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INTERACTIONS OF PROTIST AND BACTERIA: A MATHEMATICAL MODEL

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INTERACTIONS OF PROTIST AND BACTERIA – A MATHEMATICAL MODEL

by

MATTHEW LE

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ABSTRACT

INTERACTIONS OF PROTIST AND BACTERIA –
A MATHEMATICAL MODEL

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The University of Texas at Arlington, 2014

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Relationships between interacting organisms generally have several key variables that describe the dynamics of their specific relationship. And the results from those symbiotic relationships are important in that both species are affected in a significant, observable way. With this in mind, it is found that the characteristic actions of each of the two species affect the population size of both species. This effect, caused by the species' actions and interactions is qualitatively noted and is further interpreted and quantized.

The complicated relationship between a predator and its prey is broken down and analyzed to give better insight to the projected dynamics of their differential growth patterns in a specific environment with respect to time.

Many mathematically extreme, but biologically relevant scenarios are considered to showcase the wide scope of plausible outcomes that can be predicted by the

constructed model. These rare, but possible scenarios are scrutinized to verify the model's validity in predicting the results of many scenarios instead of just a particular common situation. This enhances the level of trust that the model can be given in predicting important results.

The relationship between a protist species, the predator in question, and a bacterial species, the protists' prey, is put under scrutiny with this model that features facets of common organism interplay.

The model that has been constructed for this scenario has an intrinsic balance in its foundation in that it is complex enough to accurately depict the population dynamics of this specific predator-prey relationship with a high degree of detail, but also maintains a simplistic structure that can be easily manipulated to adjust for differing situations that also may be of interest to others.

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CHAPTER 1

INTRODUCTION

There is a lot of debate among biologists concerning where many organisms fit in the evolutionary tree of life, and the fashion in which many organisms are categorized also fuels the debate. As scientific understanding progresses, species and even higher categories of classification are shuffled. The protist group is a source of much debate in phylogenetics. And though the protist grouping has a variation that is much, much greater than other taxonomic groupings of other organism types and has been the source of currently irreconcilable ideas, there are still some characteristics that can be generalized for many of the members of the group.

Though there is much less uncertainty when it comes to their classification, bacteria have a wide range of characteristic qualities too, much like protists. Some of their identifying traits are able to be generalized as well.

Asexual methods of reproduction are employed by both bacterial and protist species, and the mechanics of their metabolisms stem from the same heterotrophic foundational principles. Though members of both groups are capable of photosynthesis, a type of autotrophic metabolism, a heterotrophic process of metabolism follows a predator-prey model much more closely and is more useful for the population dynamics under study.

Bacterial groups have been observed to aggregate together to form complexes that seem to be able to work together in a pseudo-multicellular fashion, but each cell remains distinct and independent. Since these occurrences are not common and the bacterial cells are observed to be independent, they are viewed as unicellular organisms.

As currently categorized, there are species of protists that are multicellular, but many species exist as unicellular organisms. In addition to that, the multicellular protist species do not exhibit the kind of sophisticated, specialized workings of a true multicellular individual with specialized tissue types. Therefore, the protists under study are also considered to be single-celled with organization that does not reflect multicellularity. Though it should be noted that eukaryotes are much more organized than their prokaryotic counterparts since eukaryotic cells have membrane-bound organelles and true nuclei.

While sizes of both groups vary significantly, in general, it has been observed that protist species are much greater in size when compared to species of bacteria. Bacteria normally fit within the range of .5 to 5 micrometers, typical for a prokaryotic cell, whereas protists' sizes usually fit within the range of 10 to 100 micrometers that is typical for a eukaryotic cell. On average, protists are about 10 times the size of a prokaryotic bacterial cell.

Factors such as mode of reproduction, metabolism, cell organization, and even details about each organism's physical size are important in formulating a model and must be considered during the research process of constructing an accurate mathematical model (Thingstad, 2000).

CHAPTER 2

MODEL CONSTRUCTION

A qualitative approach was used to first construct the skeletal structure of the protist-bacteria predator-prey model. Critically thinking about the fundamental relationship dynamics lead to the conception of the flow diagram depicted in Figure 1.1.

