

Metapopulation Model

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The metapopulation model is a combination of a simple SEIR model (without vital dynamics) combined with metapopulation formulating that follows (?). S , E , I and R have the usual meaning and the index represents region. M_{ij} is a matrix with entries that give the number of people travelling from region i to region j in a timestep (assumed to be constant in time). We model the dynamics in discrete time as given below.

$$\begin{aligned}S_i(t+1) &= S_i(t) - \beta_i(t) \frac{S_i(t)I_i(t)}{N_i(t)} + \sum_j M_{ij} \frac{S_j(t)}{N_j(t)} - \sum_j M_{ji} \frac{S_i(t)}{N_i(t)} \\E_i(t+1) &= E_i(t) + \beta_i(t) \frac{S_i(t)I_i(t)}{N_i(t)} - aE_i(t) + \sum_j M_{ij} \frac{E_j(t)}{N_j(t)} - \sum_j M_{ji} \frac{E_i(t)}{N_i(t)} \\I_i(t+1) &= I_i(t) + aE_i(t) - \gamma I_i(t) + \sum_j M_{ij} \frac{I_j(t)}{N_j(t)} - \sum_j M_{ji} \frac{I_i(t)}{N_i(t)} \\R_i(t+1) &= R_i(t) + \gamma I_i(t) + \sum_j M_{ij} \frac{R_j(t)}{N_j(t)} - \sum_j M_{ji} \frac{R_i(t)}{N_i(t)} \\N_i(t+1) &= \sum_j M_{ij} N_j(t) - \sum_j M_{ji} N_i(t)\end{aligned}$$

The parameter $\beta_i(t)$ represents a time-varying and localised force of infection, with $\frac{1}{\beta}$ interpreted as the expected time between contacts. This model assumes that the incubation period is exponentially distributed with mean $\frac{1}{a}$. The parameter γ represents the typical length of time for an infected person to either recover or die. In this model, we recover a localised and time-varying reproduction number of

$$R_i(t) = \frac{1}{\gamma} \beta_i(t).$$

References