**Learning Scenario – Malaria Epidemiology Model (Vensim)**

**Basic Model:**

**Description**

This is a complicated model of the interactions between two populations – humans and mosquitoes. Each can live and die normally in isolation, but mosquitoes can also become infected with malaria, and then transmit that infection to their human victims. Depending on the initial settings, this can asymptotically approach a steady state or one or both populations can go to zero. Users can set the birth, death, and infection rates for humans and mosquitoes, as well as the recovery rate for humans.

**Background Information**

Malaria is a deadly scourge in tropical regions, particularly those without effective medical care. Its potency lies in the fact that it is spread primarily through mosquito bites, but mosquitoes themselves are immune to the disease. There is no effective vaccine for malaria, so effective solutions depend on controlling and understanding the evolution of the population of mosquitoes in an infected area. This model simulates such an area and allows students to investigate how changing certain parameters – number of mosquitoes, rate of human recovery, etc – can change the course of the epidemic.

**Science/Math**

This model works on the basic principle of HAVE = HAD + CHANGE for each of the population groups, complicated only by the fact that the CHANGE for each population often depends on the HAD for several other populations. For instance, the number of healthy villagers who are infected in a given tick depends on 5 different factors – the number of healthy villagers, the number of infected mosquitoes, the total number of mosquitoes, the bite rate, and the probability of infection transmission. In each case, the equation for determining HAVE for each population is represented graphically on the Vensim worksheet. The name of the box or arrow indicates the identity of each population, and the arrows themselves indicate what is taken into account for each population.

All of the interactions between groups are proportional, i.e. based on the size of the two groups. This means that we would expect to see exponential or Cumulative Distribution Function behavior. In practice, the sheer number of different variables that can have an impact on each function means that there is substantially greater variety in the graphs of populations over time. However, all populations eventually either reach a steady state or go to zero. By looking at the variation in groups over time, we can see some of the main interactions between humans and mosquitoes.

**Teaching Strategies**

An effective way of introducing this model is to use the fluid exchange activity. For this activity, each student is given a small, half-filled cup of water. One of the cups of water should contain 1 mol/L of a strong, colorless acid, such as HCl. The students know that one cup contains the acid (which is a marker for the disease in this simulation), but they will not know which one. Then, students move around the room and mix their water by pouring it into each other’s glasses with at least 5 other students.

Then, students can come back together and run a pH test of their cups of water to see which ones are now carrying the disease. Anywhere from 6 students to the entire class should now have the disease. The idea of this lesson is to show the ways in which diseases can spread among populations. Ask students to brainstorm ways of reducing the spread of disease. Common answers might include testing earlier and not letting the sick mix water with anyone (quarantining), exchanging less water (sanitation), or even adding a base to the water (vaccine/treatment).

**Implementation:**

**How to use the Model**

This systems model has a wide variety of parameters can that be manipulated to give a result. The important parameters are:

* Birth Rate: the number of new humans or mosquitoes born each time period, relative to their population
* Death Rate: the number of humans or mosquitoes that die of non-disease causes each time period, relative to their population
* Malaria Death Rate: the proportion of infected humans that die from malaria each time period
* Recovery Rate: the proportion of infected humans that recover each time period
* Bite Rate/Infections Transmission Probability: two parameters that impact the rate of infection for humans, given a certain number of infected mosquitoes

Each of these parameters can be manipulated by right-clicking on it and choosing “Equation”. This allows users to set the exact values for the parameters in question. A faster and more intuitive method, though a less accurate one, is to click and drag the sliders below each variable. The sliders can only be used while the simulation is running, but they will update instantly, so you can immediately see how changing the parameters changes the results.

When the applet is run, it will automatically run for 200 time periods, measuring and recording the values of each parameter at each time period. The data is then displayed on graphs displayed on top of each variable, including dependent variables that are not set by the user. Looking at the graphs gives an easy and simple way to follow the changes over time in each of the populations and the overall outcome. For more information on Vensim, reference the Vensim tutorial at: <http://shodor.org/tutorials/VensimIntroduction/Preliminaries>.

**Learning Objectives:**

1. Understand the how and why to set up an SIR model to simulate the spread of disease
2. Understand the effect of each parameter on the outcomes for each population

**Objective 1**

To accomplish this objective, discuss with students why it is important to model the spread of disease, and what sorts of parameters it would make sense to include in such a model. As the following questions:

As you ask the follow questions, use students’ answers to draw a simple diagram on the board, similar to the one that they will see in Vensim, with different groups and different factors. Be sure to explain why you’re drawing each factor in the way that you do.

1. What is the benefit of having a working SIR model? What will having a model allow us to do?
2. What are some key things that affect how a disease spreads? (Common answers: sanitation/hygiene, infectiousness, whether there is a cure/vaccine)
3. How can we model [key thing that affects how a disease spreads]? Ask this question for each answer given to question 2.
4. Malaria is carried by mosquitoes and transmitted to humans through mosquito bites. If we were going to model the spread of malaria, what populations would we need to think about?
5. Over the course of a disease spreading, people are going to be born and die. How can we account for that concept in our model?

