

Notes

Sang Woo Park

September 28, 2018

1 Gravity TSIR model

Deterministic model is given by:

$$S_{k,t+1} = S_{k,t} + B_{k,t} - I_{k,t+1}, \quad (1)$$

where

$$I_{k,t+1} = \frac{\beta_{k,t} S_{k,t} \left(I_{k,t} + \sum_{j \neq k} m_{j \rightarrow k} - \sum_{i \neq k} m_{k \rightarrow i} \right)^\alpha}{N_{k,t}} \quad (2)$$

Given parameters of m , we can construct

$$\hat{I}_{k,t} = I_{k,t} + \sum_{j \neq k} m_{j \rightarrow k} - \sum_{i \neq k} m_{k \rightarrow i}. \quad (3)$$

Then, we can allow for mixed model structure:

$$\begin{aligned} I_{k,t+1} &\sim \text{Distrib} \left(\exp \left(\log \beta_{k,t} + \log S_{k,t} + \alpha_k \log \hat{I}_{k,t} - \log N_{k,t} \right) \right) \\ \log \beta_{k,t} &\sim \text{Normal}(\beta_t, \sigma_{\beta_t}^2) \\ \alpha_k &\sim \text{Normal}(\alpha, \sigma_\alpha^2) \end{aligned} \quad (4)$$

This model can be fitted using GLM (zero-inflated to account for extinction events?) conditional on the parameters of $m_{j \rightarrow k}$. The fitted model yields profile likelihood for $m_{j \rightarrow k}$ and the parameters can be estimated.

In order to fit the model, we have to be able to reconstruct susceptible dynamics. Assuming that cases are reported where they became infected, we can write $I_{k,t} = I_{k,t}^{(r)} / \rho_t$. Then, the following equation suggests that the susceptible population can be reconstructed locally:

$$S_{k,t+1} = S_{k,t} + B_{k,t} - I_{k,t+1}^{(r)} / \rho_t, \quad (5)$$