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Mathematical modeling for sustainable aphid control in agriculture

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Mathematical modeling for sustainable aphid control in agriculture

by

Patricia Sharon Williams

A Creative Component submitted to the graduate faculty
in partial fulfillment of the requirements for the degree of
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Dr. Joshua M Peschel, Major Professor

The student author, whose presentation of the scholarship herein was approved by the program of study committee, is solely responsible for the content of this dissertation/thesis. The Graduate College will ensure this dissertation/thesis is globally accessible and will not permit alterations after a degree is conferred.

Iowa State University

Ames, Iowa

2020

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ABSTRACT

Agricultural losses to pests represent an important challenge in a global warming scenario. FAO estimates that, annually, between 20 to 40 percent of global crop production are lost to pests. We develop a mathematical model to study epidemic spreading and control in agricultural fields as a sustainable pest management tool for agriculture. The model combines the movement of aphids transmitting a virus in an agricultural field, the spatial distribution of plants in the field, and the presence of ground robot into an epidemiological Susceptible-Infected-Removed (SIR) model.

CHAPTER 1 INTRODUCTION

1.1 Importance of mathematical modeling

The sustainable intensification of agriculture is imperative for feeding a growing world population while minimizing its negative environmental impact. The world population will be between 9.6 and 12.3 billion in 2100, and for feeding these additional 2-4 billion people, a duplication (100-110%) of crop production relative to its 2005 level is needed. Today, 10% of ice-free land on Earth is used for crop cultivation, and returning half of Earth's terrestrial eco-regions to nature will mean global losses of 15–31% of cropland and of 3–29% of food calories. Thus, increasing crop yield without extending the size of cultivation areas nor by intensifying the use of current technologies is a vital complex problem to be solved in the coming years. Agricultural yield is substantially reduced by pests, which cause losses of 10-16% to crop production, which may represent real threats for entire world regions. In addition to these scenarios, there is increasing concern that climate change can increase plant damage from pests in future decades. Deutsch et al. [10] estimated that global yield losses of rice, maize and wheat grains are projected to increase in the range of 10 to 25% per degree of global mean surface warming. Thus, in a projected scenario of 2 degree Celsius warmer climate, the mean increase in yield losses owing only to pest pressure extend to 59, 92, and 62 metric megatons per year for wheat, rice and maize, respectively. These losses cover most of the globe, but they are primarily centered in temperate regions. From the agricultural point of view, a particularly important class of insect pests are the aphids (aphididae). Aphids are by far the most important transmitters of plant viruses, being reported to transmit about 50% of insect-borne plant viruses (approximately 275 virus species). There are about 4,700 aphids described from which about 190 transmit plant viruses. From the economic point of view this virus transmission by aphid represents global losses estimated on tens of millions to billions US \$ of yield loss per annum. In the UK alone

the damage on cereals made by aphids has been estimated to be around 60-120 million pounds annually. Thus, mathematical modeling is seen as an important tool to predict and mitigate the effects of viruses on agriculture.

1.2 Cyber-agricultural systems

In our modeling, we combine the movement of aphids in the agricultural landscape with the spatial distribution of plants in the field, into an epidemiological Susceptible-Infected-Removed (SIR) model. In agricultural modeling, the presence of the ground robot must be accounted for, which is often ignored. In our formulation, we account for the disturbances or in other words, perturbances brought about by the movement of the ground robot, which is oftentimes overlooked.

CHAPTER 2 METHODS AND PROCEDURES

We combine the movement of aphids in the agricultural landscape with the spatial distribution of plants in the field and the presence of the ground robot, into an epidemiological Susceptible-Infected-Removed (SIR) model.

2.1 Assumptions of our SIR model

For the development of the theoretical model to be used in this work we make the following assumptions:

1. The infection is transmitted to plants by an aphid—a vector. That is, a susceptible plant receives the infection, e.g., a virus, from an infectious plant through a vector.
2. Infection is also transmitted by plants that are at close proximity
3. Our formulation - Infection is also influenced by ground robot
4. Recovered (removed) plants represent those not only dead but also those which are useless for commercial purposes, i.e., those substantially damaged as to be used for consumption.
5. The number of plants in the field is fixed.
6. The number of infectious vectors is very large and at a given time t its amount is proportional to $I(t)$

2.2 SIR equations

These assumptions are an adaptation of the ones made by Cooke [1] for implementing a time-delay Susceptible-Infected- Recovered (SIR) model to study a vector-borne infection transmission to a given population. The corresponding equations read as follows:

$$\dot{S}_i(t) = -\beta S_i(t) \sum_j I_j(t) \quad (2.1)$$

$$\dot{I}_i(t) = \beta S_i(t) \sum_j I_j(t) - \mu I_i(t) \quad (2.2)$$

$$\dot{R}_i(t) = \mu I_i(t) \quad (2.3)$$

where S_i is the probability of plant i of being susceptible to the infection, I_i is the probability of plant i of being infective after having been infected by the disease, and R_i is the probability of plant i of being removed. Just to mention, the probability of infection in an SIR network is an NP-hard problem. $\dot{S}_i(t)$, $\dot{I}_i(t)$ and $\dot{R}_i(t)$ are the differential terms/solution of the SIR equation. The terms β and μ , are the birth and death rates of the disease, respectively. The term j at any time represents a plant/plants and it spans only to the plants that are able to spread the disease by contact to plant i . Note that $S_i(t) + I_i(t) + R_i(t) = 1$, and so, $\dot{S}_i(t) + \dot{I}_i(t) + \dot{R}_i(t) = 0$.

