

1. (i) Let X denote the number of days that an infected person remains infected. Then X is distributed geometrically, i.e. $\mathbb{P}(X = k) = \sigma^{k-1}(1 - \sigma)$. Then the expected infection length is

$$\mathbb{E}[X] = \sum_{k=1}^{\infty} \sigma^{k-1} = \sum_{k=0}^{\infty} \sigma^k = \frac{1}{1 - \sigma}.$$

- (ii) When $I_{t,j} \approx 0$, then

$$\begin{aligned} S_{t+1,j} &= S_{t,j} G_{t,j} \\ &= S_{t,j} e^{-\sum_{k=1}^m \beta_{j,k} I_{t,k}} \\ &\approx S_{t,j} e^{\sum_{k=1}^m \beta_{j,k} \cdot 0} \\ &= S_{t,j} \end{aligned}$$

Similarly, we can show $S_{t,j} \approx S_{t-1,j}$. Continuing, we get $S_{t,j} \approx S_{0,j}$.

Now we take the Taylor expansion $e^x = 1 + x + \mathcal{O}(x^2)$ to show $e^x \approx 1 + x$ when x is small. In the context of this problem, since $I_{t,j}$ is small, this means $e^{-\sum_k \beta_{j,k} I_{t,k}} \approx -\sum_k \beta_{j,k} I_{t,k}$. We can use this approximation, along with the approximation of S , to get

$$\begin{aligned} I_{t+1,j} &= S_{t,j}(1 - G_{t,j}) + \sigma I_{t,j} \\ &\approx \sigma I_{t,j} + S_{0,j} \sum_{k=1}^m \beta_{j,k} I_{t,k} \\ &= \sigma I_{t,j} + \sum_{k=1}^m A_{j,k} I_{t,k} \end{aligned}$$

We can interpret $A_{j,k}$ as the rate of infectious contact between infectious type k 's and susceptible type j 's in a fully susceptible population.

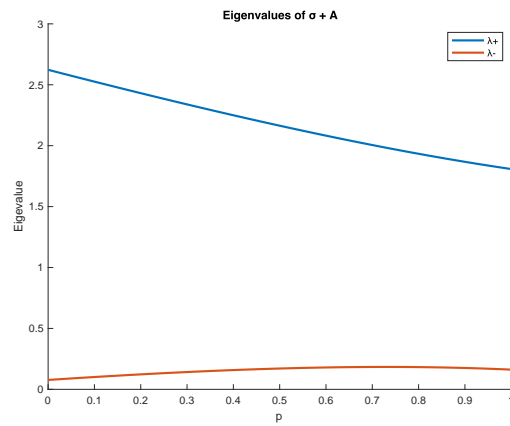
- (iii) If we define $A_{j,k} = \eta_j \beta_{j,k}$, then the system of infected individuals can be written in vector form as $I_{t+1} = (\sigma + A)I_t$, the same as in the previous problem. We can then reasonably define $\mathcal{R}_0(\eta)$ to be the maximum eigenvalue of $\sigma + A$. Such an $\mathcal{R}_0(\eta)$ would then quantify the largest increase to a component (type) of I_t .
- (iv) In this example, A is

$$A = \begin{pmatrix} 0.47p & 0.08p \\ 0.93(1-p) & 1.2(1-p) \end{pmatrix}$$

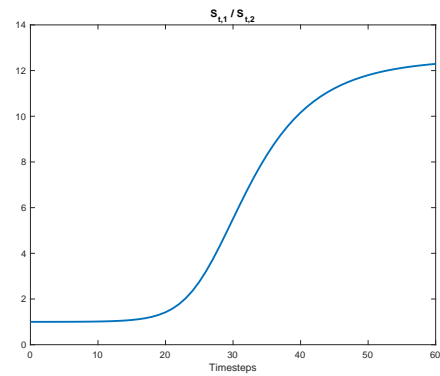
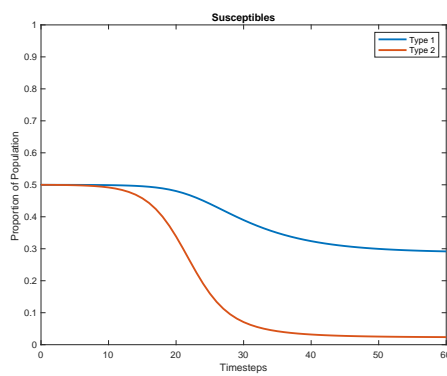
and the matrix $\sigma + A$ is

$$\sigma + A = \begin{pmatrix} 0.75 + 0.47p & 0.75 + 0.08p \\ 1.68 - 0.93p & 1.95 - 1.2p \end{pmatrix}.$$

Both eigenvalues of $\sigma + A$ as a function of $p \in [0, 1]$ are plotted below. Since we defined $\mathcal{R}_0(\eta)$ to be the maximum eigenvalue, $\mathcal{R}_0(\eta)$ is shown by the line labeled λ_+ .



(v) Solving the model numerically for 60 timesteps yields the following.



From the first figure we can see that the total number of susceptibles is decreasing, and from the second figure we can see that the number of type 1 susceptibles is growing relative to the number of type 2 susceptibles. We can evaluate the matrix A given $\eta = (1/2, 1/2)$ to get

$$A = \begin{pmatrix} 0.235 & 0.04 \\ 0.465 & 0.6 \end{pmatrix}$$

Since we interpreted $A_{j,k}$ as the rate of infectious contact between infectious type k 's and susceptible type j 's in a fully susceptible population, the sum of row j in A can be interpreted as the total rate of infectious contact with susceptible type j 's. From this it is clear that substantially less infectious contact is being made with type 1 than type 2, which explains why fewer type 1's contract the disease in the simulated model.