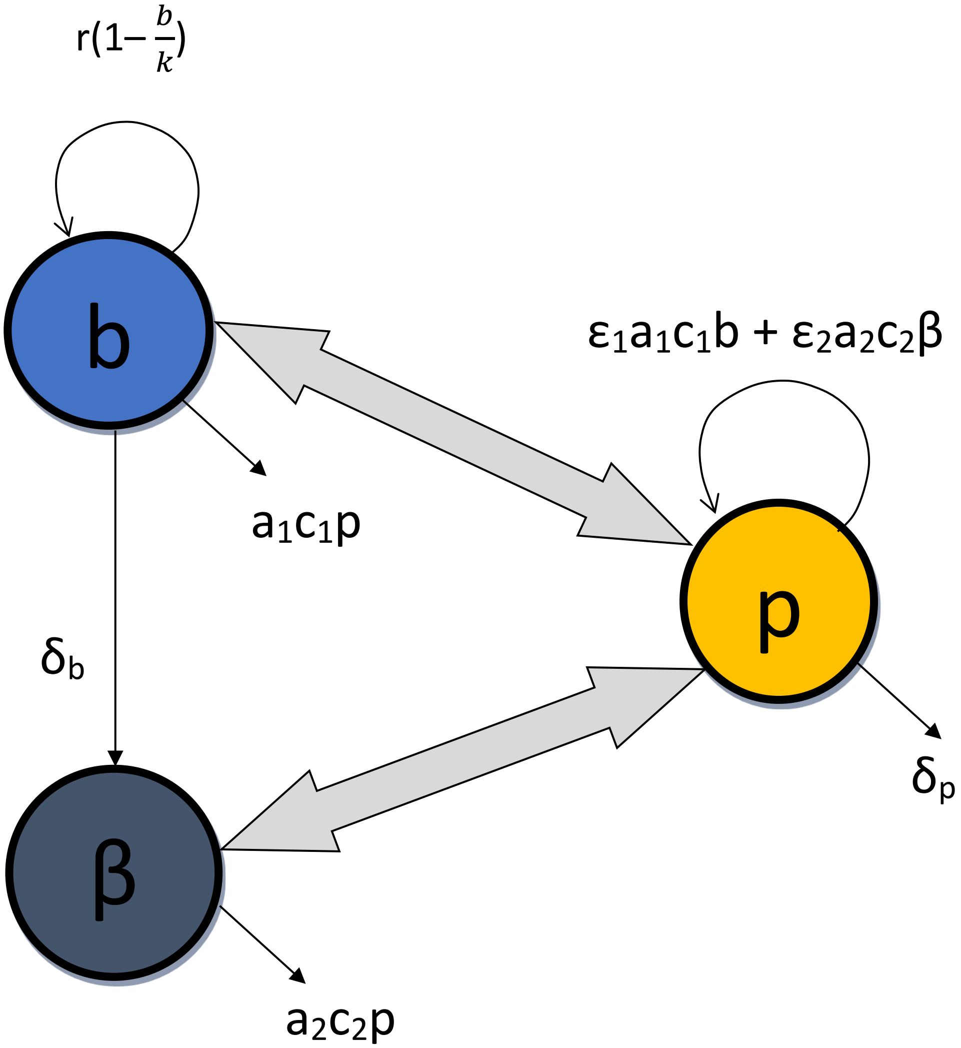

Figure 2.1: Flow diagram depicting the mathematical model of protist-bacteria dynamics.

There were three populations of interest in the model. Accounting for the following three populations led to a better understanding of how each one affects the other in its dynamics: Protists p, Living Bacteria (or simply Bacteria) b, and Dead Bacteria β. These groups represented the variables that govern the differential growth patterns of each population. Each group affected the other, and even affected the observed pattern of change for itself in a quantifiable way.

We draw an arrow going from the bacterial population to the protist population noting that there is an interaction between a predator and its prey and that the consequence of the interaction is a decrease in the bacterial population and an increase in the protist population by a factor related to the amount the bacteria decreased due to the interaction (Otto et al, 2007).

But we notice that bacteria can die due to results unrelated to their consumption by protists. We denote this by drawing an arrow from the population of living bacteria to the population of dead bacteria. Another arrow was drawn, from the dead bacteria population to the protist population showing that the protist population can experience an increase in size by consuming the organic matter of the dead bacteria. Protists also experience death, but a separate variable was not needed for the population of dead protists because we assume that the dead protists cannot affect the population sizes of the three groups of interest (HOLYOAK, 1996).

We assume that the bacterial population reproduces asexually in a way that represents logistic growth since their resources are not unlimited. This is shown graphically with the curved arrow going from the bacterial population to itself.

From this flow diagram, we derive these differential equations that describe the dynamics of each population:

1. $$\frac{\delta p}{\delta t} = \varepsilon_1 a_1 c_1 bp + \varepsilon_2 a_2 c_2 \beta p - \delta_p p$$

2. $$\frac{\delta b}{\delta t} = rb(1 - \frac{b}{k}) - a_1 c_1 bp - \delta_b b$$

3. $$\frac{\delta \beta}{\delta t} = \delta_b b - a_2 c_2 \beta p$$

Figure 2.2: Differential equations of each population of interest.

In explaining the first differential equation, the equation describing the change in the protist population, we see that the population increases in proportion (ε) to the amount of decrease experienced by the living and nonliving bacteria (a_1c_1bp and $a_2c_2\beta p$ respectively). The population of protists decreases only due to their death rate (δ_p).

The second differential equation represents the change in the population of living bacteria. The population increases in a manner similar to a logistic pattern of growth that is described by the term $rb(1 - \frac{b}{k})$ and it is decreased by the rate that protists encounter and consume bacteria and by their death rate (δ_b).

