

CARLETON UNIVERSITY

# Using Lotka-Volterra Equations to model the impact of parasitoids on the Plutella xylostella(Diamondback moth)

## BIOL 5409 Assignment #1

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A paper by (Henri E.Z Tonnand et al., 2009) was published in the Ecological Modeling journal 2009, which examined the impact of biological control of the Diamondback moth through the use of the Lotka-Volterra models. The following paper is an attempt to recreate the models from this study. Additional further insights will be drawn from the models created.

# 1.0 Introduction

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The Diamondback moth (DBM) is a dangerous pest to many cultivated plants and are now found worldwide (Henri E.Z Tonnad, 2009). The DBM arrived in North America from Europe in the mid 1800s and destroys many vegetable crops (especially from the mustard family) including; canola, mustard, broccoli, cabbage and several greenhouse plants (Duke, 2001). The impact of the DBM is most significant in the Canadian Prairies and the north central region of the United States (Duke, 2001). Currently the only method for controlling DBM population levels is with the use of pesticides, even though there are several species of parasitoids native in areas that the DBM are found (Duke, 2001) (Henri E.Z Tonnad, 2009). The cost of pesticide currently is an estimated billion dollars annually worldwide (N.S Talekar, 1993).

## **Diamondback Moth**

The life cycle of the DBM has four stages; egg, larvae, pupae and adult. It takes approximately 32 days for the DBM to mature from an egg and new generations occur every 21-51 days depending on environmental conditions (Duke, 2001).

### *Eggs*

The eggs are laid on the upper and lower leaves and can appear singly or in groups of two or three. They appear usually along a vein in the leaf where the surface is uneven and are oval with a yellowish-white color (Duke, 2001). After 5 or 6 days the eggs will hatch and the larvae will emerge.

### *Larvae*

Upon hatching the larvae will burrow itself into the leaf and begin feeding on the inside of the leaf. Once the larvae has increased in size, usually after 10 days, it will emerge from the bottom of the leaf and continue feeding (Duke, 2001). To reach maturity the larvae will moult three times and will reach maturity in 10 to 21 days depending on the environmental factors, i.e. abundance of food and temperature. Once the larvae have reached maturity they are about 12mm long (Duke, 2001).

### *Pupae*

The larvae pupae of the Diamondback moth is a fine, white, meshed cocoon that is attached to the host plant by the; stem, leaf or seed pods. This stage will last anywhere from 5 to 15 days, again depending on the environmental conditions (Duke, 2001).

### **Adult**

When the adult emerges from the cocoon it is; 8-9mm long and has a wing span of 12-15mm. The female will lay close to 160 eggs during its 16 lifespan.

The damage to vegetable crops occurs when the eggs hatch and become larvae. The larvae feed on the leaves, buds, flowers, seed pods as well as parts of the stem (Duke, 2001) which can destroy the plant, depending on its growth stage as well as the larvae density (Duke, 2001).

Pesticide sprays often lose their effectiveness because of the resistance that the DBM develops. For this reason new pesticides are constantly required, or a new solution must be developed (Asian Vegetable Research and Development Center, 1997).

### **Parasitoids**

As previously mentioned the DBM have predators. Where ever the diamond back moth is found there are parasitoids that will attack the DBM in one of its 4 stages depending on the specific species (Duke, 2001). However, these parasitoids usually are not abundant enough to keep the DBM population in check. In Europe, where the DBM originated, there are over 40 species of parasitoids that attack the Diamondback moth and therefore measures rarely need to be taken to keep the damage at a minimum (Asian Vegetable Research and Development Center, 1997).

It would seem then that a logical way to control the DBM levels would be to introduce species European parasitoids to areas where they are not normally found. The *Diadegma semiclausum*, a parasite found in Europe has been successfully used to control the Diamondback population in several countries including; Australia, New Zealand, Indonesia, Malaysia, Taiwan and the Philippines (Asian Vegetable Research and Development Center, 1997).

