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 (Li et al., 2020). 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.

$$S_i(t+1) = S_i(t) - \beta_i(t)\frac{S_i(t)I_i(t)}{N_i(t)} + \sum_j M_{ij}\frac{S_j(t)}{N_j(t)} - \sum_j M_{ji}\frac{S_i(t)}{N_i(t)}$$

$$E_i(t+1) = E_i(t) + \beta_i(t)\frac{S_i(t)I_i(t)}{N_i(t)} - aE_i(t) + \sum_j M_{ij}\frac{E_j(t)}{N_j(t)} - \sum_j M_{ji}\frac{E_i(t)}{N_i(t)}$$

$$I_i(t+1) = I_i(t) + aE_i(t) - \gamma I_i(t) + \sum_j M_{ij}\frac{I_j(t)}{N_j(t)} - \sum_j M_{ji}\frac{I_i(t)}{N_i(t)}$$

$$R_i(t+1) = R_i(t) + \gamma I_i(t) + \sum_j M_{ij}\frac{R_j(t)}{N_j(t)} - \sum_j M_{ji}\frac{R_i(t)}{N_i(t)}$$

$$N_i(t+1) = \sum_j M_{ij}N_j(t) - \sum_j M_{ji}N_i(t)$$

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

(Li et al., 2020) Li, R., Pei, S., Chen, B., Song, Y., Zhang, T., Yang, W., and Shaman, J. (2020). Substantial undocumented infection facilitates the rapid dissemination of novel coronavirus (sars-cov-2). *Science*, 368(6490):489–493.