MA4M1 Epidemiology By Example Assessed Worksheet 5

Barnaby Sproats. u1902391

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Question 1

Q1(a)

Infection-free mosquito population dynamics in a single location for are given by:

$$\frac{dL_v}{dt} = B_v - \theta L_v - \frac{L_v^2}{C}$$
$$\frac{dN_v}{dt} = \theta L_v - \mu_v N_v$$

Where L_v is the number of larvae, and N_v the number of adults. At this disease free equilibrium $(L_v^\star, N_v^\star)$, $\frac{dL_v}{dt} = \frac{dN_v}{dt} = 0$. Hence the equilibrium value for the Larvae number $L_v^\star$ can be written:

$$0 = \theta L_v^\star - \mu_v N_v^\star \implies L_v^\star = \frac{\mu_v N_v^\star}{\theta}$$

Furthermore using this result and setting $C = N_v^\star$, we can derive a value of B_v:

$$\begin{aligned} 0 &= B_v - \theta L_v^\star - \frac{(L_v^\star)^2}{C} \\ B_v &= \theta L_v^\star - \frac{(L_v^\star)^2}{N_v^\star} \\ B_v &= L_v^\star(\theta - \frac{(L_v^\star)^2}{L_v^\star \frac{\theta}{\mu_v}} \\ B_v &= L_v^\star(\theta - \frac{\mu_v}{\theta}) \end{aligned}$$

Q1(b)

As n_v is a measure of relative decrease in the adult population, we have $\tilde{N}_v = n_v N_v$. Assuming B_v is unchanged if we alter C to some value $\tilde{C}$, then:

$$\begin{aligned} B_v = \theta L_v^\star + \frac{(L_v^\star)^2}{C} &= \theta \tilde{L}_v^\star + \frac{(\tilde{L}_v^\star)^2}{\tilde{C}} \\ N_v^\star(\mu_v + \frac{\mu_v^2}{\theta^2}) &= \frac{\mu_v}{\theta} n_v N_v^\star \theta + \frac{\mu_v^2}{\theta^2} n_v^2 N_v^\star \frac{1}{\tilde{C}} \\ \mu_v + \frac{\mu_v^2}{\theta^2} &= \mu_v n_v + \frac{\mu_v^2}{\theta^2} n_v^2 N_v^\star \frac{1}{\tilde{C}} \\ \theta^2 \mu_v (1 - n_v) + \mu_v^2 &= \mu_v^2 n_v^2 N_v^\star \frac{1}{\tilde{C}} \\ \tilde{C} &= \frac{\mu_v n_v^2 N_v^\star}{\theta^2(1 - n_v) + \mu_v} \end{aligned}$$

A plot of $\tilde{C}$ against n_v is in figure 1.