Now, have students open up Vensim and look at the Malaria Epidemiology model. Discuss the ways in which the Vensim model is similar to or different from the one you created as a class. For instance, it is likely that your students will suggest some form of cure in the model, but Vensim does not consider treatment to be a viable option.

**Objective 2**

To accomplish this objective, have students run the model without changing any parameters. Explain how the results are displayed on the model: the simulation runs for 200 time steps, and then displays the quantities of each population at each time step on their own graphs. The graphs aren’t particularly detailed or well-scaled, but they give quick and easy insight into the overall population changes over time. The simulation with default settings goes to completion – the number of humans drops to zero, as they all die of disease. Ask the following questions:

1. What does it mean to say that the number of humans eventually goes to zero? Is this a realistic scenario?
2. What are some ways we could ensure that humans don’t just die off from the disease?

Now, have students implement one of their proposed modifications (common solutions: set birth rate of humans to 0.125, change malaria death rate to 0.05, change infection transmission probability to 0.575) and note the changes. Ask the following questions:

1. What is happening to the population of humans over time now?
2. This model says that the disease will eventually stabilize and the same proportion of people will be infected at all times. Do you think that’s realistic? Why or why not?
3. How could we improve this model to take into account the fact that infection rates aren’t always constant?

**Extensions:**

1. Expand the model to include the possibility of immunity
2. Compare the results of the simulation to real-world data regarding the spread of malaria

**Extension 1**

Ask students to think about what it would mean if there was a possibility that some healthy people could be immunized from the disease, as with a vaccine. Discuss how that might be applied to the model, and then have students add a new group and a new relationship between that group and health people. Once students have added this new feature, ask the following questions:

1. What does it mean to say that we have a separate group of immune people?
2. Are there any other groups we need to connect immune people to besides healthy people?
3. With this change, does the long-term human population increase, decrease, or stay the same? Why do you think that is?
4. Why do we only let healthy people become immune? Why not sick people?

**Extension 2**

Ask students to go online and research historical malaria rates in any area of Sub-Saharan Africa (excluding South Africa). Students should specifically look for rates of infection by the smallest time step possible. Compare these to the results of students’ models, and have students try to change their parameters to make the pathology of the disease match the real-world infection rates as closely as possible. Then, ask the following questions:

1. In the real world, what is the general relationship between population and malarial infection rates?
2. Does the real-world data more closely match a single epidemic that goes to completion, or a long-term steady state? Why do you think this is? Would your answer be different for different countries? Why or why not?
3. What are some factors that affect the spread of malaria in the real world that we haven’t taken into account in our model? How could be include some of them?

**Related Models**

**Epidemic (Vensim)**

<http://www.shodor.org/refdesk/BioPortal/model/VSepidemic?level=introductory>

This model is useful as an extension to the malaria model to study a different type of virus – swine flu. Like the malaria epidemiology model, this model investigates the effect of disease on a population of humans over time. However, rather than including a separate category for another species (and infection agent), the swine flu model only deals with humans. However, it adds additional categories for immunized and quarantined people. This is a great way to show students an example of some of their suggestions in a separate applet. The display system for the epidemic (Vensim) model is also significantly more detailed, providing side-by-side comparisons of the number of healthy, sick, recovered, immunized, and quarantined over time.

**Disease Model**

[www.shodor.org/featured/DiseaseModel/](http://www.shodor.org/featured/DiseaseModel/)

This model provides an excellent way to compare the systems model of malaria used here with an agent model. In a system model, the process is entirely determinate, calculating proportions mathematically from time-step to time-step. However, an agent model introduces an element of randomness since the individual actors are sprites, not populations. The decisions each sprite makes about where to move determine the course of the infection. This is also a great launching platform for a discussion of the relative merits of both systems. Ask students to think about the advantages and disadvantages of each type of model, and brainstorm a few situations where each model would be clearly better.

**Rabbits & Wolves**

[www.shodor.org/interactivate/activities/RabbitsAndWolves](http://www.shodor.org/interactivate/activities/RabbitsAndWolves)

One similar process to epidemic spread that might be counterintuitive to a lot of students is that of a predator-prey model, such as Rabbits & Wolves. The virus can be thought of as the predator, reproducing at the cost of increasing the chance of death for its host, while the humans would be the prey, attempting to avoid their predator at all costs and able to live without killing other species. Like in an epidemic, the settings on Rabbits & Wolves determine whether the interaction between predator and prey goes to completion or reaches a steady state.

An important distinction to make here is that, as a pseudo-random agent model, Rabbits & Wolves is inherently unstable. Eventually, sheer chance will have either all the wolves or all the rabbits die off, regardless of the initial conditions. Meanwhile, a Vensim model that goes to equilibrium will stay at equilibrium until the end of time. Ask students to discuss which behavior they think is more realistic, and why.