2.3 Major differences

Although my work is an implementation of Allen-Perkins [2], there are certain very important distinctions between the paper and my work. A time delay τ , is assumed in the paper, which is the time taken for the infectious agent to develop in the vector, when it is infected by a plant. For relatively low time delays the results in the disease propagation on plants are very similar to those without time-delays according to the paper. Also, when the the aphid mobility is relatively large, the time delay does not affect significantly the propagation rate of the disease. As a consequence, this time delay τ becomes trivial and we ignore this time delay in our work. We also ignore the presence of trap crops, because it is not our concern as to whether or not trap crops are present or how they are arranged. The distance Δ between plants, as assumed in the paper, doesn't necessarily contribute to our modeling, and hence we eliminate it in our formulation. The paper assumes only uni-directional movement of aphids, i.e., it can move from some plant i to plant j and cannot move from plant j to plant i in the future. Now, why this is true is ambiguous - at any time, an aphid can move back and forth and has no reason not to.

2.3.1 Ground Robot

In agriculture, a ground robot traverses between the rows of crops in an agricultural field. It is used for various purposes like picking fruit, measuring moisture content, visually analyzing the plant for health, etc.,. Often, these robots are ignored when it comes to mathematical modeling. As these robots traverse, they tend to make an impact on the movement of the aphids. They thus contribute in some way, as a perturbation to the movement of the vector. In our formulation, we consider the presence of a ground robot. We model this as a perturbation factor (like a noise) in our programming.



Figure 2.1 Ground Robot

2.4 Vector traversal

A vector can hop to any plant at a given time. It can hop to distant plant in the field too. It doesn't necessarily have to hop to the immediate neighbor. So we have to factor this into the SIR equations:

$$\dot{S}_i(t) = -\beta S_i(t) \sum_j f_{ij} I_j(t) \quad (2.4)$$

$$\dot{I}_i(t) = \beta S_i(t) \sum_j f_{ij} I_j(t) - \mu I_i(t) \quad (2.5)$$

$$\dot{R}_i(t) = \mu I_i(t) \quad (2.6)$$

where f_{ij} is a function of the “separation” between the plants i and j , and j spans to all the plants in the field. There are two possibilities of accounting for this separation between plants. The first one is to consider the Euclidean distance between the corresponding two plants. We know from basic Mathematics that the Euclidean distance between two points is $\rho_{ij} = \sqrt{(x_i - x_j)^2 + (y_i - y_j)^2}$, where x_i and y_i are the Cartesian coordinates of the plant i in the plane. Now this distance does not capture all the subtleties of the real separation between the plants. Plants can be of different heights, and a third coordinate should be introduced. In this case we can consider that the probability f_{ij} of moving from plant i to plant j is proportional to certain function of this distance - decaying as a power-law $f_{ij} \propto \rho_{ij}^{-s}$ or decaying exponentially $f_{ij} \propto \exp(-\lambda \rho_{ij})$, where $s; \lambda \in \mathbb{R}^+$. The second approach is to consider the plant-to-plant separation in terms of the number of hops that an aphid needs to take to go from plant i to plant j using other intermediate plants. Let's consider that the aphid has an exploration radius equal to r . This means that if the aphid is on plant i it can hop directly to a plant which is at a distance smaller than r from i . In order to hop to a plant k separated by two radii from i it has to use two steps. That is, if we connect two plants by an edge, if their geographic separation is $\rho_{ij} \leq r$, then the plant-to-plant (topological) separation d_{ij} is given by the number of edges in the shortest path connecting the two nodes. Thus it can be viewed as a graph $G = (V;E)$ with vertices V and edges E . In this case we again can consider that the probability f_{ij} of moving from plant i to plant j is proportional to certain function of this distance, e.g., decaying as a power-law $f_{ij} \propto d_{ij}^{-s}$ or decaying exponentially $f_{ij} \propto \exp(-\lambda d_{ij})$ where $s; \lambda \in \mathbb{R}^+$. We'll see more about how d is formulated later in the chapter.

2.4.1 Rationale for our model

Air currents can transport aphids through long geographic distances. We exclude these unintentional movements of aphids through air currents and we identify some factors that favor the use of topological inter plant separation. Please see figure 2.2 for the illustration. The following are the

three main factors that are based on the main behavioral characteristics of the aphids' exploratory movement inside the crop fields:

- a) ***First come, first served*** - An aphid flying in one direction will land in the first available plant independently of the distance at which it is, from its starting position.
- b) ***A bird in the hand is worth more than two in the bush*** - The probability that an aphid moves from a plant i to another plant j decays with the number of other plants in the path between i and j .
- c) ***Go back before it's too late*** - An aphid flying in one direction without plants would prefer to return to its starting point.