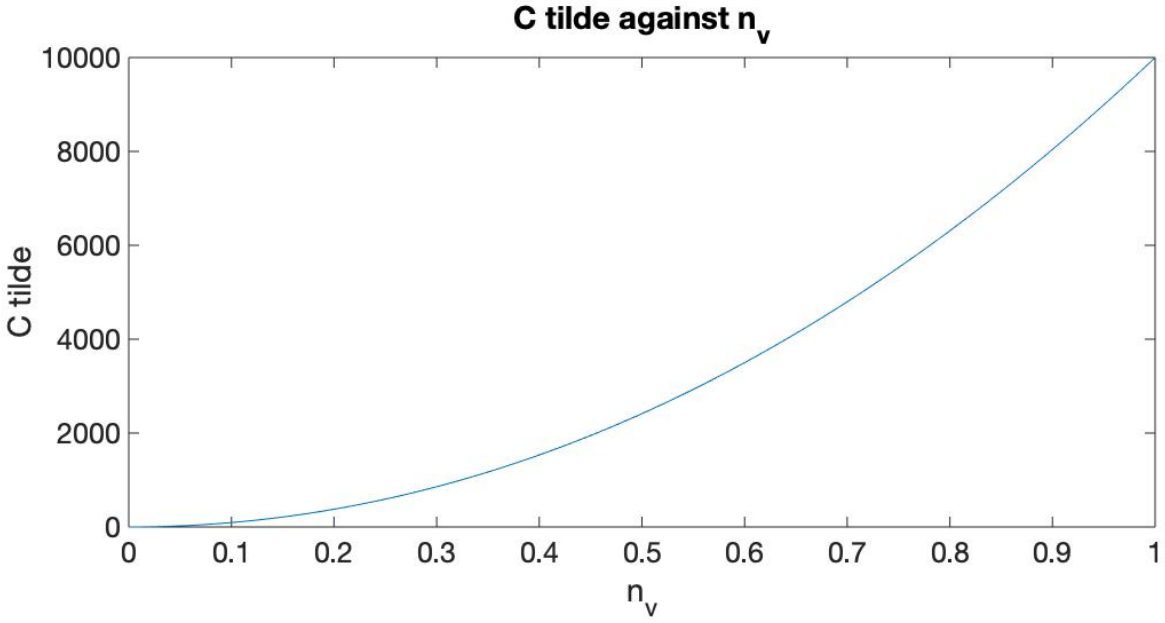

Figure 1: $\tilde{C}$ against n_v.

Finally, this has used that for a given n_v:

$$\tilde{L}_v^\star = \frac{\mu_v \tilde{N}_v^\star}{\theta} = \frac{\mu_v n_v N_v^\star}{\theta}$$

Question 2

Q2(a)

To calculate R_0 within farm 1, we use the next generation matrix approach. This amounts to finding the dominant eigenvalue of the next generation matrix $K = -T\Sigma^{-1}$. Here T is the matrix of transmissions and Σ the matrix of transitions. In this case, $K_{11} = 1$ and $K_{ij} = 0$ for all other components of K. This being a diagonal matrix, the eigenvalues are the diagonal elements, 1 and zero. Hence the dominant eigenvalue, and therefore R_0, is equal to 1.

Q2(b)

In figure 2, find a plot of the spatial kernel $K(d) = \exp(-bd^2)$ (left) and a schematic of farm location with relative connectivity marked on (right).

Q2(c)

In figure 3 the infection dynamics for the No Control (NC) strategy are plotted. In each location, each curve qualitatively fits the standard SIR style, having one peak before decaying to zero. As the infection begins in location 1, we observe it to peak first at 150 days and have the highest peak at around 90 infected. The second location is the only farm with any substantial connection to farm 1 as seen in figure 2 (right). Due to

