

# Milestone V

Linsey A. Norris  
Justin Tanjuako  
Charlotte Wentzien  
Addison Yanito

December 14, 2006

## 1 Introduction

## 2 Introduction

The plasmodium *Physarum polycephalum* is a large unicellular, multinuclear amoeba-like slime mold that forms a network of tubes through which nutrients and chemical signals flow [2,3]. It spreads out into a sheet-like shape in search of food sources. It is believed that chemical signals initiated by detection of food set in motion mechanical wave oscillations that lead to the development and growth of the tubes, called pseudopodia, that transport food and chemical signals throughout the organism. One would assume that the tubes form in a pattern which transports the most nutrients with the least amount of work while also preserving robustness; that is, the network with the least likelihood of disruption due to outside influences. The ultimate goal of our research is to observe how the mold evolves in into an efficient tubular network when faced with limited food sources. To accomplish this, we must develop a mathematical model to predict and explain the network formation while considering the biological influences. The study of the formation of efficient networks has many other applications, and understanding how it occurs in nature can help in the planning and subsequent implementation of artificially created networks.

The wave propagation in the protoplasm is the mechanism by which the mold spreads in different directions, and the network expansion continues due to the patterns of changes in thickness and shuttle streaming in the plasmodium [6]. According to Nakagaki, the driving force for the shuttle streaming is the hydrostatic pressure in the tubes, and the location size and number of tubes are dependent on the location and size of the food sources. In addition to availability of food, the overall health and growth of *Physarum* is influenced by light and temperature. As it grows, it progresses through several life stages based on its reaction to the external factors. If food becomes too limited, the plasmodium begins to form fruiting bodies called sporangia. They contain masses of spores which either reproduce or release cells that will produce new feeding plasmodia. Another form the plasmodium can reach is a steady state, when it forms a hardened tissue called sclerotium.

In previous work by Nakagaki and Kobayashi, the slime mold navigated through a maze to find local food sources [1,3], and it was able to do so using the shortest routes. Those pseudopodia that reached dead ends in the maze formed a single thick pseudopodium spanning the minimum distance between the food sources. The tubes created between the food sources depended upon the amount of food at each location. For example, when the amount of food was limited, multiple tubes led to each food source.

Overall, we would like to be able to understand the complex assembly of the simple unicellular structure the slime mold creates to survive. As we progressed through our project, we attempted to understand the mathematical discrete network structures to develop a model that could create a prediction of an efficient and robust resource distribution network. We mathematically analyze the global and local networks within the plasmodium in order to understand the slime mold at any level. This type of resource distribution network play crucial roles in biology as well as in simulated models in science. By understanding *Physarum polycephalum* we hope to be able to understand how network can be formed to maximize efficiency and robustness.

## 2.1 Relevance to Existing Work

Much research has been performed regarding evaluation of slime mold networks. In general, these networks are very efficient in that food is distributed in a manner in which all resources are used in combination with minimal connections. They also find ways to survive and often continue to grow when the network is disrupted. Currently, mathematical models exist to attempt to explain how slime mold networks will form, live and decay, but they have limitations. Based on experimentation and observations, basic rules can be determined which can be combined to form a slime mold algorithm. Once an accurate model is developed, we can apply the slime mold model to other networking problems.

Creating mathematical models that are similar to problems in nature can be important, because they can be applied to modeling problems we face in the world. For example, complex networks in our society, such as road placement and the internet, are difficult to optimally configure [4]. Ideal solutions would be those in which the path between a finite number of points is the shortest and which is least likely to be disrupted. Although there exist algorithms in finding the shortest path, these algorithms are usually inefficient to compute. However, slime mold provides an optimal solution naturally when placed with food sources representing nodes. The natural algorithm of the slime mold can solve maze problems in which the mold finds the shortest distance between two food sources when it has many paths from which to choose. Initially the slime mold uses all solutions and, over time, eliminates the solutions which are not optimal. Extracting a mathematical algorithm to model the natural networking of slime mold would be useful for modeling more complex networks since the slime develops an optimal solution based on the food sources.

Strogatz wrote about a series of networks that are being studied and exist in the world around us [8]. By studying the different ways to model and approach these networks, we are able to analyze patterns that seem pertinent in networks. Strogatz was able to conclude

that the length and clustering effect of the nodes strongly affects the network. In his article, he gave several examples of mathematical structures that can be used to describe the slime mold: lattices, random graphs, coupled dynamical systems, statistical physics, chains, grids, and fully connected graphs.

## 2.2 Previous Models That Were Considered

Strogatz did not go into detail about how to create any particular models based on the mathematical structures he found. We considered this research to develop a simple model based on rules about the entire network of the slime tubes. In this global model, we wanted determine how the slime mold would grow based on controlling the placement of an initial small living section of slime mold and the food sources. We created a model for the generation of the resource distribution network and were able to use our model to predict the resulting colony network on a global scope as a top-down approach to slime mold growth. The model we created was able to quickly determine all the possible paths of the slime mold, and then find the shortest/thickest route to the food sources.