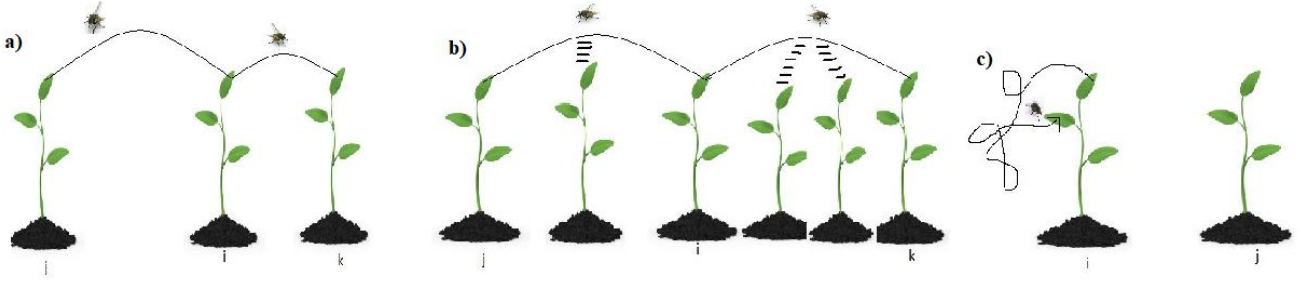


Figure 2.2 Illustration of the three factors

2.5 SIR model with topological distances

Using the topological interplant separation which is appropriate for our modeling purposes as a consequence of the previous hypothesis, the SIR model becomes:

$$\dot{S}_i(t) = -\beta S_i(t) \sum_j \tilde{A}_{ij} I_j(t) \quad (2.7)$$

$$\dot{I}_i(t) = \beta S_i(t) \sum_j \tilde{A}_{ij} I_j(t) - \mu I_i(t) \quad (2.8)$$

$$\dot{R}_i(t) = \mu I_i(t) \quad (2.9)$$

where $\tilde{A} = \sum_{d=1}^{d_{max}} d^{-s} A_d$, $d \leq d_{max}$, d_{max} is diameter of the graph. By diameter we mean the largest separation between two plants in terms of steps, and the matrix A_d captures the (long-range) mobility of the pest between plants (See Fig. 2.3).

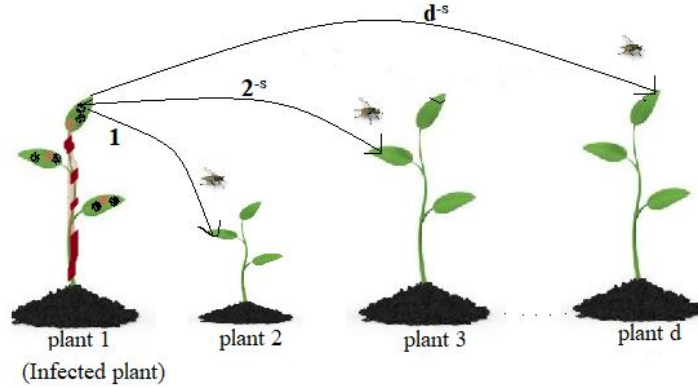


Figure 2.3 Hop of an aphid from infected plant to susceptible plant separated by d steps, given by d^{-s}

The d -path adjacency matrix A_d gives us the all the possibilities of movement of the aphid. We will always consider a connected network here. Let $d_{ij} = d$ be the shortest-path distance between the nodes i and j in a network G . The adjacency matrix in general is defined by,

$$A = \begin{cases} 1, & \text{if } d_{ij} = d. \\ 0, & \text{otherwise.} \end{cases} \quad (2.10)$$

The term ' s ' is an empirical aphid mobility parameter. If s is infinite, then the aphid has poor mobility and so all entries of the adjacency matrix become zero, except for those which become 1. On the other hand, if s is very low, then the aphid has excellent mobility and so every entry of the adjacency matrix becomes 1, suggesting that the hops are equiprobable, independent of separation.

2.6 Computational arrangements

2.6.1 Construction of the network

For our formulation, we assume a small grid of plants, just the main cultivar, as we are not interested in the trap crops. We assume a rectangular arrangement of 12 plants, that is a 3x4 grid.

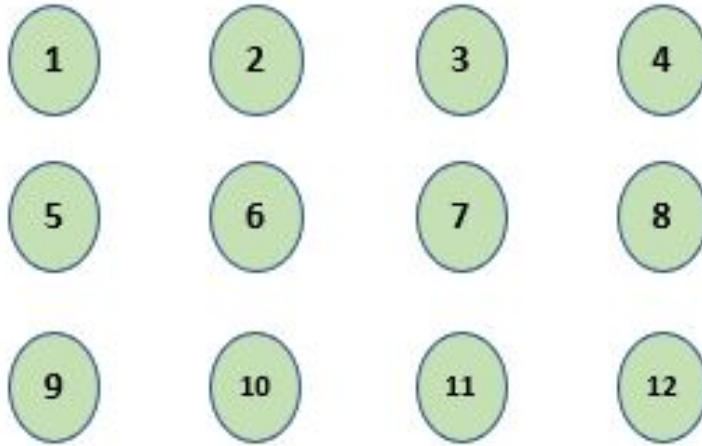


Figure 2.4 3x4 grid of nodes

The aphid can travel from any plant to any other plant. For the sake of simplicity, we don't assume the diagonal movement of aphids, i.e., from node 1 to node 6, or from node 10 to node 7, etc., though we assume bidirectional movement of aphids. We also assume that the aphid doesn't start go back to it's starting point, at a given time (We'll see this in the next section).