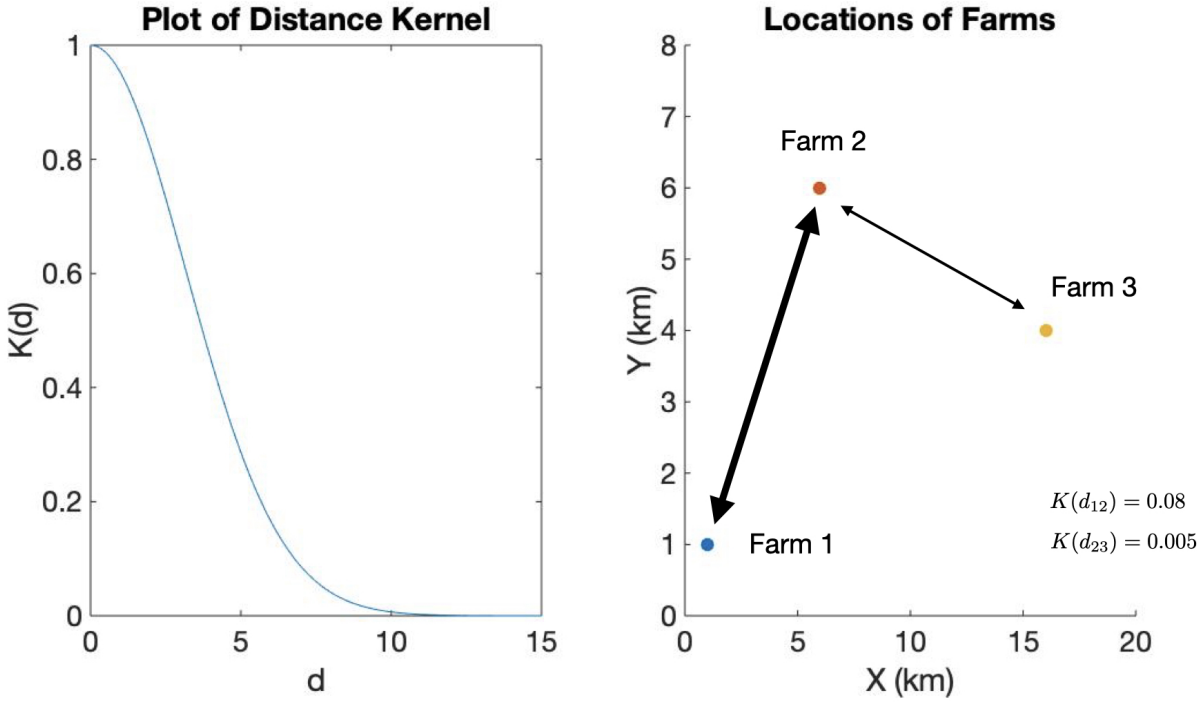

Figure 2: Left: Distance Kernel. Right: Locations of farms and relative connectivity. The Kernel between farms 1 and 3 is so close to zero it can be neglected and so it is no marked.

a decent connectivity, infected mosquitoes can quickly travel to this location, inducing a curve that peaks around the same time as that in location 1. However, as the transmission is not perfect, fewer infected mosquitoes penetrate into farm 2, and the peak is lower at 45 infected.

As farm 3 is not really connected to farm 1, it can only be infected via farm 2. Therefore, due to the reduced mosquitoes in farm 2, it takes longer for sufficient infected mosquitoes to cumulate in farm 3 for the disease to take off, and is seen by a delayed peak at 240 days of around 40 infected.

In figure 4 the cumulative deaths and abortions are plotted which follow a similar pattern. Farm 1 has the most, with farm 2 having less but stabilising at a similar time. Farm 3 achieves a similar number to farm 2 but after a delay. For cumulative abortions farms 2 and 4 overlap, as time scale for abortions is significantly greater than the delay in farm 3. The reason cumulative abortions takes so long to stabilise is that we require R_{hi} to vanish. With no infections, $\dot{R}_{hi} = -\mu_h R_{hi}$ which corresponds to exponential decay with decay constant $\mu_h = 1/10 years^{-1}$. Thus it takes $\ln(2) \times 10 \approx 7$ years for R_{hi} to half its original value..

Q2(d)

The duration was calculated using MATLAB's find function to locate the respective times each farm had less than 1 infected. Then the duration of the entire disease is the maximum of these times and in this case found to be 314 days. Then, we sum the final elements in the cumulative deaths and abortions class for each farm to give total deaths and abortions. Then taking a death to cost \$250 and an abortion \$50, we found the total