Intially, we considered using Dijkstra’s algorithm (using graphs and vertices) as a favored method to solve the shortest path algorithms. We determined that the Steiner minimum tree was found to be the most efficient network due to its minimum tube length as well as solving the shortest path. This model allowed us to start analyzing the slime mold; however, we found that it was too general an approach and we needed a better model.

We then proceeded to consider a model from Nakagaki’s work [2], in which fault tolerance and total length were the tools used to evaluate slime mold networks globally. The formula we used to determine  $\alpha$  is as follows:

$$\frac{TL}{FT} = \alpha$$

where TL was the total length of all the tubes in the network and the FT was the fault tolerance of the network based on the connections. We found that this formula was only of use to analyze the efficiency of an established network and thus was not able to determine how the network would develop. It was only useful only tell one about the current steady state.

By testing these and several other models not detailed here, we were able to discover what we concluded to be the best possible model. By continually refocusing our goals on the central issues of efficiency and robustness of the slime mold, we were able to find the optimal solution to these problems.

### 3 The Problem

Our previous work studying self assembling slime mold involved developing a global model for slime mold network growth. The Steiner minimum tree was found to be the most efficient network due to its minimum tube length. Following Nakagaki’s work, fault tolerance and total length were tools used to evaluate slime mold networks globally. However, the use of a global model to project the growth of slime mold is inconsistent to the actual biology of slime mold, in that all network decisions are made at the cellular level. In other words, a single slime mold cell contributes to the network formation by sending a chemical signal, cAMP (Cyclic adenosine monophosphate) to it’s neighboring cells which each send a following cAMP signal to it’s neighbors as well. The result is a well designed resource distribution network, formed by single cell interactions. Accordingly, developing a local model which describes the decisions of each cell is an important basis for this self assembling network problem. The foundation of our model is derived from the flux model used in Nakagaki’s “Intelligence: Maze-Solving by an Amoeboid Organism.”

The problem we are addressing is development of a model for the generation of the resource distribution network of the tubes. With a small amount of plasmodium in a petri dish with food sources at certain points we will be able to apply the model we create in order to predict the resulting network of food transportation tubes. As we observe the early growth of the slime mold, the problem is to determine how the organism will form and where veins will develop to search out food. Locally, we need our model to predict how the growth will extend outward in search of food and where food tubes will form. Over time, we will predict which veins will stay and which should disappear, and whether or not new ones will form. Thus our model will have to take into account the placement of the food sources relative to the initial mold placement, which will then allow us to apply our model and test it for accuracy.

### 4 The Model

#### 4.1 Flux Model

The model which we wish to develop is based on the ideas Kobayashi introduced when he studied how slime would evolve through a maze [1]. His model (Equation 1 below) suggested that when two food sources are connected by more than one tube, the slime will choose the most efficient path between the two nodes based which tube has the highest plasmodium flux. Thus, for our model, given an existing network of connected nodes (food sources), we will model flux through each connecting tube and determine which tubes will become primary passageways for flow of nutrients.

$$\Phi_{ij} = \frac{D_{ij}}{L_{ij}}(p_i - p_j). \tag{1}$$

where  $p_i$  is the pressure at the node,  $L_{ij}$  is the length of the segment and  $D_{ij}$  is the conductivity

Similarly to Kobayashi’s assumptions, we are assuming that the flow of food through each tube follows a Poiseuille (model for tube flow), and thus we can determine the flux through each tube as,

$$\Phi = \frac{\pi R^4}{8\eta} \left( \frac{\Delta P}{\Delta x} \right) \quad (2)$$

where,  $R$  is the radius of the tube,  $\eta$  is the viscosity of the liquid (protoplasm),  $\Delta P$  is the change in pressure between two ends of a tube and  $\Delta x$  is the length between the two nodes.

## 4.2 Assumptions

*Physarum polycephalum* requires nutrients (oat flakes), moisture, warmth, and air to survive [10]. In our research, we can assume that the moisture is supplied by the agar medium that is contained in our petri dishes. Also, we will assume that warmth and air are controlled at a constant value in the lab. However, the variables, which we will be able to control and vary as necessary are the quantity and the location of the food to determine the distribution network of the tubes. We will vary this to be able to test our model using different formations of slime mold to be able to understand how the slime mold interacts at a local and global approach.

When approaching the model of solving the efficiency of the network, we need to make certain assumptions about the discrete network of tubes.

1. Since we will be studying the steady state process of our network of tubes, time will not be a factor in our model.
2. We will hold viscosity at a constant. Viscosity is how well fluid can travel through a medium. The definition by Seifriz is as follows: an internal function of a fluid or a gas, and when pressure is applied friction occurs which affects how much the substance will respond to the external forces [7]. From Seifriz, although protoplasm is often of a high viscosity, it varies due to changes in consistencies from anywhere to that of water to a firm jelly. These changes are influenced by physiological activity, development, reproduction, injury, mitosis, and death. For our constant, we used the results of micro dissection suggested by [7]. We will use the value of  $\eta = 1$ . Their conclusion was that the viscosity of protoplasm ranges from a degree that is given in Figure 3.
3. We will also be setting the change in pressure as a constant in our model. From [11], we know that the pressure has to follow Darcy’s laws and Kirchoff’s laws; thus, since we are holding the pressure constant between two nodes, we can set  $\Delta p = 1$ .