Table 2.1- Parameters and symbols of the mathematical model

Term	Symbol	Units	Estimated Parameter value for the most Biologically Probable Scenario (Standard)
The rate of change in the amount of protists	$\frac{\delta p}{\delta t}$	# protists/(cm^3*h)	N/A
The rate of change in the amount of bacteria	$\frac{\delta b}{\delta t}$	# bacteria/(cm^3*h)	N/A
The rate of change in the amount of dead bacteria	$\frac{\delta \beta}{\delta t}$	# dead bacteria/(cm^3*h)	N/A
The number of bacteria	b	# bacteria/cm^3	Initial value - 1000000
The number of protists	p	# protists/cm^3	Initial value – 1
The number of dead bacteria	β	# dead bacteria/cm^3	Initial value – 0
Efficiency factor of bacteria consumption	ε_{1*}	# protists/# bacteria	ε_1=((2k-b)/2k)α
Efficiency factor of dead bacteria consumption	ε_2	# protists/# dead bacteria	$1*10^{-3}$
Probability of ingesting a living bacterium upon meeting	a_1	N/A	1.00
Probability of ingesting a dead bacterium upon meeting	a_2	N/A	.75
Contact rate of bacteria and protist	c_1	cm^3/(h*# protists)	$3.8*10^{-6}$
Contact rate of dead bacteria and protist	c_2	cm^3/(h*# protists)	$1.9*10^{-6}$
Per capita death rate of protists	δ_p	1/h	$7*10^{-3}$
Per capita death rate of bacteria	δ_b	1/h	$1*10^{-1}$
Reproductive factor of bacteria	r	1/h	1
Carrying capacity of bacteria	k	# bacteria/cm^3	10000000
Efficiency factor of bacteria consumption	α	# protists/# bacteria	1/200

* ε_1=((2k-b)/2k)α

Note: h - hours, cm - centimeter

The third differential equation measures the rate of change in the population of dead bacteria. Their population grows with the rate of death of living bacteria (δ_b) while the population shrinks with the rate of encounter and consumption by protists ($a_2c_2\beta p$).

When considering the efficiency factor for living bacteria, it was taken into account that bacteria generally have a greater nutrient density when they are experiencing a relatively rapid growth (when there are fewer bacteria) and have less nutrient density when they are experiencing a relatively slow growth (when there are many bacteria) (Briony, 2011). This idea is shown by the term $((2k-b)/2k)$, which multiplies with α to equal the efficiency factor, ε_1. Biologically speaking, populations spend most of their time near or below their carrying capacity, but it is possible for the population to temporarily shoot above carrying capacity, so in order to keep the efficiency terms positive for values of $b > k$, k is multiplied by 2 in the efficiency equation (we assume $b < 2k$ is always true).

Using this model, we assign numerical values to the parameters in a way that optimizes the accuracy of the model to realistic scenarios with its ability to predict the results of other scenarios of interest.

CHAPTER 3

PARAMETER RATIONALE

The efficiency factor of bacterial consumption by protists isn't defined as a constant parameter. It depends on the size of the bacterial population b, and an intrinsic conversion factor α, which could vary between different species of bacteria and protists. In this model, α is defined as 1/200, meaning that the protist population experiences an increase of 1 per a decrease of 200 in the bacterial population. Several factors were weighed before consensus was established for the numerical value of 1/200: Given the large difference in size between the bacteria and protists, we assume that there must be a large amount of bacteria consumption before a protist acquires the necessary energy and organic material to reproduce viable offspring. Initially, a range of 1/100 and 1/1000 was accepted for the conversion factor, but to narrow the scope of the α factor, the average was taken of those two numbers that gave approximately 1/182. This was rounded down to 1/200 for the reason of preserving modesty in the conversion factor. It should be noted that 1/200 represents the maximum efficiency factor, for when the population of bacteria is very small. As bacteria accumulate, each individual bacterium will have a lower concentration of organic nutrients, so the amount of bacteria that need to be eaten for the protists to experience an increase goes up.

Stemming from this rationale, the efficiency factor of consuming dead bacteria (ε_2) was given a numerical value of 1/1000, much less than 1/200. The factor ε_2 is held constant, unlike the efficiency factor for the consumption of living bacteria. The reason for this is that, with the level of complexity of this particular model, it is impossible to tell what the population size of bacteria was when the specific bacterium died. To remedy this problem, we make the value for ε_2 a constant. ε_2's value is depressed in relation to the possible values for ε_1 because we assume that the dead bacteria could have died because they weren't able to ingest the critical amount of nutrients they needed in order to survive; following that notion, it was reasoned that they would therefore have a decreased concentration of nutrients in comparison to their living counterparts. The organic material of the dead bacteria could also degrade before the protists have the chance to ingest the matter, which would further decrease the value for ε_2.

Values for the probability of ingestion (a) upon contact were 1.00 and .75 for living bacteria and dead bacteria respectively. While assigning these numbers to the probabilistic parameters, we assume that there is a 100% chance that a protist will ingest a living bacterium when they come into contact because it would be favorable for the protist to do so. And we assume that the probability of a protist to ingest a non-living bacterium would be less than the probability of ingesting a living bacterium because protists can exhibit selective behavior concerning whether or not to expend their energy on consuming something that has a low density of nutrients.