### **Lotka-Volterra Model**

The Lotka-Volterra equation is often used to model a predator-prey relationship. For this study we will use a modified set of equations (equation 1.1, 1.2 (Henri E.Z Tonnad, 2009)) to model the predator-prey relationship between the Diamondback moth and a mixed group of parasitoids. While the Lotka-Volterra equation has been used in many different studies, in many different biological fields, no study has ever tried to predict and assess the impact of a parasitoid (Henri E.Z Tonnad, 2009). In the study performed by (Henri E.Z Tonnad, 2009) their hope was that by using the empirical data they would be able to mathematically estimate the parameters and fit the Lotka-Volterra equations to the field data sets (Henri E.Z Tonnad, 2009). The purpose being, if the results confirmed the positive impact of the pests on the population

of Diamondback moths, then such modeling techniques could be used for pest management for this system and potentially others as well (Henri E.Z Tonnad, 2009).

The goal of this study is to confirm the model and subsequent results of the study by (Henri E.Z Tonnad, 2009) and demonstrate further uses of such models. To verify the results of the simulation, results will be compared to the theoretical results they generated.

## 2.0 Methods

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### Lotka-Volterra Model

As previously stated, the following equations, 1.1-2, will be used to estimate the populations of the Diamondback moth and the parasitoids. For the purpose of this model all parasites, both indigenous and released, will be counted as a single species.

$$\text{equation 1.1} \quad \frac{dX}{dt} = \alpha_1 x - \beta_1 x^2 - \gamma_1 xy$$

$$\text{equation 1.2} \quad \frac{dY}{dt} = -\alpha_2 y - \beta_2 y^2 + \gamma_2 xy \text{ (Henri E.Z Tonnad, 2009)}$$

In this equation alpha, beta and gamma correspond to the estimated parameter values found in Table 1 of the study done by (Henri E.Z Tonnad, 2009).

### Creating the Models

In order to recreate the results they generated and be able to compare them the same steps were followed. A series of five simulations were run with the first being Werugha before release and the last being Tharuni following release.

A basic model could easily be coded in R to represent this. It would have the following form:

```
parameters <- (alpha, beta, gamma.....) #initialize the parameters
yo <- c(x,y) #set initial conditions
time <- seq(0,t,0.01) #generate time sequence
```

```
calc<-function(parameters){insert equation}  
results <- ode(y=y0,time,calc,parameters)
```

While this is easy to code initially it becomes time consuming to be changing the parameters and initial values for each data set.

Therefore to make user input easier and more efficient a simulation was made that produce all five results simultaneously. To do this the code was broken into several parts. First was a definition of universal variables, i.e. variables that are called upon in several functions, next are several defined functions that perform all the calculations and return the results and finally the executables, i.e. the calling of each function.

## Variables

This section included the following:

- definition of the initial population sizes
- main time sequence for the ode's
- dimensions of the data structure required

The reason the parameters were not defined here, is because if in the future the parameters were calculated instead of given it would be easier to implement since they already defined in a function

## Functions

The functions are the backbone of the simulation. By having all the required calculations isolated in separate functions it is not only easier to navigate through the simulation, but if in the future changes were to be made to the model it would easier to add or change the model. The functions that where made include:

- Calculation Function
- Parameters Function

- Plot function
- Graph Function
- Graph2 Function
- Prediction Function
- Average Function

The calculation function will be used to call up the pre-built *ode* function. This will be used to generate a matrix for the solutions to equations 1.1-2.

As mentioned before the parameters function is currently used to define the parameters that were given, however, it would be simple to adapt this function to estimate the parameters.

The plot function is used to set up and provide all the necessary information for the calculation function, then take the results and store them in a single ordered matrix. This allows all five graphs to be produced at once without having to manually adjust and change the settings.

The graphing function takes the final results matrices and separates and organizes the results to be displayed.

The second graphing function can be run instead of the first to graph the five unique phase plots.