For Model 3 we will hold pressure, radius, and viscosity constant.

$$\Delta p = 1$$

$$R = 1$$

$$\eta = 1$$

For Model 4, we will hold only pressure and viscosity constant. We will measure the radius by taking the average radius over each tube. Considering the radius of the tube is a more complicated problem in that tubes with longer length but larger radii may be more favorable than shorter tubes of smaller radii due to the  $R$  being raised to the fourth power. This will be the final model used in our calculations.

$$\Delta p = 1$$

$$\eta = 1$$

**NOTE: Model 1 and Model 2 are given below.**

#### 4.2.1 Model 1- Simplified Model

First, we chose to have only the change in length vary in order to simplify the model to make sure that we were able to test our model. Thus, we will hold the radius, viscosity, and pressure of the tube as constants:  $c_1$ ,  $c_2$ , and  $c_3$  respectively.

$$\Phi = \frac{\pi * c_1^4}{8c_2} \left( \frac{c_3}{\Delta x} \right) \quad (3)$$

From the previous work of Kobayashi as well as Strogatz, we will hold these constants as follows.

$$c_1 = 1$$

$$c_2 = 1$$

$$c_3 = 1$$

Thus, the equation becomes a function of the change in the length. We will only run two tests on computerized models with this equation. Although trivial, for explanation purposes, we want to demonstrate the basic properties that our model can emulate.

#### 4.2.2 Model 2- A More Complex Model

Now, we consider the thickness of each tube and hold  $R$  no longer constant. The model for flux is therefore,

$$\Phi = \frac{R^4 \beta}{\Delta x} \quad (4)$$

where  $\beta = \frac{\pi \Delta P}{8\eta}$  with  $\Delta P = 1$  and  $\eta = 1$ . Considering the radius of the tube is a more complicated problem in that tubes with longer length but larger radii may be more favorable than shorter tubes of smaller radii due to the  $R$  being raised to the fourth power. We will investigate the same tube networks with this more accurate model.

## 4.3 Procedures

### 4.3.1 Procedure of Selecting and Measuring Tubes

To demonstrate how our model is used, we will estimate the values of the radius and change in length based on the picture of the slime network. When observing the computer models that were created, we will automatically assign the values of the radius and change in length as to just focus on the calculations. To select the tubes from a slime mold culture, we will follow the below procedure.

- (a) We will load the image into Photoshop Elements (P.E), a photo-editing program, and set the contrast to 85. This will eliminate the minor tubes that are barely visible and will emphasize the larger tubes.
- (b) After this eliminates, the smaller tubes, we then choose to eliminate any open-ended tubes, that is, any tube that is not connected between two food sources.
- (c) Next, we will label each of the remaining tubes starting with 1 to  $x$ , where  $x$  is the number of tubes in the network.
- (d) We will then measure each tube by each grid square which is simulated in P.E. to determine the change in length,  $\Delta x$ .
- (e) To measure the radius, we will choose ten evenly spaced points along the tube and measure the radius by grid size once again.
- (f) We will then proceed to calculate the flux of all the tubes.

### 4.3.2 Procedure for Removing Tubes and Determining the Steady State Network

Now that we have values for the length and radius of each tube in addition to having them numbered. We can now calculate fluxes through each tube and begin to eliminate non-optimal tubes. The result is a steady state network solution which we believe is optimal for food distribution in the slime network.

4. Fluxes through tubes connected by two food sources can be calculated by using our model since we have all the values associated with the model.
5. In the case where tubes are connected to other tubes such as with the steiner tree, calculate the flux through each tube using the method for the special case mentioned in the section above.
6. After calculating the fluxes of all the tubes, we will then proceed to remove particular tubes based on the flux through each tube. We look at each set of two nodes in the network.

7. If only one tube is connecting a pair of two food sources, the tube will remain.
8. If more than one tube is connecting the same two food sources, we compare the flux between all tubes connecting the same two sources. The tube with the largest flux value is the optimal tube and all other tubes are deleted.
  - (a) If there are no steiner points between the two food sources, we will compare all the fluxes between these two sources, and select the tube with the greatest flux. The rest of the tubes between these two sources will be eliminated.
  - (b) If there are steiner points between the two food sources, we will then calculate the steiner point using Kirchoff's laws (as described below). After calculating this, we will then proceed to eliminate the tubes based on flux once again.
9. The resulting network is a system of food sources with the maximum of one tube connecting a particular pair of food sources. This is our steady state solution.