In determining the appropriate magnitude of c_1 and c_2, knowledge about the contact rates of motile and non-motile objects became critical. Two non-moving objects will never come into contact if, initially, they are separated. If one of those objects were motile, though, then their rate of contact would be greater (non-zero). It was then reasoned that if both objects were in motion, their rate of contact would be the most frequent of all three possible cases (Gonzalez et al, 1993). For this reason, the value for the contact rate of living bacteria and protists (c_1) was given a greater numerical value than the contact rate of non-living (non-moving) bacteria and protists (c_2).

The per capita death rate for protists and for bacteria was calculated by finding the reciprocal of the average lifespan of the organism. The reciprocal of the average lifespan has special significance in that it implies the chance of death of a cell per unit time (hours in this case). This value can vary significantly with different species or bacteria and protist. These per capita death rates can also be affected by the environment as well. A harsh environment can increase the per capita death rates of these species for example.

The reproductive factor r is given a numerical value of 1. This makes biological sense in that it implies a bacterial colony can double its size in just an hour under ideal conditions, which is perfectly feasible. The value for r can be adjusted to account for different biological circumstances that would affect the reproductive factor such as the use of different bacterial strains for study or varying environmental conditions.

The carrying capacity k is dependent on many factors. Its value is affected by the habitable space of the environment, the available amount of nutrients, the degree of interaction between biotic factors in the environment (competition between different bacterial species for example), the degree of efficiency of the bacteria utilizing the necessary biotic and abiotic resources, and environmental considerations among other factors. Since bacteria are relatively small and efficient, a high value—10,000,000—was assigned to k. Adjusting any of the factors that k is dependent on can alter the carrying capacity and give rise to different, but somewhat comparable dynamics.

CHAPTER 4

MODEL PREDICTIONS

Exploring the dynamics of this model based on the differential equations and the assigned numerical values for their parameters described earlier, we arrive at the graph depicted in Figure 2. The x-axis corresponds to time measured in hours, while the y-axis corresponds to the number of cells/cm^3 (log-scaled). From this graph, we can see that the protist population starts off low but increases, following a sigmoid shaped curve that is characteristic of a logistic growth model. The amount of living and non-living bacteria grow very fast initially and level off somewhat before declining. Perhaps incoincidentally, the living and non-living populations of bacteria begin to decline when the protist population begins to level off.

In a scenario with modified parameter values and initial values for the protist and bacteria populations, we observe an immediate decline in the bacterial population and an immediate rise in the protist population. The population of living bacteria continues to descend for the majority of the experiment while the protist population eventually tapers off and remains relatively constant for the remainder of the experiment. This scenario is depicted in Figure 3. This graph resulted from increasing the initial values of the protist population and the bacteria population. The rate of contact between the protist and the living bacteria was also increased. With a higher rate of contact between predator and prey, it follows that the bacteria population decreases more in this scenario than in the standard model.

In Scenario 2, depicted in Figure 4, bacteria immediately begin to decline while the protist population is relatively unchanged. This scenario had many modified variables. The initial amount of bacteria was equal to twice the carrying capacity, k, and each bacteria had a reduced reproductive factor r. The contact rate between the protists and the living bacteria was increased compared to the standard model, and the efficiency factors were very low for the consumption of both living and non-living bacteria.

In Scenario 3, we start out with a higher number of protists than in the standard model. The population of protists experiences a linear pattern of decline while the bacterial population remains virtually the same throughout the breadth of the experiment's time frame as shown in Figure 5. In this particular scenario the rate of contact and probability of ingestion of both the living and non-living bacteria is reduced to a fraction of the values proposed in the standard. The death rates of both the protist and bacterial populations are elevated as well.