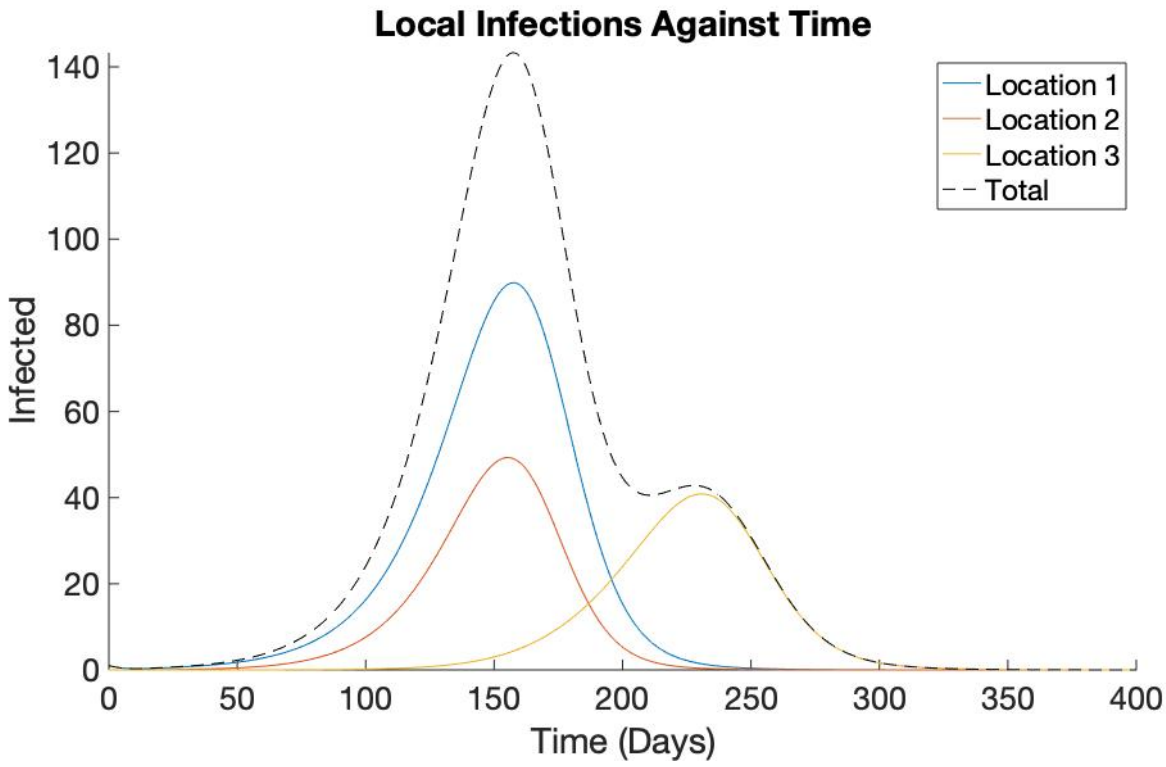

Figure 3: Infection dynamics for No Control (NC) strategy,

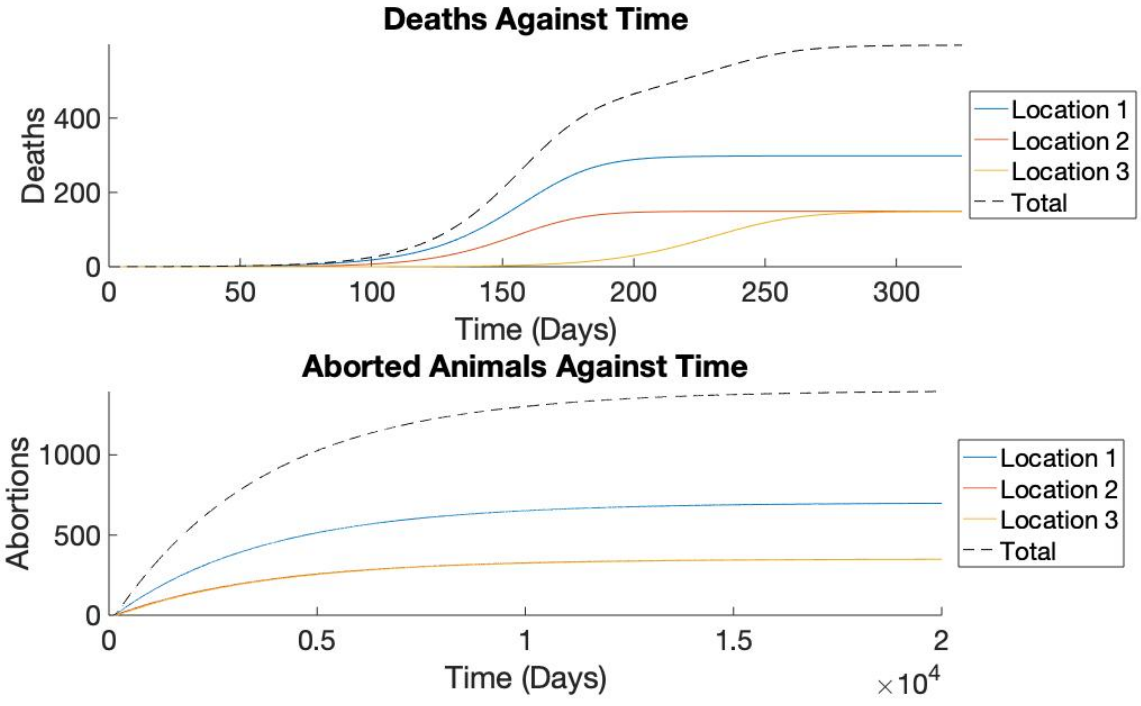

Figure 4: Cumulative deaths and abortions due to No Control (NC) Strategy.

cost of the disease to be \$219,550.

Strategy	Duration (days)	Cost ($)
NC	314	219,550
VC→ VC $n_v = 0.1$	339	165,550
VC→ NC $n_v = 0.1$	322	227,050
VC→ VC $n_v = 0.4$	412	245,950
VC→ NC $n_v = 0.4$	320	227,050

Table 1: Comparison of fundamental objectives for each strategy