#### 4.3.3 Special Case: Calculating flux through tubes connected at a steiner point

In many cases, the slime mold will connect tubes at an intermediary point between food sources. Doing so often minimizes the total length of tubes in the network. An example of this process occurring is when three sources are connected by a Steiner minimum tree as shown in the following picture;

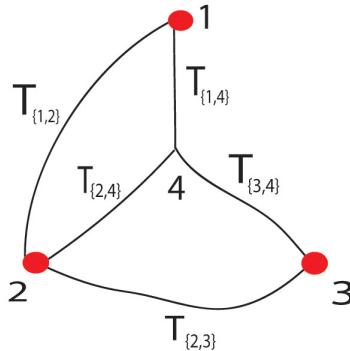


Figure 1: Steiner Tree Figure.  $T_{i,j}$  corresponds to the tube connecting nodes  $i$  and  $j$ .

The steiner point at node 4 complicates the problem in that when comparing fluxes between tubes  $T_{1,2}$  and  $T_{1,4} + T_{2,4}$ , the two tubes connected through node 4 have individual fluxes. The same problem occurs when comparing the flux through  $T_{2,3}$  and  $T_{2,4} + T_{3,4}$ . This occurs due to the a pressure drop between the food sources and the steiner point which is less than 1. In the normal case, the pressure drop between two nodes is equal to 1. To solve this problem, we assume food is flowing from node 1 through  $T_{1,4}$  and the flow splits to tubes  $T_{2,4}$  and  $T_{3,4}$ . This allows us to apply Kirchoff's Law at the steiner point and conclude that all fluxes going through the point sum to zero. Using our flux equation and Kirchoff's Law, we have 4 equations with 4 unknowns.

$$\Phi_{1,4} = \frac{c_1 R_{1,4}^4}{\Delta x_{1,4}} (P_1 - P_4) \quad (5)$$

$$\Phi_{2,4} = \frac{c_1 R_{2,4}^4}{\Delta x_{2,4}} (P_2 - P_4) \quad (6)$$

$$\Phi_{3,4} = \frac{c_1 R_{3,4}^4}{\Delta x_{3,4}} (P_3 - P_4) \quad (7)$$

$$\Phi_{1,4} - \Phi_{2,4} - \Phi_{3,4} = 0 \quad (8)$$

In each equation,  $c_1 = \frac{\pi}{8\eta}$ , and  $R_{i,j}$  and  $\Delta x_{i,j}$  can be determined through measurements. Currently, we do not have an equation to model pressure at a given node but we assume All pressures besides  $P_4$  are assumed to be known. Therefore, our 4 unknowns are  $\Phi_{1,4}, \Phi_{2,4}, \Phi_{3,4}$ , and  $P_4$ . The resulting matrix equation is,

$$\begin{bmatrix} 1 & 0 & 0 & \frac{c_1 R_{1,4}^4}{\Delta x_{1,4}} \\ 0 & 1 & 0 & \frac{c_1 R_{2,4}^4}{\Delta x_{2,4}} \\ 0 & 0 & 1 & \frac{c_1 R_{3,4}^4}{\Delta x_{3,4}} \\ 1 & -1 & -1 & 0 \end{bmatrix} \begin{bmatrix} \Phi_{1,4} \\ \Phi_{2,4} \\ \Phi_{3,4} \\ P_4 \end{bmatrix} = \begin{bmatrix} \frac{P_1 c_1 R_{1,4}^4}{\Delta x_{1,4}} \\ \frac{P_2 c_1 R_{2,4}^4}{\Delta x_{2,4}} \\ \frac{P_3 c_1 R_{3,4}^4}{\Delta x_{3,4}} \\ 0 \end{bmatrix} \quad (9)$$

which can be solved to determine the separate fluxes. Once  $\Phi_{1,4}, \Phi_{2,4}$  and  $\Phi_{3,4}$  are determined, fluxes between tubes can now be compared.

#### 4.3.4 3 Node Steiner Simulated Example

Considering the network above containing the steiner point;

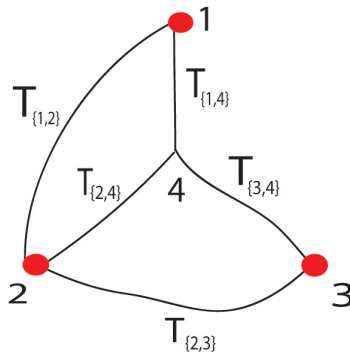


Figure 2: Steiner Tree Figure.  $T_{i,j}$  corresponds to the tube connecting nodes  $i$  and  $j$ .