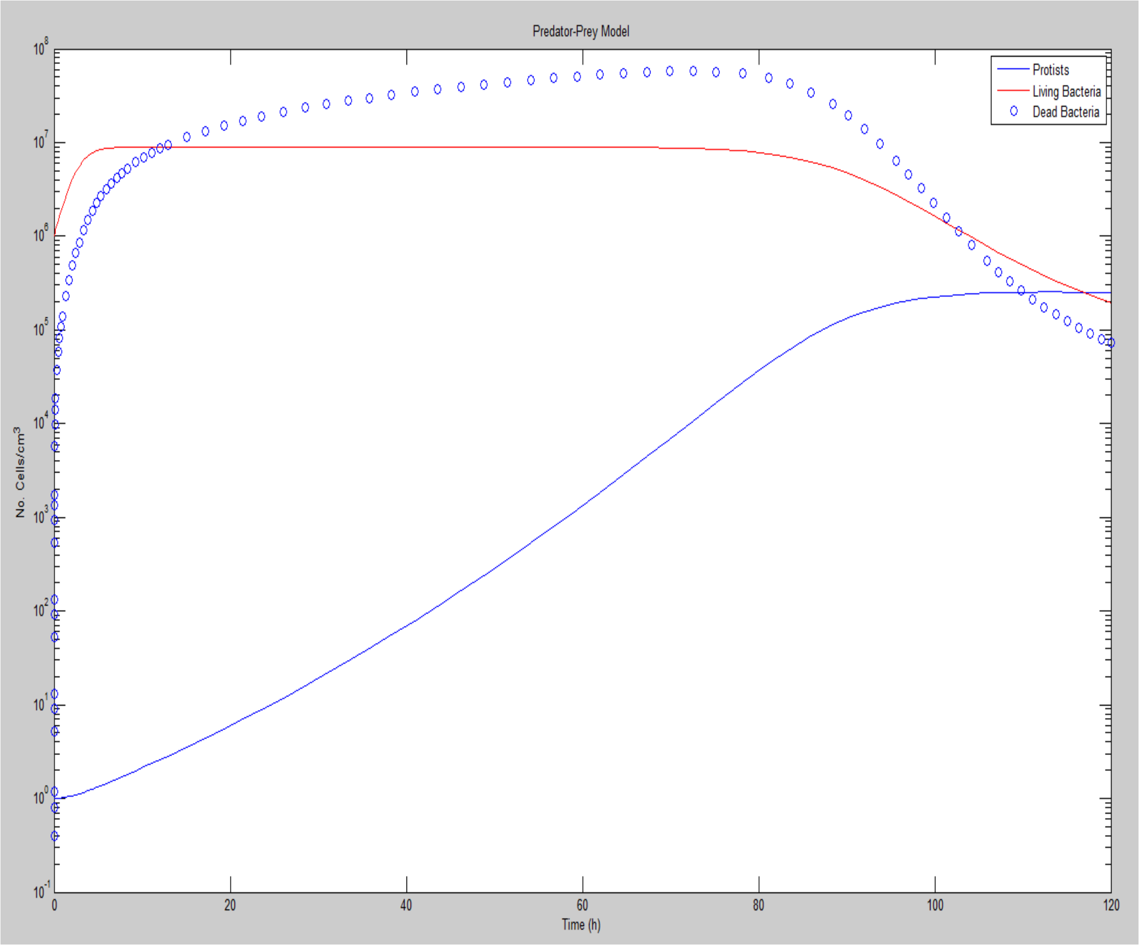

Figure 4.1: Standard, Graphical representation of the predator-prey model with standard parameter values.