Question 3

Q3(a)

In figure 5 we plot the infection dynamics for infected adult mosquitoes and infected larvae when our vector control constant $n_v = 0.1$. This reduction of mosquito carrying capacity successfully lowers and delays the peak in the VC→ NC stragegy. Furthermore it drastically reduces the same peak in the VC→VC strategy,

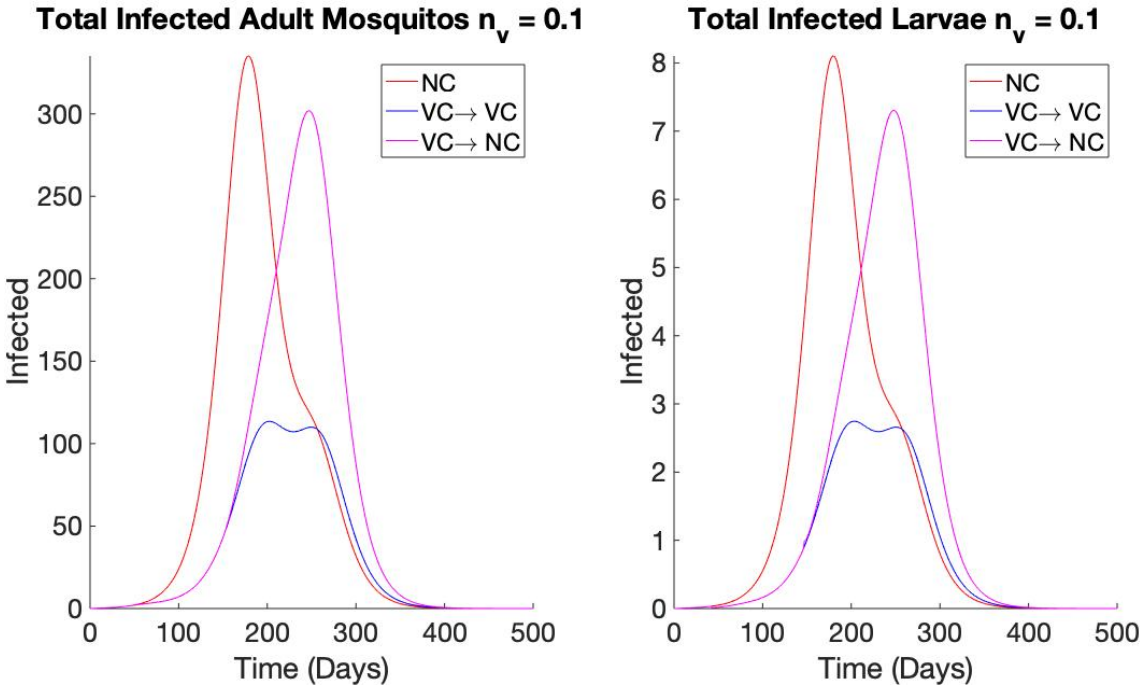

Figure 5: Infected adults and larvae over each strategy with $n_v = 0.1$.