2.6.2 Adjacency matrix

If trap crops were implemented, which we don't assume in our modeling, the strength of the aphid mobility between two plants of the main cultivar i_d and i_{d+1} , with shortest-path i_1, i_2, \dots, i_d and i_{d+1} , will be modified as follows:

$$\tilde{A} = \begin{cases} d^{-\gamma s}, & \text{if there is at least one trap crop between the two plants.} \\ d^{-s}, & \text{otherwise.} \end{cases} \quad (2.11)$$

where, $\gamma \geq 1$ is the trap strength; As γ increases, trap strength increases and the probability of infection decreases. But in our formulation, we assume no trap crops. So, it is permanently the second case of the above equation (2.11). Therefore, the adjacency matrix that we use in our formulation is as follows:

$$\tilde{A} = \begin{bmatrix} 0 & 1 & 2^{-s} & 3^{-s} & 1 & 2^{-s} & 3^{-s} & 4^{-s} & 2^{-s} & 3^{-s} & 4^{-s} & 5^{-s} \\ 1 & 0 & 1 & 2^{-s} & 2^{-s} & 1 & 2^{-s} & 3^{-s} & 3^{-s} & 2^{-s} & 3^{-s} & 4^{-s} \\ 2^{-s} & 1 & 0 & 1 & 3^{-s} & 2^{-s} & 1 & 2^{-s} & 4^{-s} & 3^{-s} & 2^{-s} & 3^{-s} \\ 3^{-s} & 2 & 1 & 0 & 4^{-s} & 3^{-s} & 2^{-s} & 1 & 5^{-s} & 4^{-s} & 3^{-s} & 2^{-s} \\ 1 & 2^{-s} & 3^{-s} & 4^{-s} & 0 & 1 & 2^{-s} & 3^{-s} & 1 & 2^{-s} & 3^{-s} & 4^{-s} \\ 2^{-s} & 1 & 2^{-s} & 3^{-s} & 1 & 0 & 1 & 2^{-s} & 2^{-s} & 1 & 2^{-s} & 3^{-s} \\ 3^{-s} & 2^{-s} & 1 & 2^{-s} & 2^{-s} & 1 & 0 & 1 & 3^{-s} & 2^{-s} & 1 & 2^{-s} \\ 4^{-s} & 3^{-s} & 2^{-s} & 1 & 3^{-s} & 2^{-s} & 1 & 0 & 4^{-s} & 3^{-s} & 2^{-s} & 1 \\ 2^{-s} & 3^{-s} & 4^{-s} & 5^{-s} & 1 & 2^{-s} & 3^{-s} & 4^{-s} & 0 & 1 & 2^{-s} & 3^{-s} \\ 3^{-s} & 2^{-s} & 3^{-s} & 4^{-s} & 2^{-s} & 1 & 2^{-s} & 3^{-s} & 1 & 0 & 1 & 2^{-s} \\ 4^{-s} & 3^{-s} & 2^{-s} & 3^{-s} & 3^{-s} & 2^{-s} & 1 & 2^{-s} & 2^{-s} & 1 & 0 & 1 \\ 5^{-s} & 4^{-s} & 3^{-s} & 2^{-s} & 4^{-s} & 3^{-s} & 2^{-s} & 1 & 3^{-s} & 2^{-s} & 1 & 0 \end{bmatrix} \quad (2.12)$$

As we can see, the adjacency matrix gives the number of steps an aphid takes to traverse between two plants - say, for it to go to node 1 from node 9 (Refer to fig. 2.4), the shortest path it takes will be 9 to 5, and then 5 to 1. So, it takes 2 steps and hence the element in the 1st column of the 9th row gives us this information. Also, as mentioned earlier, the aphid doesn't travel to its starting point at a given time t.

2.6.3 Acceleration factor

The major factor that needs to be considered in our modeling is the acceleration from the Ground robot. Often, in agricultural modeling, or cyber-agricultural systems, the presence of the ground robot is overlooked. It is used for various purposes like, measurement of moisture content,

visual analysis of plant health, crop-picking, etc,. Thus, it has a very big impact on the movement of the aphid and in fact the movement of the disease itself. Hence we include a noise or in other words, a random perturbation factor to account for the movement of this ground robot.

CHAPTER 3 IMPLEMENTATION

Matlab software was used to implement our model and visually analyze the results. It came in handy especially because all the variables could be expressed in familiar mathematical notation (See Appendix for code).

3.1 Specifics of the code

3.1.1 Initial distribution

The variables $S_i(t)$, $I_i(t)$ and $R_i(t)$, which are the probabilities respectively of the susceptibility, infection and removal, were normally distributed (`normrnd()` in Matlab). For $S_i(t)$ which is 'S' in our code, a mean of 0.09 and a standard deviation of 0.01 were assumed. Similarly, the mean and standard deviation of $I_i(t)$, which is 'I' in the code was 0.08 and 0.002 respectively. Now, we don't work on live data and our concern is about the robustness of the model. Hence, the assumptions of the mean and standard deviation were made based on the values that the paper, which used live data.

3.1.2 Initial removal probability

Removal probability is always zero initially. This is because we assume that none of the plants are infected in the beginning of time and so, there is null probability of a plant being removed at the beginning of time. Hence, $R_i(t)$ which is 'R' in our code is zero initially.

3.1.3 Adjacency matrix

As mentioned in the previous chapter, the Adjacency matrix is a 12x12 matrix, owing to the 4x3 grid of plants. Written using eq. 2.11, the adjacency matrix (see eq. 2.12) is a hollow symmetric matrix. A hollow matrix has all the elements along its main diagonal as zeros.

3.1.4 Time

For our model to work, we need a synchronization, or something like what's called a clock in electronics. In the Matlab code, the maximum time, t_{max} was taken as 7. This t_{max} can be the number of hours, number of days, number of weeks or number of months.