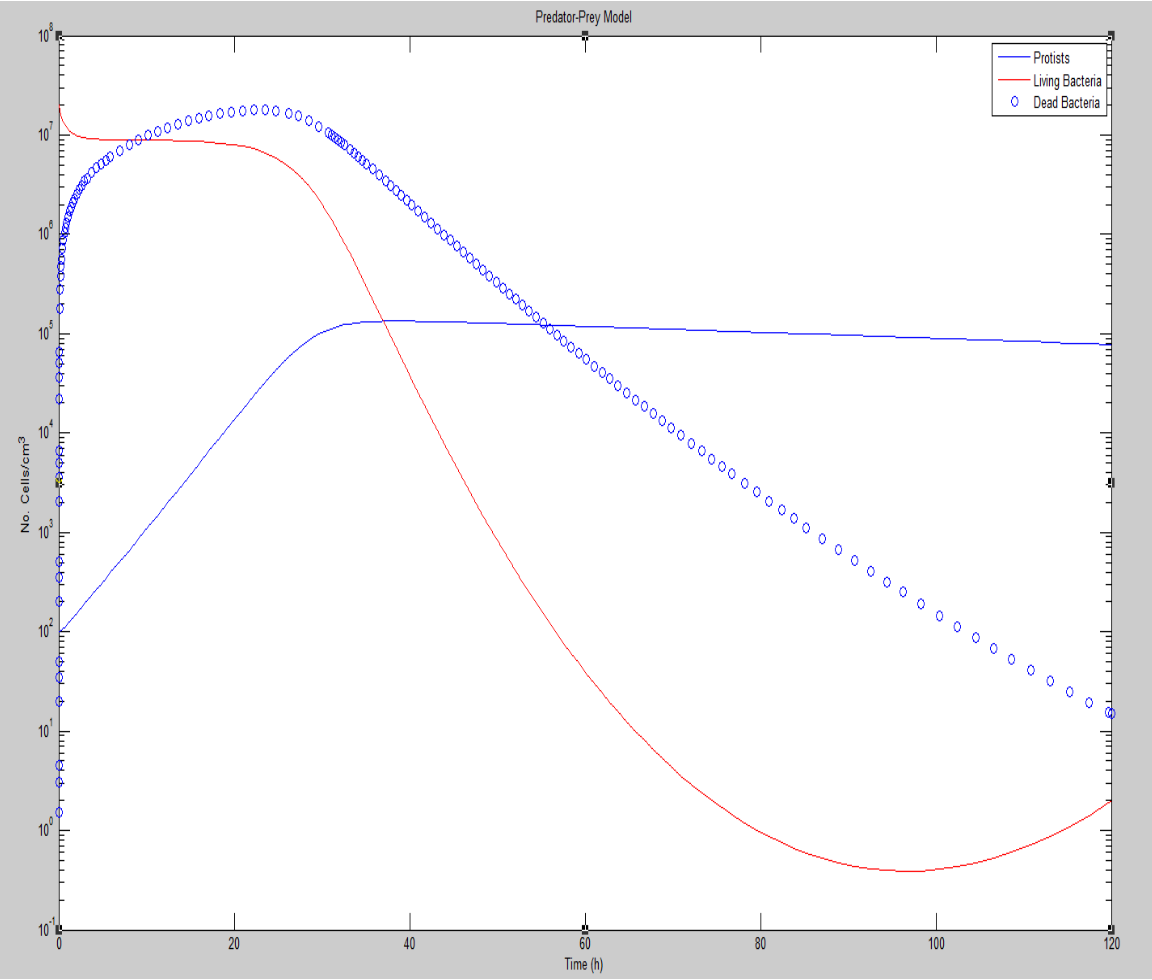

Figure 4.2: Scenario 1, Graphical representation of the predator prey model with modified parameter values: b (initial value) = $2*10^7$, p (initial value) = 100, $c_1 = 9.8*10^{-6}$.

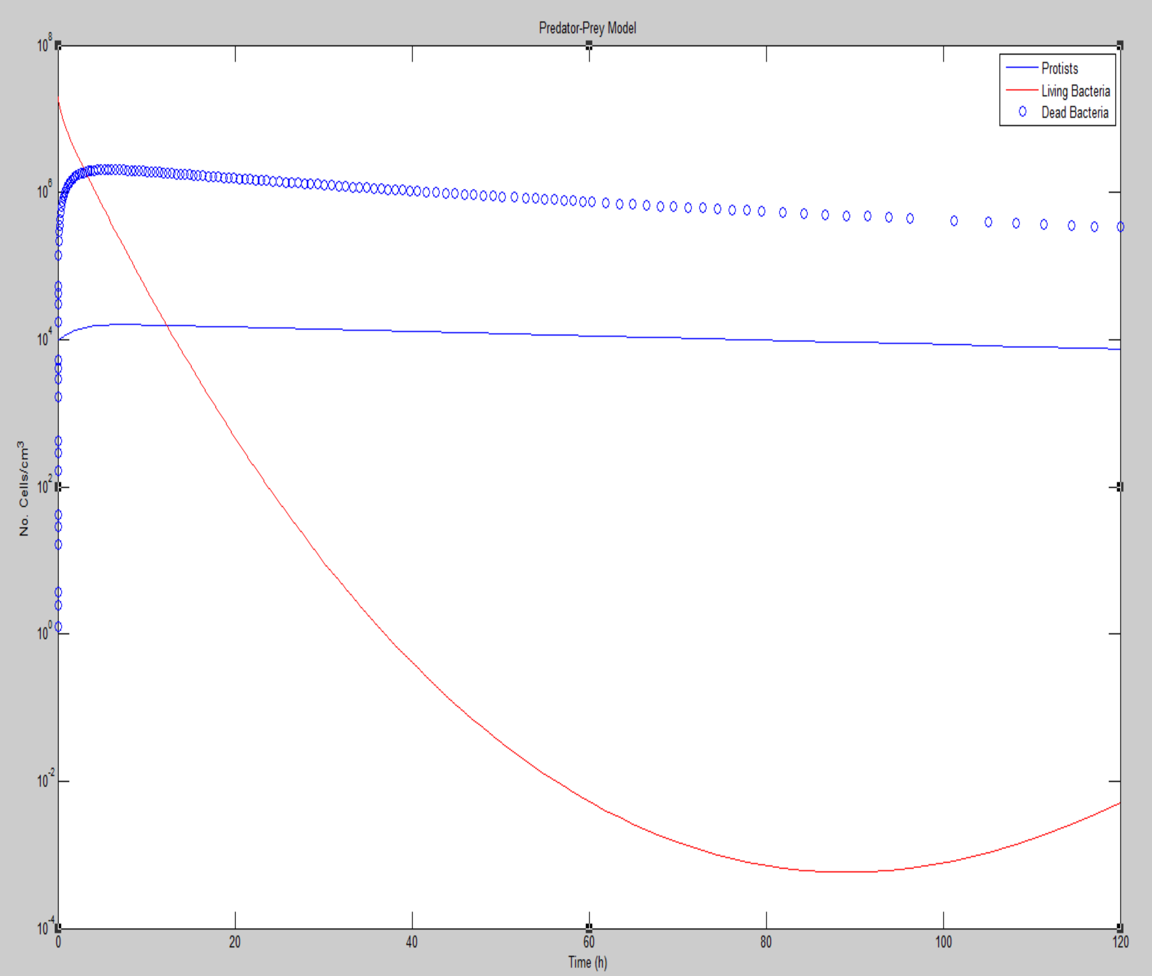

Figure 4.3: Scenario 2, Graphical representation of the predator-prey model with modified parameter values: b (initial value) = $2*10^7$, p (initial value) = $1*10^4$, $c_1 = 7.6*10^{-5}$, r = .8, $\alpha = 2000$, $\varepsilon_2 = 5*10^{-4}$.

