p_{11} = p_{12} = p_{21} = p_{22} = p = \lambda/N$ .