We will calculate the fluxes through each tube using the matrix equation in the previous section. Although we do not have a model for pressure at a given node, we assume  $P_1, P_2$ , and  $P_3$  to be  $1/2, 1/4$ , and  $1/4$  respectively. The following matrix represents the system:

$$\begin{bmatrix} 1 & 0 & 0 & \frac{c_1 R_{1,4}^4}{\Delta x_{1,4}} \\ 0 & 1 & 0 & \frac{c_1 R_{2,4}^4}{\Delta x_{2,4}} \\ 0 & 0 & 1 & \frac{c_1 R_{3,4}^4}{\Delta x_{3,4}} \\ 1 & -1 & -1 & 0 \end{bmatrix} \begin{bmatrix} \Phi_{1,4} \\ \Phi_{2,4} \\ \Phi_{3,4} \\ P_4 \end{bmatrix} = \begin{bmatrix} \frac{1}{2} \frac{c_1 R_{1,4}^4}{\Delta x_{1,4}} \\ \frac{1}{4} \frac{c_1 R_{2,4}^4}{\Delta x_{2,4}} \\ \frac{1}{4} \frac{c_1 R_{3,4}^4}{\Delta x_{3,4}} \\ 0 \end{bmatrix} \quad (10)$$

The following values are used for each tube:

$$T1,2 : R_{1,2} = 1.1, \Delta x_{1,2} = 7.0$$

$$T1,4 : R_{1,2} = 2.0, \Delta x_{1,2} = 3.5$$

$$T2,4 : R_{1,2} = 1.0, \Delta x_{1,2} = 4$$

$$T3,4 : R_{1,2} = 1.1, \Delta x_{1,2} = 3.2$$

$$T2,3 : R_{1,2} = 0.9, \Delta x_{1,2} = 6.3$$

The matrix equation with these values is:

$$\begin{bmatrix} 1 & 0 & 0 & 1.80 \\ 0 & 1 & 0 & .100 \\ 0 & 0 & 1 & .180 \\ 1 & -1 & -1 & 0 \end{bmatrix} \begin{bmatrix} \Phi_{1,4} \\ \Phi_{2,4} \\ \Phi_{3,4} \\ P_4 \end{bmatrix} = \begin{bmatrix} .900 \\ .025 \\ .045 \\ 0 \end{bmatrix} \quad (11)$$

This system yields the solution:

$$\begin{bmatrix} \Phi_{1,4} \\ \Phi_{2,4} \\ \Phi_{3,4} \\ P_4 \end{bmatrix} = \begin{bmatrix} -.083 \\ -.030 \\ -.053 \\ .546 \end{bmatrix} \quad (12)$$

The results are reasonable in that all the fluxes are flowing in the same direction. We can finally compare the fluxes between tubes  $T_{1,2}$  and  $T_{1,4} + T_{2,4}$ .

Using our flux model for a normal case,  $\Phi_{1,2} = .082$ . We compare flux to magnitude of  $|\Phi_{1,4} + \Phi_{2,4}| = .113$ . These results indicate that  $T_{1,2}$  will disappear and the connected tubes  $T_{1,4}$  and  $T_{2,4}$  will remain.

The same method is used to determine the fluxes between tubes  $T_{2,3}$  and  $T_{2,4} + T_{3,4}$ .  $\Phi_{2,3} = .041$  and  $|\Phi_{2,4} + \Phi_{3,4}| = .083$ . We predict that the connected tubes of  $T_{2,4}$  and  $T_{3,4}$  will be the optimal selection.

## 5 Analysis

### 5.1 Computer Analysis Models: Using Model 1 and Model 2

#### 5.1.1 2 Node Simulation

The simulated computer model is a two node network as seen in Figure 4. Tubes are indicated as black lines and the red circles are food sources. We will proceed to use Model 1 (without radius taken into account) to calculate the flux values and thus determine the

proposed network solution.

We calculated all the possible fluxes as seen in . By using our procedures, we then determined the optimal solution as seen in Figure 5.

Then, by comparing all the fluxes in model 1 (as seen in Table 1) we found out that the one with the greatest flux between two nodes would survive. Thus, by using Model 1, our solution (Figure ?? is that tube 3 would be the optimal solution.

### 5.1.2 3 Node Simulated Model

We proceeded to a computer simulated three node model (as seen in Figure 6 ) and then wish to apply Model 1 and Model 2 to this problem. By applying both of these models, we show that although Model 1 is easy to apply, Model 2 will be the most effective model to use when we calculate our slime mold analysis.

From Table 2, we calculated the fluxes. After calculating these values, we then used our procedures for removing tubes to find the efficient network of slime mold. We will first look at model 1 then followed by model 2. From this, we then compare the all possible combination of nodes.

1. For  $N1$  and  $N2$ , we compare tubes: 2, 3, and 8.
2. From model 1, the resulting tube that will remain is tube 2.
3. From model 2, the resulting tube that will remain is tube 3.
1. For  $N2$  and  $N3$ , we compare tubes: 4, 6, and 9.
2. From model 1, the resulting tube that will remain is 9.
3. From model 2, the resulting tube that will remain is 6.
1. For  $N3$  and  $N1$ , we compare tubes: 1, 5, and 7.
2. From model 1, the resulting tube that will remain is 5.
3. From model 2, the resulting tube that will remain is 1.

Therefore, for model 1, the resulting network that will survive is shown in Figure 7. For model 2, the resulting network that will survive is shown in Figure 8.

## 5.2 Slime Mold Analysis

### 5.2.1 Slime A Sample

We used a sample grown from Slime A (Figure 9) to test our model from Equation 4 (Model 2). We then proceeded to follow the procedures for selecting and measuring tubes to input the data (as seen in Table 3) in order to calculate the fluxes. Finally, we followed the procedures for removing tubes and found that the resulting network will be tubes 1, 3, 4, 7, 8, and 9.