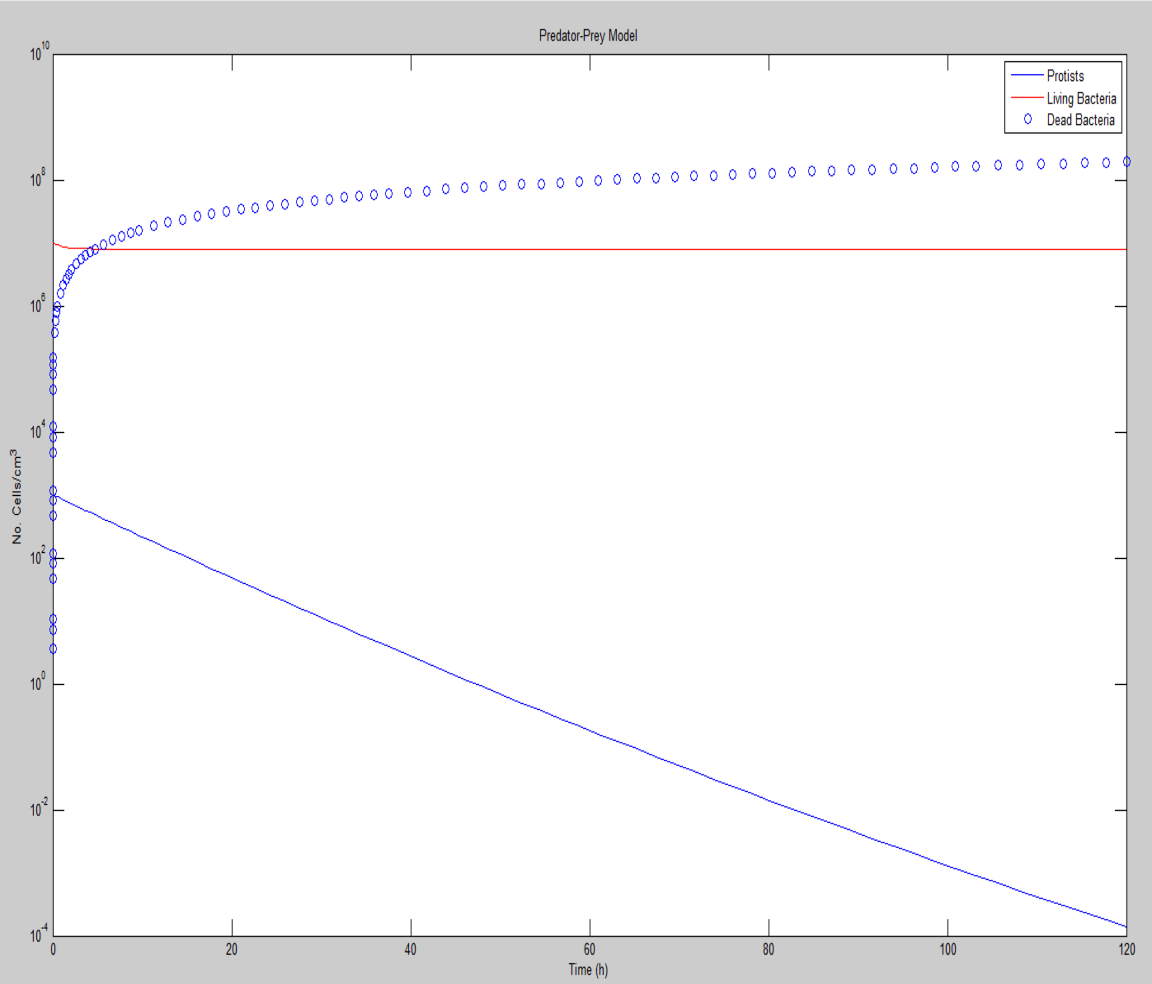

Figure 4.4: Scenario 3, Graphical representation of the predator-prey model with modified parameter values: b (initial value) = $1*10^7$, p (initial value) = $1*10^3$, $a_1 = .75$, $a_2 = .50$, $c_1 = 8*10^{-7}$, $c_2 = 5*10^{-7}$, $\delta_p = 1.7*10^{-1}$, $\delta_b = 2*10^{-1}$.

CHAPTER 5

DISCUSSION

In the standard we see an initial increase in the bacterial population. The bacterial population remains somewhat steady until the protist population experiences a lot of growth. This makes biological sense in that the bacterial population can’t be expected to decrease until the concentration of its predator is significant enough to offset their positive growth and cause a decline in the bacterial population. The same is true for the non-living bacteria. We also see that the protist population begins to level off once the bacterial population and dead bacterial population begin to decrease. If the time span of the model was stretched even farther, we may have seen a decline in the protist population since its resource for energy and organic material start to diminish.

Like in the standard, Scenario 1 shows that the living and non-living bacteria experience declines once the population of protists rises to a size that is comparable to the population of the other two groups. And, although slight, there is a noticeable decrease in the protist population for the remainder of the experiment. This could possibly reflect the shrinking population of living and non-living bacteria, as a decline would be expected for a predator population per consequence of their corresponding prey’s population shrinkage.