In figure 6 we plot the infection dynamics for infected adult mosquitoes and infected larvae when our vector control constant $n_v = 0.4$. As n_v is slightly closer to 1, the VC→VC and VC→NC curves are closer to the NC curve. Hence the peaks are higher and less delayed. Results of fundamental objectives are plotted in table 1.

The duration of the disease is often unaltered except for the VC→ VC strategy for $n_v = 0.4$ as reducing carrying capacity flattens the curves, trading peak height for duration. The real difference comes in cost. For $n_v = 0.4$, VC→ VC is the most expensive as, whilst less animals die or are aborted, we pay for intervention over the entire disease duration. However for $n_v = 0.1$, we cut off the peak of infective mosquitoes and larvae

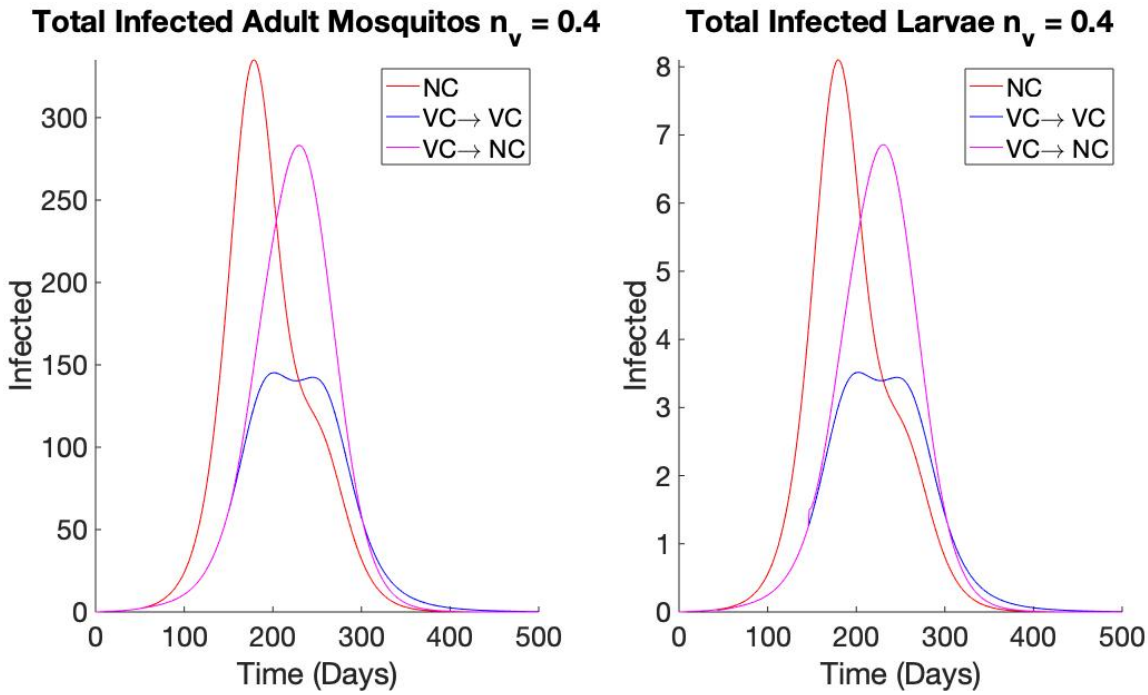

Figure 6: Infected adults and larvae over each strategy with $n_v = 0.4$.