3.1.5 $\dot{S}_i(t)$, $\dot{I}_i(t)$ & $\dot{R}_i(t)$

The values of $\dot{S}_i(t)$, $\dot{I}_i(t)$ & $\dot{R}_i(t)$, which is 'dS', 'dI' and 'dR' in our code is initially assumed to be zero. We declare this as a 12x7 matrix of zeros (`zeros()` in Matlab). The reason behind the 12 is that we have a 4x3 grid, i.e., 12 plants and the number 7 comes from the maximum time that's assumed, as mentioned in the previous section.

3.1.6 Birth and death rates of the disease

Birth rate β and death rate μ are assumed to be 0.5 each. We are not trying to characterize any particular disease. For instance, if $\mu = 1$, say, the recovery is too fast to see the spatial propagation, and conversely, when $\mu = 0$, the dynamics would be SI dynamics. We want to lie between these two limiting cases and that's why we assume such values for β and μ .

3.1.7 Perturbation factor from the ground robot

To factor in the perturbation, we include a random noise into our Infection variable on the right hand side of the SIR equations. We cannot really measure perturbation, or measure how much of a disturbance is created by the robot. We make use of `rand()` command in Matlab in order to model this perturbation factor.

3.2 Looping and decision control

Nested looping was made use of. Starting with $t_{max}=1$ and N (number of nodes) = 1, at each stage, the possibilities, or in other words, the neighboring plants that the aphid can explore, were checked. This is crucial, because at every node, the possibilities of exploration to other nodes in the field are the different. This is evident when we consider the aphid sitting in the nodes that border the field/grid. For example, if an aphid were in node(plant) 7 (refer fig. 2.4), its possibilities of exploration are node 3, node 6, node 8 and node 11. Therefore, it can go in all four directions. On the contrary, if it was on a node at the edge of the field, or on one of the four corners of the field, then the exploration possibilities differ. For example, in the same grid (fig. 2.4), if an aphid were in node 5, it can travel to node 1, node 6 or node 9. This is obvious to us humans, but this needs to be accounted for meticulously in our code. Hence, looping and if statements were used.

CHAPTER 4 RESULTS

As discussed in the previous chapter, we used looping and decision control for our mathematical model. In the realization, the assumption was that the propagation was initialized by infecting a single susceptible plant on the border of the field. The following results were obtained.

4.1 Probability of susceptibility

Graph shows the probability of susceptibility for all the 12 plants over time. We assumed normal distribution of the initial probability of susceptibility. There is a noise factor from the acceleration of the ground robot. Hence, we get the graph.

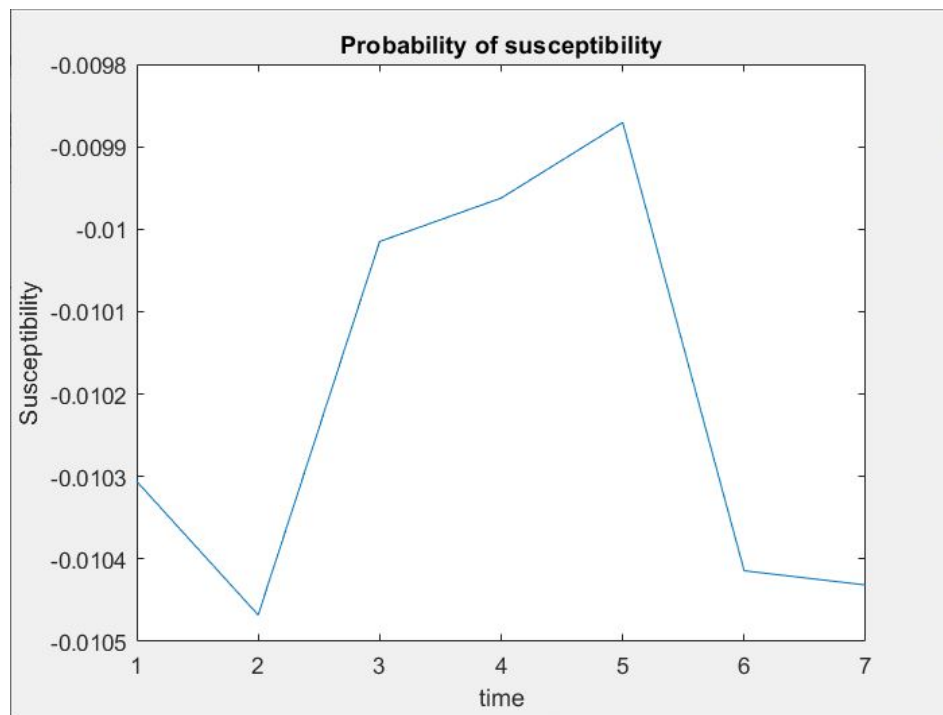


Figure 4.1 Probability of Susceptibility vs. time

dS =

-0.0073	-0.0060	-0.0071	-0.0073	-0.0070	-0.0070	-0.0062
-0.0115	-0.0115	-0.0108	-0.0116	-0.0105	-0.0111	-0.0120
-0.0094	-0.0096	-0.0110	-0.0108	-0.0127	-0.0114	-0.0112
-0.0053	-0.0071	-0.0080	-0.0064	-0.0070	-0.0061	-0.0070
-0.0090	-0.0117	-0.0127	-0.0106	-0.0095	-0.0095	-0.0111
-0.0152	-0.0159	-0.0154	-0.0142	-0.0171	-0.0132	-0.0116
-0.0148	-0.0128	-0.0142	-0.0134	-0.0164	-0.0135	-0.0142
-0.0115	-0.0121	-0.0115	-0.0124	-0.0106	-0.0104	-0.0126
-0.0071	-0.0077	-0.0075	-0.0066	-0.0061	-0.0071	-0.0070
-0.0109	-0.0109	-0.0096	-0.0099	-0.0104	-0.0071	-0.0109
-0.0103	-0.0105	-0.0119	-0.0098	-0.0107	-0.0102	-0.0097
-0.0079	-0.0071	-0.0075	-0.0061	-0.0075	-0.0083	-0.0071