### 5.2.2 Slime 1 Sample

Also, we used a sample grown from Slime 1 (Figure 10) to test our model again. Next, we followed the same procedure for Slime Team 1. We inputted the data into Table 4 in which we calculated the fluxes. We then found that the resulting network will be tubes 2, 4, 7, 11, and 12.

## 5.3 What does the model tell us about the problem

The model which we proposed will help us determine the steady state solution of the slime mold and which factors will play a role in determining how the slime mold reacts. However, after calculating our two node computer model using both models, we have determined that we will no longer use the model 1 due to its simplicity (change in length is the only variable) and thus does not generate accurate results. By implementing model 2, we are able to predict the steady state solutions of a slime mold tubular network. By using this model on our experiments in the lab as well as other team's samples, we will be able to use our flux model to calculate the steady state solution for which tubes will form an efficient network.

## 5.4 What does the problem tell us about the model

As we observe the beginning of the slime mold colony, the problem is to determine how the colony will form and where veins will develop to search out food. As this continues, the slime mold will reach a state where the mold then begins to no longer grow, and starts to form tubular networks preparing to go into a steady state form. We know that slime mold is not only dependent upon the robustness in terms of the length.

As we seek to further our model, we hope to find other variables that the problem will tell us that we can further apply to our model.

## 6 The Experiments

When culturing *Physarum*, it is a fairly easy process to grow the slime mold. We are given petri dishes in which there is an agar medium that will supply the *physarum* plasmodium with the water and air it needs. Then we place oatmeal flakes in particular arrangements to

allow food sources for the slime to grow. Finally, we take the plasmodium from the samples that we are given and place it into the petri dish to allow the mold to grow. We then place the dishes in a drawer to allow the mold to grow in the dark. Incubation at room temperature is optimal.

We have begun to grow cultures of Physarum in the MEClab. Each experiment has been cultured for two days and have been recorded onto graph paper for easier calculations of length and radii.

## 6.1 Experiment 1

Within a small petri dish of Agar, we placed a small portion of Physarum in the center with a low quantity of food. This was to help the Physarum grow, but also allow it to expand once the food source was depleted and search for other food sources. There are 4 food sources (nodes) placed strategically within the dish. A central node over the original Physarum and three surrounding nodes which form an equilateral triangle.

The result after a couple days was incredible. A full petri dish of slime mold grew with excellent beginning tube formations. This was the culture we used for our competition, where we had the other teams decide which tubes would survive and which would die. This resulted in what may possibly be the stable state of the Physarum. We did the measurements on photoshop like our models early to hypothesis which tubes would remain and which would die. A very interesting result came about when longer tubes connecting the outer nodes would be more probable to remain than some of the shorter tubes connecting the central node with an outer.

After about a week of watching and waiting for the culture to reach a steady state The results were very interesting. From the center node, a tube connected to one surrounding node, from that point on the triangular formation, a tube wrapped around the entire petri dish connecting the other two nodes in a big circle. The culture was very similar to our hypothesis, except for being off by one non-surviving tube. This gave us a better trust about our flux model and felt our hypothesis' for the other teams cultures would be more accurate.

## 6.2 Experiment 2

In a larger petri dish containing Agar made by a student, a small amount of Physarum was placed in the center of the dish and allowed to grow out for a couple days (similar to Experiment 1). The result after two days was not as intense as Experiment 1, however, there was a small amount of outward growth around the central node. With this taken into consideration, we removed the randomly placed food sources and replaced them with three surrounding nodes like Experiment 1. The difference is that each node is placed at a different length from the central node.

A short, medium, and long distance were chosen. Without an intense tube structure, we can predict a possible tube structure by observations of past milestone competitions. Also, we will use our calculations to state a well formed hypothesis on how a tube structure might grow.

Sadly, The culture never managed to grow definite tube formation. The culture stained the agar yellow in certain spots and looked like it was trying to grow, but no success came out of it. We had to let it go.

### **6.3 Experiment 3**

In this experiment we used another small petri dish with agar already inside. A small bit of Physarum was placed near the edge of the dish with food on top. Growth was weak in this experiment; however we are only using two nodes this time. Once a tube structure has been grown, we will determine which tubes will remain and which will stay. If we are successful with our calculations, our experiment should be similar to our 2 node computer model in the previous section.

After two days of growth, experiment 3 showed multiple tubes branching outward for the other node. We could see multiple paths from one node to the other, and could easily identify which tubes had a better chance of survival than others.

However, this culture did not make it as well. After about two days since the last time we checked on it, a serious infection managed to grow over the entire petri dish. A specimen that had such good potential was lost that day.

### **6.4 Experiment 4**

Using a small petri dish, four food sources were placed around the edge to form a square formation. In the center we placed a paper of mold with some food on top. Each surrounding node was about equal lengths from the center node.

