

For the stochastic compartmental model: for each country/region we have the following equations (we will write down the stochastic version which we solve below).

$$\frac{dS_i}{dt} = -\lambda_i S_i + w_i R_i$$

$$\frac{dI_i}{dt} = \lambda_i S_i - \gamma_i I_i$$

$$\frac{dR_i}{dt} = \gamma_i I_i - w_i R_i$$

where the force of infection λ_i is given by:

$$\lambda_i = \beta_i \sum_j m_{ij} \frac{I_j}{N_i}$$

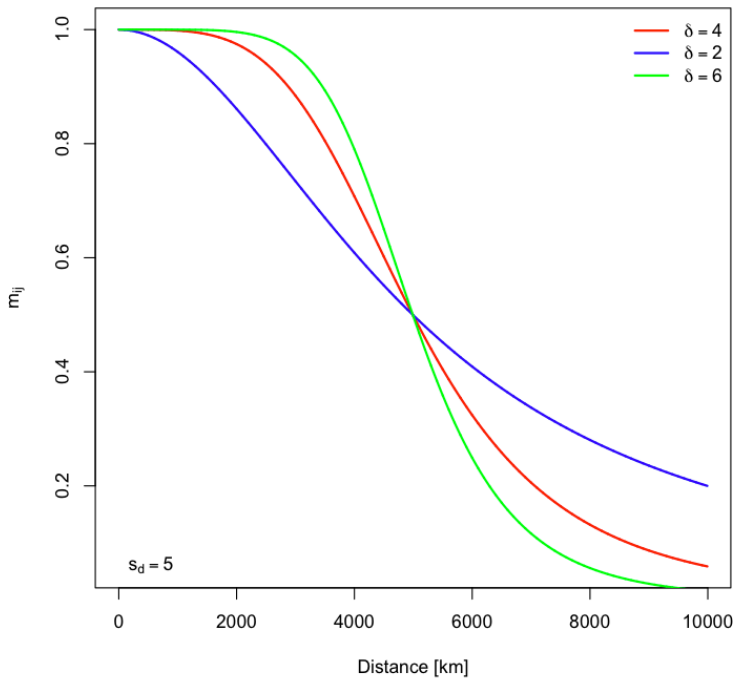
note that we have N_i in the denominator above which means that we have made an implicit assumption that transmission takes place in population i , presumably resulting from the movement of an infectious individual from population j . We could have made the other assumption: that transmission is due to individual from population i travelling to population j and picking up the infection during this travel time. This will require putting N_j in the denominator above.

The recovery rate, γ_i , can be different (or the same for all countries/regions). The rate that immunity wanes is w_i and I have set it to four years.

The coefficients, m_{ij} , measure the strength of interaction between populations and we will assume that it has an off-set power-law dependence on the distance between the centroids of the populations (r_{ij}):

$$m_{ij} = \frac{1}{1 + (s_d/r_{ij})^\delta}$$

The power determines the mixing between the populations and s_d is the distance (in km) below which the kernel function is saturated. We can decide not to have an off-set and we can start with $\delta=-4$. The matrix will be normalized by ensuring that the sum over rows equals 1. By looking at the median value of our distance matrix we can set the distance s_d . Below is a plot of m_{ij} with $\delta=-2$ (blue), -4 (red) and -6 (green) and $s_d=5$ km, seems that we may even want to set it to a smaller number (2km like in the Mills/Riley paper?)



We will be solving the stochastic version of the three equations for S_i , I_i and R_i

$$S_{i,t+1} = S_{i,t} - N_{i,S,t}^{inf} + N_{i,t}^{lst}$$

$$I_{i,t+1} = I_{t,i} + N_{i,S,t}^{inf} - N_{i,I,t}^{rec}$$

$$R_{i,t+1} = R_{i,t} + N_{i,t}^{rec} - N_{i,t}^{lst}$$

where we will calculate the probability of population i to be infected as:

$$p_i^{inf} = 1 - \exp(-\lambda_i \cdot \Delta t)$$

(see above for the definition of λ_i), the probability of this population to recover as:

$$p_i^{rec} = 1 - \exp(-\Delta t \cdot \gamma_i)$$

and the probability to lose immunity as:

$$p_i^{lst} = 1 - \exp(-\Delta t \cdot w_i)$$

with Δt being the time step. Using these two probabilities we can calculate the number of infected/recovered for each country as:

$$N_{i,S,t}^{inf} = rbinom(1, S_i, p_i^{inf})$$

$$N_{i,I,t}^{rec} = rbinom(1, I_i, p_i^{rec})$$

$$N_{i,I,t}^{lst} = rbinom(1, R_i, p_i^{lst})$$

I am using the term 'country' in a loose way here. It can mean country/state/region/country etc.