Figure 4.2 $\dot{S}_i(t)$

The negative entries in the matrix dS owes to the negative sign before β in the SIR equations. None of the other variables in the $\dot{S}_i(t)$ equation can possibly contribute to these negative values. Since these are values of probability, it is a quasi probability distribution that allows a negative probability for some events. For further clarification on why these negative values are valid, let's look at the following analysis:

We know that,

$$\frac{dS}{dt} = -\beta S_i(t) \sum_j A_{ij} I_j(t)$$

$$\frac{dS}{S} = \left\{ \left(-\beta \sum_j A_{ij} I_j(t) \right) \right\} dt$$

Integrating on both sides,

$$\ln(S) = [-\beta \sum_j A_{ij} I_j(t) * t] + c \quad (4.1)$$

The constant of integration, 'c' can be found from some 'side' conditions or initial conditions, i.e., $t = 0$, for example. Therefore,

$$S = \exp([- \beta \sum_j A_{ij} I_j(t) * t] + c) \quad (4.2)$$

This 'S' value cannot be negative at all, neither can it exceed 1, thus making it a valid probability value.

4.2 Probability of infection

Graph shows the probability of infection for all the 12 plants over time. The graph has very low infection probability values. Now, in the real world, it can't and will never be this low. We get this owing to the initial normal distribution and also to the noise from the acceleration.

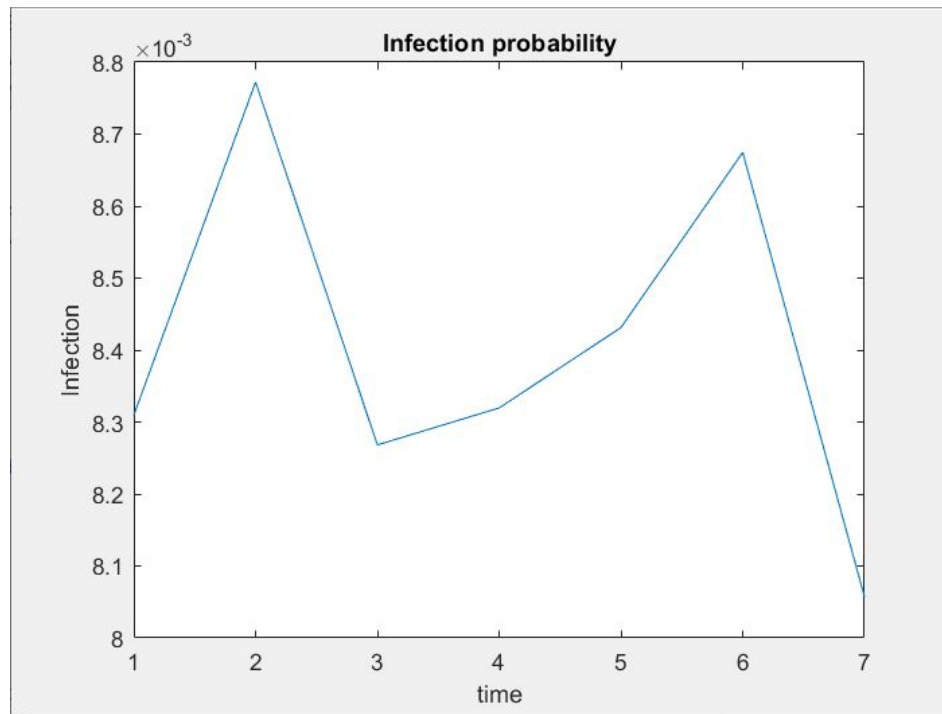


Figure 4.3 Probability of Infection vs. time

This will look very different in the real world, where trap crops are used. The strength of the trap crops play a major role in the propagation of the disease. If there was a row of strong trap crops or in other words, secondary crops between two rows of the main cultivar, then the aphid would either get attracted to the trap crop more than the main cultivar, or will get repelled by it, thus preventing the untouched row of the main cultivar, unaffected (push-pull mechanism). Hence, the probabilities might vary in the real world scenario. Besides, we did not consider diagonal

dI =

0.0055	0.0044	0.0054	0.0054	0.0053	0.0052	0.0046
0.0095	0.0097	0.0089	0.0098	0.0087	0.0091	0.0100
0.0079	0.0079	0.0092	0.0089	0.0105	0.0096	0.0094
0.0040	0.0054	0.0060	0.0049	0.0053	0.0046	0.0052
0.0074	0.0097	0.0105	0.0088	0.0079	0.0080	0.0094
0.0135	0.0138	0.0135	0.0124	0.0150	0.0116	0.0101
0.0128	0.0112	0.0124	0.0117	0.0144	0.0117	0.0124
0.0096	0.0100	0.0095	0.0102	0.0089	0.0086	0.0105
0.0053	0.0057	0.0056	0.0051	0.0046	0.0053	0.0051
0.0091	0.0091	0.0080	0.0082	0.0086	0.0059	0.0092
0.0086	0.0087	0.0100	0.0082	0.0089	0.0085	0.0081
0.0059	0.0054	0.0057	0.0046	0.0057	0.0063	0.0053

Figure 4.4 $\dot{I}_i(t)$

movements of aphids, for the sake of simplicity. This might also have an impact on the probability of infection and will bring about significant changes in the graph.