After about a week of waiting, the resulting growth was amazing. Four tubes connecting each outer node with the central node were formed. Outer tubes connecting neighboring outer nodes were grown or in the process of growth.

We used this culture for Milestone V. We are supposed to remove one of the nodes and use our equation to model how the slime will react. Will it kill the broken tubes or perhaps connect them? We decided to remove the middle node, creating four severed tubes pointing inward. After a weekend of growth, the final stable state will have been set.

## 7 Results

### 7.1 Strengths

We have a strong base to work with by finally being able to create a model that will be able to simulate how the slime mold develops after there are a number of tubes formed. We are able to calculate the possible outcome of tubular structures in the final steady state of the Physarum. We used the ability to start simple, dealing with only the length of each tube, and from there we furthered our calculations by adding the radius of each tube. The model and calculations were able to give us a possibly more accurate solution to the way Physarum form to. Using our drawn models and our data organization, we can move towards actual cultures of Physarum and be able to predict what the final form of tubes will look like.

### 7.2 Weaknesses

As of right now, the calculations are made using two unknown values and allowing the change of pressure and viscosity to be constant. Our problem is that the pressure is dealt in time, so it is constantly changing, creating a difficult ability to calculate the pressure at one given time everywhere. If we were able to calculate viscosity and pressure, the accuracy as to which tubes will survive would increase significantly.

Also, our equation is a simple model, eliminating multiple functions of the Physarum. Relying on one equation to predict how a biological organism will react in a natural setting is somewhat ignorant. However, it seems when looking at Physarum in a more in-depth fashion, more physics and biological characteristics are implemented, making our heads hurt for days trying to understand it.

## 8 Summary and Conclusions

Through further investigation dealing with our code and numerous equations we had written down, we decided to do away with the code and simplify the equations to be used. We focused on the Kobayashi model that led us to delving more into the central issues. This model has allowed us to not only see slime mold at a local level to analyze it but as well determine the global structure of the tubular network. By applying our model to networks, we have been able to come to a better understanding as to how Physarum will grow. Initially, we simplified the equations to a point where anybody can calculate the needed data. After realizing that this model was too simplistic, we implemented the next model with less parameters held constant. By implementing the new model, we were able to determine a more probabilistic model that we hope to further develop to obtain more accurate results in later tests.

## References

- [1] R. Kobayashi, A. Tero, and T. Nakagaki. Mathematical model for rhythmic protoplasmic movement in the true slime mold. *JOURNAL OF MATHEMATICAL BIOLOGY*, 53(2):273–286, August 2006.
- [2] T. Nakagaki. Smart behavior of true slime mold in a labyrinth. *RESEARCH IN MICROBIOLOGY*, 152(9):767–770, November 2001.
- [3] T. Nakagaki, R. Kobayashi, Y. Nishiura, and T. Ueda. Obtaining multiple separate food sources: behavioural intelligence in the physarum plasmodium. *PROCEEDINGS OF THE ROYAL SOCIETY OF LONDON SERIES B-BIOLOGICAL SCIENCES*, 271(1554):2305–2310, November 2004.
- [4] T. Nakagaki, H. Yamada, and M. Hara. Smart network solutions in an amoeboid organism. *BIOPHYSICAL CHEMISTRY*, 107(1):1–5, January 2004.
- [5] T. Nakagaki, H. Yamada, and A. Toth. Maze-solving by an amoeboid organism. *NATURE*, 407(6803):470–470, September 2000.
- [6] T. Nakagaki, H. Yamada, and A. Toth. Path finding by tube morphogenesis in an amoeboid organism. *BIOPHYSICAL CHEMISTRY*, 92(1-2):47–52, August 2001.
- [7] William Seifriz. Viscosity values of protoplasm as determined by microdissection. *Botanical Gazette*, 70:360–386, 1920.
- [8] S. H. Strogatz. Exploring complex networks. *NATURE*, 410(6825):268–276, March 2001.
- [9] A. Takamatsu, R. Tanaka, H. Yamada, T. Nakagaki, T. Fujii, and I. Endo. Spatiotemporal symmetry in rings of coupled biological oscillators of physarum plasmodial slime mold. *PHYSICAL REVIEW LETTERS*, 8707(7):078102, August 2001.
- [10] A. Tero, R. Kobayashi, and T. Nakagaki. A coupled-oscillator model with a conservation law for the rhythmic amoeboid movements of plasmodial slime molds. *PHYSICA D-NONLINEAR PHENOMENA*, 205(1-4):125–135, June 2005.
- [11] A. Tero, R. Kobayashi, and T. Nakagaki. Physarum solver: A biologically inspired method of road-network navigation. *PHYSICA A-STATISTICAL MECHANICS AND ITS APPLICATIONS*, 363(1):115–119, April 2006.
- [12] P. Xu, B. M. Yu, M. J. Yun, and M. Q. Zou. Heat conduction in fractal tree-like branched networks. *INTERNATIONAL JOURNAL OF HEAT AND MASS TRANSFER*, 49(19-20):3746–3751, September 2006.