The factors of efficiency for living and non-living bacterial consumption play quite a role in explaining the dynamics observed in Scenario 2. The efficiency factors for the consumption of either type of bacteria must be artificially low in order to predict the dynamics shown in this scenario. Protists experience very little change in their population size while the living bacteria decline dramatically. The only way to account for a huge decline in the bacterial population and a very little change in the protist population was to depress the efficiency factor by a substantial amount. The contact rate between protist and bacteria also needed to be increased to result in a higher rate of consumption upon meeting. This could reflect the possibility of either or both organisms traveling at faster speeds. The biological explanation of depressed efficiency factors could be that the bacteria do possess key nutrients that the protists need, but only in a very dilute amount that causes a huge decrease in the bacteria's population while only increasing the protists' population by an amount (that actually is counteracted by δ_p to yield a slight downward trending slope).

In order to keep the bacterial population relatively constant, as shown in Figure 5, the initial amount of bacteria was equal to the carrying capacity. The initial amount of bacteria was equal to k because for values of $b > k$, we'd expect b to decrease, and for values of $b < k$, we'd expect it to increase. So, to keep b relatively stable, b was made to be equal to k. To retard the decreasing effects of protists' consumption of bacteria, a_1 and c_1 values were decreased. As a result, the population of bacteria experienced less of a decline and was more stabilized than in other scenarios where a_1 and c_1 were greater. To manipulate the dynamics of the protist population in a negative fashion, we also decreased the values for a_2 and c_2, which would decrease the net gain that protists would experience from consuming dead bacteria. The per capita death rates for both protists and bacteria were raised as well to give rise to these dynamics. The combination of all these changes to the parameters could reflect the use of a harsh, convoluted environment that increases the per capita death rate of each organism and decreases their contact rate due to impediments caused by placement of physical structures.

From comparing all the graphs, considering their specialized values for certain parameters, it seems that the bacteria only experience a decline in their population when the protist population and the rate of ingestion upon meeting are high enough to combat the rate of growth that the bacteria experiences. Adjusting any of the factors significantly can cause a shift in the curve of the respected plot of the population affected. Changes made to just one parameter have the potential to affect more than just one of the three groups under study because the groups interact so much with each other. This model reflects possible realistic scenarios in that the results displayed in the previous figures make intuitive biological sense when compared to well-known biological phenomena observed in the field. The model doesn’t predict anything that seems to be out of the ordinary.

This model has great utility. It retains a level of simplicity in its basic structure that can be built upon to form more complex models for more complex scenarios. As the model becomes more complex, it will most likely be able to predict biologically important events with greater accuracy and detail.

REFERENCES

Briony LL. 2011. Addressing Prey Selection and Predator Fitness: Ingestion by, and Growth of, Ochromonas Danica on Multiple Bacterial Prey. [Internet]. [cited 2014 Oct. 10]. x Available from:http://dspace.uta.edu/bitstream/handle/10106/9605/foster_uta_2502m_11321.pdf?sequence=1

Gonzalez, J.M., E.B. Sherr and B.F. Sherr. 1993. Differential feeding by marine flagellates on growing versus starving, and on motile versus nonmotile, bacterial prey. MarineEcology Progress Series 102:257-267.

MARCEL HOLYOAK, SHARON P. LAWLER. "PERSISTENCE OF AN EXTINCTION-PRONE PREDATOR-PREY ." *Ecology* (1996): 1867-1879 .

Thingstad, T. F. Elements of a theory for the mechanisms controlling abundance, diversity, and biogeochemical role of lytic bacterial viruses in aquatic systems.*Limnol. Oceanogr.* 45, 1320–1328 (2000).

Otto, S.P. and Day, T. 2007. A Biologist’s Guide to Mathematical Modeling in Ecology and Evolution. Princeton University Press, Princeton, New Jersey.

BIOGRAPHICAL INFORMATION

Matthew was born in Fort Worth, Texas and spent the majority of his childhood in Grand Prairie, Tx. Matthew chose to attend The University of Texas at Arlington due to financial means and to stay close to family. With a passion for pursuing a career in the health field he decided to join Dr. Mario Romero-Ortega's regenerative neurobiology lab in the bioengineering department. There he was a part of a pioneer field of helping patients with disabilities dealing with loss of function in nerves, specifically limbs. During his work there he was a part of two major projects. The biosynthetic nerve implant team focused on repairing nerve injuries over a long gap and the neuroma team focused on limiting neuroma formation and pain. As part of this lab he was one of the authors on multiple papers currently being produced and has presented his project at conferences like ACES and won the Dean's award. Given another opportunity Matthew was able to be a part of the Undergraduate Training in Theoretical Ecology Research (UTTER) mentored by numerous professors including Dr. James Grover, Dr. Hristo Kojouharov, Dr. Christopher Cribs-Zaleta and others. Here he learned about the interdisciplinary field of mathematical biology involving how to model real life biological scenarios. His work with the UTTER program has resulted in multiple posters and papers that were presented nationwide at numerous research conferences and won him several awards. Matthew is grateful for the opportunities extended to him through UTA and aspires to one day work as a professional in the health care field.