To provide an example of the usefulness of the model, (Henri E.Z Tonnad, 2009) used their model to find the best initial release numbers for the parasitoids to control the population. While their methodology isn't explained, similar results were reconstructed in the predictions function. This function was rather complex in that it simulated the equations 1.1-2 over many different initial population values of DBM as well as several different initial population values of the parasitoid. This was done to determine if there was a optimal value, and if there was to prove the usefulness of using purely mathematical models to estimate real world scenarios. For this simulation the model will be run for only the first 100 iterations, instead of a 1000, and will be run for

densities of DBM from 0 to 25 in steps of 0.1. The initial populations of parasitoids that will be used will be (0.49,0.69,1.38,5,20,100). The first 3 appear in the original study, however for a better understanding of the trends three additional values were added.

The averaging function is used to estimate where the equilibrium lies if the model has not run till stabilization.

By following these steps in creating the model, an accurate reproduction of the original model was able to be made.

## 3.0 Results

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As previously mentioned the simulation will generate all the necessary graphs as seen in figure 1.1 and the phase plots in 2.0. However, for the purpose of examination the plots were separated.

### **Werugha Before Release (Fig 1.2 and Fig 2.1)**

The parameters were set for the pre-release parameters as found in the region of Werugha before any parasitoids were released. The model predicted that there would be a damped oscillation that reached a maximum peak of approximately 12 DBM per plant and a minimum of approximately 2 DBM per plant before damping to an equilibrium of approximately 5.2 DBM per plant. While the density levels of the parasitoid oscillated slightly they never rose greater

than approximately 1.6 and soon settled at around 0.6 parasitoids per plant. This is further demonstrated in the phase plot by the helical shape that winds inward towards 5.2, 0.6.

### **Werugha After Release (Fig 1.3, Fig 2.2)**

After the parasitoids were released in the Werugha region the density of DBM per plant decayed rapidly to less than 1 DBM per plant, however it soon rose again, which suggests a low frequency oscillation that would soon settle to approximately 2.1 DBM per plant. The density of the parasitoid seemed to remain steady at approximately 0.2, however upon examining the phase diagram it is obvious that it is oscillating between a high of 0.23 and a low of 0.14.

### **Tharuni Before Release (Fig 1.4, 2.3)**

The parameters were set for the pre-release parameters as found in the region of Tharuni before any parasitoids were released. The model predicted that there would be a damped oscillation that reached a maximum peak of approximately 10 DBM per plant and a minimum of approximately 2.6 DBM per plant before damping to an equilibrium of approximately 6 DBM per plant. While the density levels of the parasitoid oscillated slightly they never rose greater than approximately 1.6 and soon settled at around 0.6 parasitoids per plant, with the minimum reaching approximately 0.15. This is further demonstrated in the phase plot by the helical shape that winds inward towards 6.1, 0.58.

### **Tharuni After Release 1 (Fig 1.5, 2.4)**

After the release of parasitoids into the region, the density of the DBM dropped rapidly, to a low of approximately 3.3 DBM per plant, then overshooting to a new high of approximately 4.1 DBM per plant, before settling to equilibrium of approximately 3.8 DBM per plant and 0.1 parasitoids per plant. This appears as a spiral on the phase diagram that settles at

approximately 3.8 and 0.8 respectively. We also notice from the phase plot that the density of the parasitoids reached a high of 0.38 and a low of almost 0.07.

## **Tharuni After Release 2 (Fig 1.6, 2.5)**

Similar to the previous release, the results were that of an oscillation with an eventual equilibrium at a lower population density. However the frequency of the oscillation was higher with a larger difference between the minimum and maximum. The density first rose to over 11 DBM per plant, then quickly fell to a low of approximately 1.7 DBM per plant followed by an overshoot to approximately 5.8 DBM per plant. The population density of the DBM eventually settled to approximately 3.6 DBM per plant. The parasitoid densities oscillated as well, clearly demonstrated in fig 2.5, where it reached a maximum at 1.35 and a minimum of approximately 0.1 before settling near 0.35. These oscillations are clearly seen in the phase diagram.