## 9 Appendix

TABLE I

Viscosity value*	Descriptive term	Percentage of gelatine†	Substances having an equivalent viscosity‡
1. ....	Watery	0.0	Water
2. ....	Very liquid	0.05	.....
3. ....	Liquid	0.2	.....
4. ....	Slightly viscous	0.4	.....
5. ....	Rather viscous	0.5	Paraffine oil.....
6. ....	Decidedly viscous	0.6	.....
7. ....	Very viscous	0.7	Glycerine
8. ....	Extremely viscous	0.8	Bread-dough
9. ....	Gel	1.0	Vaseline
10. ....	Rigid gel	2.0	Firm gelatine

\*The abbreviation v.v. will be used for viscosity value.

†A 1 per cent dispersion is a mixture of 1 gm. of gelatine in 99 cc. of water.

‡All substances were examined at room temperature, 18° C.

Figure 3: Table of Viscosity Values

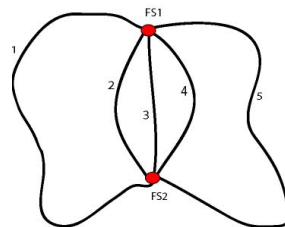


Figure 4: Computer Model of 2 Food Sources

2 Node			
Tube	R (average radius)	$\Delta x$ (change in length)	$\Phi$ (flux ( $\Delta x$ ))
1	0.3	11	0.0355
2	0.2	6	0.0650
3	0.1	3	0.1300
4	0.3	4	0.0975
5	0.35	13	0.0300

Table 1: Node 2 Table



Figure 5: Node 2 Model 1 Solution

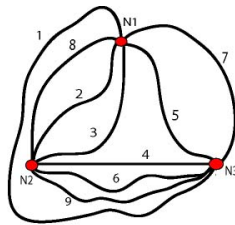


Figure 6: Computer Model of 3 Food Sources

3 Node				
Tube	R (average radius)	$\Delta x$ (change in length)	$\Phi$ (flux ( $\Delta x$ ))	$\Phi$ (flux ( $\Delta x, R$ ))
1	0.3	22	0.0177	1.4359E-04
2	0.3	7	0.0557	4.5129E-04
3	0.4	9	0.0433	1.1093E-03
4	0.2	10	0.0390	6.2400E-05
5	0.1	6	0.0650	6.5000E-06
6	0.3	10	0.0390	3.1590E-04
7	0.2	10	0.0390	6.2400E-05
8	0.4	8	0.0488	1.2480E-03
9	0.1	6	0.0650	6.5000E-06

Table 2: Node 3 Table

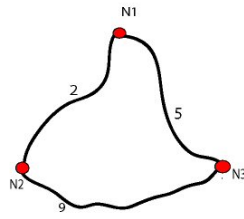


Figure 7: Node 3 Model 1 Solution

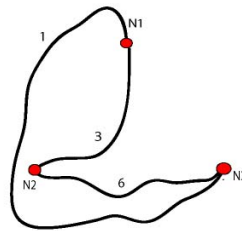


Figure 8: Node 3 Model 1 Solution

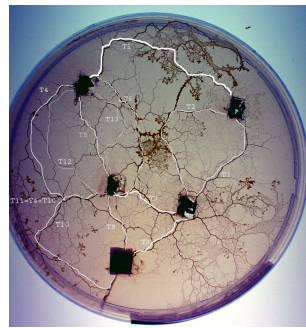


Figure 9: Slime A Proposal

Tube	COMPA	
	R (average radius)	$\Phi$ (flux $(\Delta x, R)$ )
1	0.4	3.8400E-04
2	0.3	1.5795E-04
3	0.3	2.4300E-04
4	0.35	2.3410E-04
5	0.25	1.2695E-04
6	0.3	1.6626E-04
7	0.35	7.3155E-04
8	0.25	1.6927E-04
9	0.2	7.8000E-05
10	0.2	2.6000E-05
11	0.2	1.5600E-05
12	0.1	2.0526E-06
13	0.1	2.4375E-06

Table 3: Slime A Table

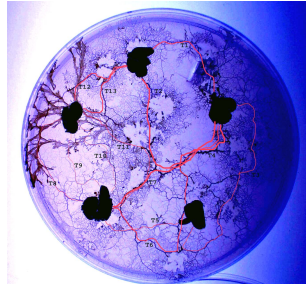


Figure 10: Slime 1 Proposal

COMP1			
Tube	R (average radius)	$\Delta x$ (change in length)	$\Phi$ (flux ( $\Delta x$ , R))
1	0.3	15	2.1060E-04
2	0.45	31	5.1589E-04
3	0.15	35	5.6411E-06
4	0.4	16	6.2400E-04
5	0.2	14	4.4571E-05
6	0.3	18	1.7550E-04
7	0.4	23	4.3409E-04
8	0.1	20	1.9500E-06
9	0.1	14	2.7857E-06
10	0.15	17	1.1614E-05
11	0.2	21	2.9714E-05
12	0.25	11	1.3849E-04
13	0.2	14	4.4571E-05

Table 4: Slime 1 Table