4.3 Probability of removal/recovery

Graph shows the probability of removal for all the 12 plants over time. The initial probability of removal/recovery, i.e., $R_i(t)$, which is present on the right hand side of the SIR equations is assumed to be zero initially. This is because, at the beginning of time, we assume that none of the plants are infected enough to be removed or thrown away. We must remember according to our initial assumption that removed plants represent those not only dead but also those which are useless for commercial purposes, i.e., those substantially damaged as to be used for consumption. If time was increased to 100 or 1000 instead of 7, then we would be able to visually make sense of the probability of removal. The constraint on time being 7 (hours, days, weeks or months), limits the exact visualization of the results.

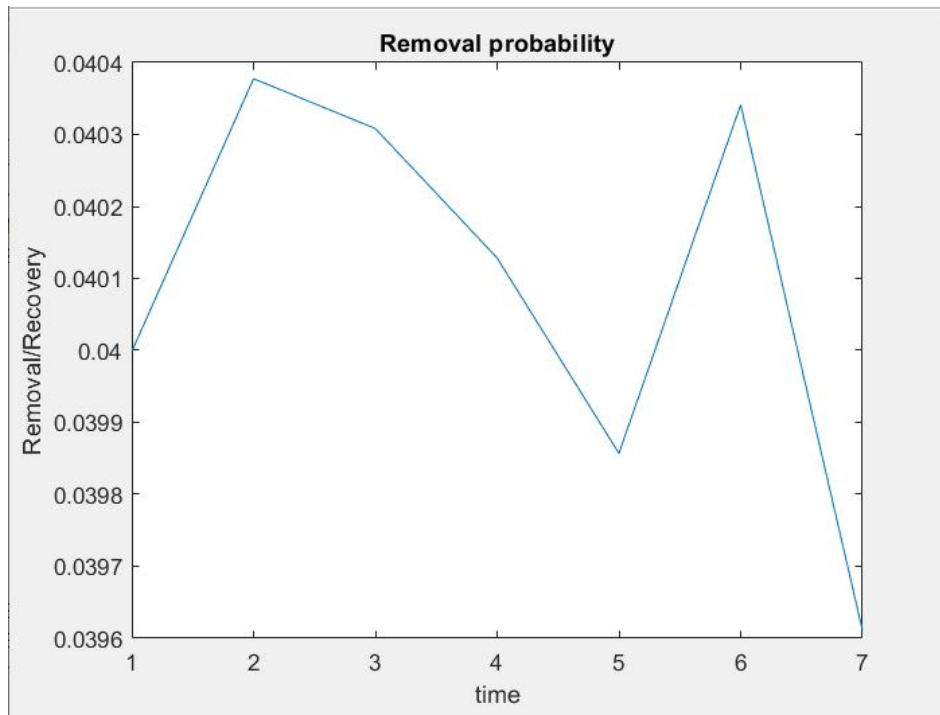


Figure 4.5 Probability of Removal vs. time

dR =

0.0402	0.0404	0.0387	0.0412	0.0401	0.0399	0.0403
0.0404	0.0383	0.0409	0.0384	0.0391	0.0410	0.0404
0.0396	0.0405	0.0400	0.0400	0.0404	0.0379	0.0391
0.0398	0.0388	0.0399	0.0381	0.0407	0.0395	0.0398
0.0420	0.0401	0.0409	0.0410	0.0409	0.0387	0.0379
0.0377	0.0407	0.0406	0.0409	0.0393	0.0396	0.0411
0.0422	0.0403	0.0404	0.0400	0.0404	0.0406	0.0394
0.0403	0.0411	0.0413	0.0399	0.0401	0.0408	0.0388
0.0410	0.0410	0.0409	0.0375	0.0408	0.0390	0.0397
0.0383	0.0393	0.0402	0.0406	0.0405	0.0395	0.0386
0.0394	0.0403	0.0393	0.0378	0.0409	0.0401	0.0400
0.0397	0.0391	0.0393	0.0377	0.0399	0.0397	0.0394

Figure 4.6 $\dot{R}_i(t)$

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APPENDIX A MATLAB CODE

```

1 clear all
2 close all
3 %defining parameters
4 N=12; %total no. of plants-->3x4 and is fixed throughout our modeling
5
6 %birth and death rate of disease
7 beta=0.5;
8 mu=0.5;
9
10 %insect mobility
11 s1=2.5;
12 s2=4;
13 s=s1; %s1-->high mobility of aphid; s2-->low mobility of aphid;
14 tmax=7;
15
16 %Let's assume that there is no trap crops; With no trap crop at all,
17 %according to the paper
18 %Hollow symmetric matrix
19 A = [0 1 2^-s 3^-s 1 2^-s 3^-s 4^-s 2^-s 3^-s 4^-s 5^-s;
20      1 0 1 2^-s 2^-s 1 2^-s 3^-s 3^-s 2^-s 3^-s 4^-s;
21      2^-s 1 0 1 3^-s 2^-s 1 2^-s 4^-s 3^-s 2^-s 3^-s;
22      3^-s 2^-s 1 0 4^-s 3^-s 2^-s 1 5^-s 4^-s 3^-s 2^-s;
23      1 2^-s 3^-s 4^-s 0 1 2^-s 3^-s 1 2^-s 3^-s 4^-s;
24      2^-s 1 2^-s 3^-s 1 0 1 2^-s 2^-s 1 2^-s 3^-s;
25      3^-s 2^-s 1 2^-s 2^-s 1 0 1 3^-s 2^-s 1 2^-s;
26      4^-s 3^-s 2^-s 1 3^-s 2^-s 1 0 4^-s 3^-s 2^-s 1;