Strategy	Expected Duration (days)	Expected Cost ($)
NC	314	219,550
VC→ VC	296	239,490
VC→ NC	297	227,990

Table 2: Comparison of expected values of fundamental objectives for each strategy

which drastically reduces deaths and abortions. This causes saving in spite of prolonged VC reduction, leading to the cheapest strategy. Both VC→NC strategies have the same cost as deaths and abortions are similar, and we pay for intervention over the same 15 week time period and lie between VC→VC for $n_v = 0.1$ and VC→VC for $n_v = 0.4$.

Q3(b)

We assume $n_v \sim$ Beta(2,5). For a given metric O, let $O_S(n_v^\star)$ denote the value of this metric under strategy S, with n_v fixed to $n_v^\star$. Then, the expected value of O_S over all n_v, taking our prior into consideration, is given by:

$$\mathbb{E}[O_S] = \int_0^1 O_S(n_v) f(n_v)\, dn_v$$

Where $f(n_v^\star)$ is the PDF of a Beta(2,5) distribution, evaluated at $n_v^\star$. This was computed via the trapz numerical integrator in MATLAB. Here, for each n_v, the duration and cost are found as in Q2(d), where for cost we add on the intervention costs The results are presented in table 2.

We see that both VC strategies reduce the duration of the disease by about 2 and a half weeks. However, the VC→ VC strategy is the most expensive, followed by the

VC→ NC strategy, followed by NC. Hence, policy makers a reduction value the 2 week reduction, we rank them VC→ NC, VC→ VC, NC. However, if we value the $7,000 saving more, we could rank them NC, VC→ NC, VC→ VC.

Q3(c)

We assume that after 15 weeks, we can remove all uncertainty in n_v. Hence, we can model its distribution as a Dirac delta function $\delta(n_v - n_v^\star)$ where $n_v^\star$ is the true value of n_v. Then our our expected value for O under strategy S is:

$$\mathbb{E}[O_S] = \int_0^1 O_S(n_v)\delta(n_v - n_v^\star)\, dn_v = O_S(n_v^\star)$$

In other words the expected value is just the model evaluated at $n_v^\star$. Therefore, in figure 7, we plot how the duration and cost of the disease varies with n_v.