## **Prediction**

Since the prediction model seemed to have run longer than in the study, it showed that at a high enough initial population of DBM, they might actually drive themselves to extinction. With an initial parasitoid value and DBM of 0.49 and approximately 3 respectively, the DBM peaked at almost 10 DBM per plant after two weeks. The same extinction could occur with the parasitoid. With an initial value of 100 per plant, it seemed to control the population at first, however with higher DBMs as well as maybe more time the parasitoids may drive themselves to extinction. The best result occurred at an initial population density of 0.69, however a value of 1.38 reached equilibrium at approximately the same value. For the remaining higher initial values, it would appear that, while they do keep the population in control, when the DBM density is low, when faced with a higher density they did not perform as well.

## 4.0 Discussion

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By creating purely mathematical models I was able to generate results that matched the results of the study. The results showed that not only would introducing parasitoids into the environment reduce the overall population of Diamondback moths but it would help control the population by keeping the levels at a more steady and predictable level. The paper by (Henri E.Z Tonnad, 2009) stated in their introduction that if they were able to match the empirical results and support the idea that the introduction of parasitoids into the population would have a positive effect, than they would have proven that purely mathematical models can be used to help manage the population of Diamondback moths by introducing new species of parasitoids. By being able to reproduce their results, I have been able to support their argument.

I did however experience several difficulties with their experimental process and will go through them in the order I experienced them.

The first problem I encountered was with their parameters. They stated that they estimated the parameters using a series of very complex equation. The problem is this. Since this is a paper on the feasibility of using purely mathematical models to simulate biological events, they should have included more details on how they got the parameters. As it stands, the paper would be of no use to modeling other regions since the parameters are specific to that region and they give no mention of how they could be adapted to fit different locations. However, if their intent is solely to prove the point and not to provide help to future work, then the information given is sufficient.

The next problem was with their timing, i.e. what an iteration represents in real time. To create the scale for my figures I had to reference "landmarks" on my graphs to ones that appeared in

theirs and extrapolate the necessary information to convert the scale from iterations to weeks. Along the same note they seemed to have used a larger step size, which in my opinions was not sufficient for the task. Finally their simulation run time was not sufficient in several graphs to accurately depict certain trends. For example in Fig 1.2 I have depicted 4 cycles which is enough to show that it approaches equilibrium and that it oscillated. As they show it, they only have 1.5 cycles which barely indicates oscillation and does not hint at the fact that it will reach equilibrium. The only reason for this oversight is if they felt that a natural event would not reach equilibrium, in which case the parameters should have more accurately reflected that. The next is in figure 1.3. They show that the population decays to a steady state, when in-fact the model predicts a very low-frequency oscillation that actually reaches equilibrium at a significantly higher density than their graph shows. Similarly to before their version of fig 1.4 leads the viewer to think that the density is oscillating with little decay. If this is what they wished to model, than the parameters where wrong, because my model shows a eventual equilibrium. The most significant difference lay in figure 1.5 and 1.6. While the equilibrium values remain close to the same, the shape of their curves show zero oscillation while my model shows that there would be some.

The final problem I ran into was with their prediction graph. At first glance it looks like the results are completely different, however with an understanding of what is happening, the reason is because since they did not provide any sort of scale between iterations and weeks, my 2 week point may be different from theirs. It is my opinion that my model, as seen in figure 7, actually demonstrates the results in a better fashion. Since my model ran for longer with more variables it is clear why there is a maximum parasitoid population, even if we disagree on the exact value.

Before the model could be used for any real method of controlling Diamondback moth populations a couple changes would have to be made. The *parameters function* would have to be changed so that it would be able to generate a set of estimated parameters for a given area. Next, the *prediction function* would have to be made more powerful and the entire model would have to be run on a powerful computer. That is to say, with the model as it is, it takes

approximately 15 seconds to run. However, in order to be of any use the function would have to generate the same graph for every iteration and for more possibilities in order to ensure that the choices that are made are indeed the most appropriate. For example, as the model is it runs for 100 iterations 251 times for 6 different parasitoid values or 150 600 times. To be more accurate the model should run for 1000 iterations for 500 different DBM concentrations and 100 different parasitoid populations 50 000 000 times as well.

# 5.0 References

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## Works Cited

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