```

```

27     2^-s 3^-s 4^-s 5^-s 1 2^-s 3^-s 4^-s 0 1 2^-s 3^-s;
28     3^-s 2^-s 3^-s 4^-s 2^-s 1 2^-s 3^-s 1 0 1 2^-s;
29     4^-s 3^-s 2^-s 3^-s 3^-s 2^-s 1 2^-s 2^-s 1 0 1;
30     5^-s 4^-s 3^-s 2^-s 4^-s 3^-s 2^-s 1 3^-s 2^-s 1 0;];
31
32 %Initial conditions/values
33 Smean=0.09;
34 Sstddev=0.01;
35 S=normrnd(Smean,Sstddev,[12,7]);
36 Imean=0.08;
37 Istdddev=0.002;
38 I=normrnd(Imean,Istdddev,[12,7]);
39 R=0;
40
41 dS=zeros(N,tmax);
42 dI=zeros(N,tmax);
43 dR=zeros(N,tmax);
44
45 for t = 1:tmax
46     for i = 1:N
47         Q=0;
48         a = rand(1); %acceleration factor for the robot
49         if (i==6) || (i==7)
50             for j = i+1
51                 Q = Q + A(i,j)*(I(j,t)+a);
52             end
53             for j = i-1
54                 Q = Q + A(i,j)*(I(j,t)+a);
55             end
56             for j = i+4
57                 Q = Q + A(i,j)*(I(j,t)+a);
58             end
59             for j = i-4

```

```
60     Q = Q + A(i, j) * (I(j, t) + a);
61     end
62 end
63 if (i==2) || (i==3)
64     for j = i-1
65         Q = Q + A(i, j) * (I(j, t) + a);
66     end
67     for j = i+1
68         Q = Q + A(i, j) * (I(j, t) + a);
69     end
70     for j = i+4
71         Q = Q + A(i, j) * (I(j, t) + a);
72     end
73 end
74 if (i==10) || (i==11)
75     for j = i-1
76         Q = Q + A(i, j) * (I(j, t) + a);
77     end
78     for j = i+1
79         Q = Q + A(i, j) * (I(j, t) + a);
80     end
81     for j = i-4
82         Q = Q + A(i, j) * (I(j, t) + a);
83     end
84 end
85 if i==1
86     for j = i+1
87         Q = Q + A(i, j) * (I(j, t) + a);
88     end
89     for j = i+4
90         Q = Q + A(i, j) * (I(j, t) + a);
91     end
92 end
```

```
93     if i==5
94         for j = i+1
95             Q = Q + A(i, j) * (I(j, t) + a);
96         end
97         for j = i-4
98             Q = Q + A(i, j) * (I(j, t) + a);
99         end
100        for j = i+4
101            Q = Q + A(i, j) * (I(j, t) + a);
102        end
103    end
104    if i==9
105        for j = i+1
106            Q = Q + A(i, j) * (I(j, t) + a);
107        end
108        for j = i-4
109            Q = Q + A(i, j) * (I(j, t) + a);
110        end
111    end
112    if i==4
113        for j = i-1
114            Q = Q + A(i, j) * (I(j, t) + a);
115        end
116        for j = i+4
117            Q = Q + A(i, j) * (I(j, t) + a);
118        end
119    end
120    if i==8
121        for j = i-1
122            Q = Q + A(i, j) * (I(j, t) + a);
123        end
124        for j = i-4
125            Q = Q + A(i, j) * (I(j, t) + a);
```



```

126         end
127         for j = i+4
128             Q = Q + A(i, j) * (I(j, t) + a);
129         end
130     end
131     if i==12
132         for j = i-1
133             Q = Q + A(i, j) * (I(j, t) + a);
134         end
135         for j = i-4
136             Q = Q + A(i, j) * (I(j, t) + a);
137         end
138     end
139
140     dS(i, t) = (-beta) * S(i, t) * Q;
141     dI(i, t) = (beta * S(i, t)) * (Q - mu * (I(i, t) + a));
142     dR(i, t) = mu * (I(i, t) + a);
143
144 end
145 end
146
147 display(dS)
148 display(dI)
149 display(dR)
150
151 %Graphs
152 figure(1)
153 DS=transpose(dS);
154 m=mean(DS, 2);
155 plot(m)
156 xlabel('time')
157 ylabel('Susceptibility')
158 title('Probability of susceptibility')

```

```
159
160 figure(2)
161 DI=transpose(dI);
162 k=mean(DI,2);
163 plot(k)
164 xlabel('time')
165 ylabel('Infection')
166 title('Infection probability')
167
168 figure(3)
169 DR=transpose(dR);
170 l=mean(DR,2);
171 plot(l)
172 xlabel('time')
173 ylabel('Removal/Recovery')
174 title('Removal probability')
175
176 figure(4)
177 plot(m)
178 hold on
179 plot(k)
180 hold on
181 plot(l)
```