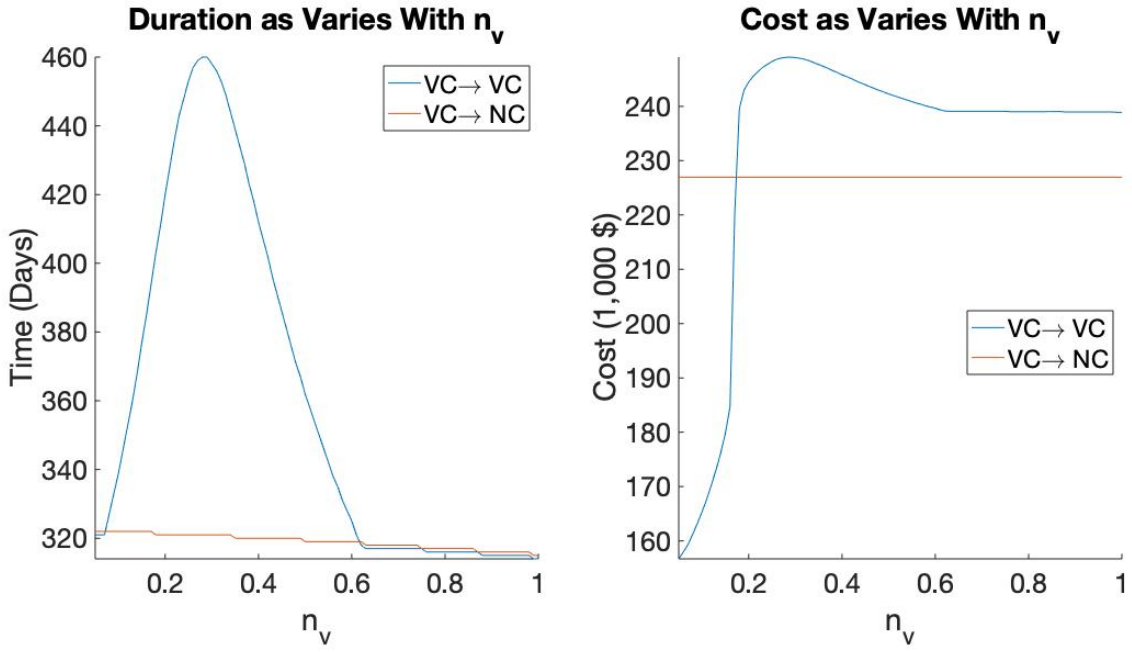

Figure 7: How diease duration and cost vary with n_v.

We see that for all n_v values, the duration for the VC→ NC remains steady at around 320 days. For VC→ VC, duration increases to around 460 days for non-extreme values. Meanwhile, for costs VC→ NC is fixed. Meanwhile for low values of n_v the costs for VC→ VC are remarkably cheap, as the duration, and abortions are greatly reduced. However as n_v increases costs become greater surpassing that of VC→ NC around $n_v = 1.8$. Using active adaptive management, if after 15 weeks of monitoring we saw $n_v < 1.8$, we would choose strategy VC→VC, other wise choose strategy VC→NC.

Question 4

Q4(a)

There are several other considerations to make when considering policy analysis. Most important is our fundamental objectives. Here we have studied duration and cost. How-

ever, RVFT infections often occur in locations like Sub-Saharan Africa, where livestock can be crucial to income. Therefore, we may also want to consider livestock deaths and abortions as part of the policy maker's fundamental objectives, over say duration. The disease being prolonged may matter less if fewer animals die.

It is also important to consider other interventions. Vaccination of livestock is a potential method for controlling RVFT, hence it is worth considering if they are applicable, or using active adaptive management to monitor their effectiveness. That said, as mentioned this disease is prevalent in developing regions so high cost strategies may not be an option. Alternately, the control of restricting livestock trade and eduction of the population can prevent the spread of disease, at a lesser price.

Next, the timing of this intervention is important. The OIE states that infections flare up after rain and flood, as they lead to mosquito eggs hatching and beginning infections. Hence, if controls were implemented during or just before heavy rainfall, any growing infection can be efficiently stopped, which will reduce the disease severity, disease duration and the cost of intervention.

Therefore, data can have a real influence on strategy recommendation. We have seen earlier that prolonged vector control is expensive. However, with adequate climate data, we could intervene before the disease takes off, which could potentially reduce n_v below the 1.8 threshold to be cost-effective. Related to this example, data in what parameters like n_v or vaccine efficiency have significant influence on strategy recommendation. For example, if the data for n_v is inconclusive, we would recommend the VC$\rightarrow$NC strategy instead to avoid the negative effects of the VC$\rightarrow$VC strategy when n_v is above 1.8.

Q4(b)

Whilst our model is effective, there are several ways we could make it more realistic/practical.

First, we may add to our model the ability to track the explicit relocation of animals. Currently only the distance kernel is used to model disease transfer from farm to farm, which solely accounts for disease transfer via mosquitoes. However, if infected animals are frequently traded, this will lead to dynamics unaccounted for by our model. For example, in our case farms 1 and 3 have little contact, but farm if 1 frequently trades animals to farm 3, farm 3 will have a greater influx of infected animals than our current model predicts.

Second, we could update our kernel to better capture the geography of the region. Presently we are using a UK kernel, whilst RVFT infections mainly occur in Africa or the Arabian peninsula. Furthermore, the kernel used solely depends on distance. If, for example, there is a hill between farm 1 and 2, mosquitoes may be unable to make the journey, the rate of disease transfer between farms 1 and 2 will be less than expected by the current model.

Third, we could modify our implementation of VC to occur slightly before infections begin. This would help us examine whether pre-emptive action taken before rainfall induces an infected outbreak could significantly reduce the outbreak. Furthermore, we could use a stochastic, not deterministic model as this would allow us to calculate the probability of disease extinction due to pre-emptive intervention.