Of Men, Mice, and Hanta

Team 59
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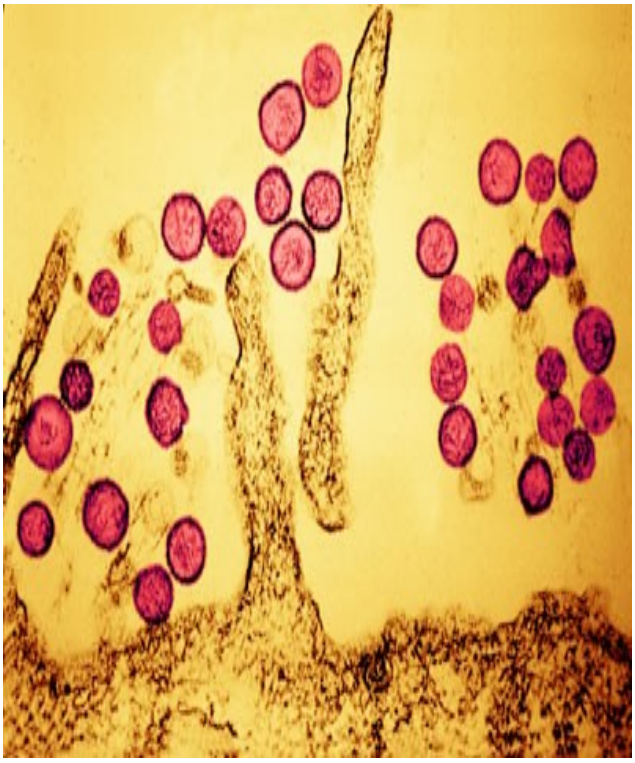

New Mexico Supercomputing Challenge- Final Report
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Executive Summary

Hantavirus is a prominent disease in New Mexico. Our team has conducted research on Sin Nombre, a Hanta Virus, and has made a model to represent this disease by showing how it spreads through a mouse colony. Since Sin Nombre is a vector borne disease the spread in mice will be very indicative to the spread from the mice to humans. We modeled the disease in an agent based system with two models and we looked into how to model it mathematically with an SIR model. We used Starlogo TNG and Netlogo, both of which we have some experience in. We attempted a mathematical Java model, but there were several complications in making it work on our computers so we did not finish it. We did not get to add global warming, so we do not have complete results, but if we did we think the virus would amplify in the mouse population, and therefore in humans.

Introduction

In the last few decades a significant number of so far unknown or underestimated pathogens have emerged as fundamental health hazards of the human population despite extensive research and increasing capabilities of

modern medicine to contain and eradicate infectious diseases. Almost all incidents caused by such emerging pathogens could be ascribed to viruses that are animal borne or have expanded their host range and crossed species barriers. The ability of an infectious agent to adapt to changing environmental conditions and variations in human behavior, population development, nutrition, education, social, and health status are relevant factors affecting the correlation between pathogen and host. Hantaviruses belong to the emerging pathogens that have gained more and more attention in the past decades. The serotypes of hantaviruses, Hantaan (HTN), Seoul (SEO), Puumala (PUU), and Dobrava (DOB) viruses predominantly cause hemorrhagic fever with renal syndrome (HFRS), characterized by renal failure, hemorrhages, and shock. Hantavirus outbreaks in the United States of America at the beginning of the 10^{th} decade of the past century have fundamentally changed our knowledge about the appearance of the hantavirus specific clinical feature, mortality, origin, and transmission route in human beings. The hantavirus pulmonary syndrome (HPS) was first recognized in 1993 in the four corners area of the United States and had a lethality of more than 50%. Although the causative virus was first termed in

relation to the geographic region where the outbreak occurred, the analysis of the individual viruses indicate that that the causing virus of HPS was a genetically distinct virus, and was thus named Sin Nombre, or “No Name” virus. Ever since, epidemiologists have struggled to study the long-term dynamics of its principal host, the deer mouse (peromyscus maniculatus). The goal of our project is to model the effects of global warming on hantavirus spread in New Mexico. Hantaviruses do not harm their hosts, but can produce a severe disease in humans. Hantaviruses also alter the behavior of their deer mouse hosts, causing them to become more aggressive and less mindful of territory. Hantaviruses spread in murid rodents through the entry of saliva into wounds. Hanta is also spread in rodent excreta to humans, via the aerosol route . Modeling the effect of Hanta in a mouse colony, therefore, will directly predict the incidence of the virus in humans. We focused on the spread of the disease in a mouse colony in the four corners area of the United States, where the 1993-1994 outbreaks occurred. Since these outbreaks were thought to occur because of the favorable climactic conditions (brought in part by the El Niño southern oscillation), we want to introduce climate change into the model. We wish to accomplish this with both a Netlogo and a

Starlogo TNG agent-based model.

Description of the Problem:

In the spring of 1993, a cluster of patients with an acute and highly lethal cardiopulmonary disease came to the attention of health officials in the Four Corners area (New Mexico, Colorado, Utah and Arizona) of the southwestern United States. All of the victims were otherwise healthy young athletes. The etiologic agent was determined to be a novel hantavirus, now known as Sin Nombre (SN), which is spread by infected rodents. Sin Nombre is a Hantavirus, a genus of the family Bunyaviridae, and has been endemic in the United States for several decades. Cases of this disease have been recognized from 1959, 1975, and 1978 and later. After the 1993 outbreak, which extended well into 1994 and ultimately affected 52 patients, subsequent cases in the Four Corners region and elsewhere in the United States occurred sporadically. From 1995 through 1997, an average of 4 patients per year received diagnoses of HCPS in the Four Corners states. Despite extensive media attention and public health campaigns during and after the 1993-1994 outbreak, the extent to which the public became informed about ways to avoid exposure to hantaviruses has been little assessed. The 1993 outbreak is believed to have emerged because of the unusual climatic conditions of

1991 and 1992, including the El Nino southern oscillation which brought increased precipitation to the Four Corners area. Ever since, a continuous effort has been maintained to study the long-term dynamics of Sin Nombre's principal host, the deer mouse (Peromyscus maniculatus). Sin Nombre is spread through inhalation of the dried feces, urine, and saliva of murid rodents (deer mice). Although Sin Nombre is not harmful to its rodent hosts, a severe disease known as Hantavirus Cardiopulmonary Syndrome (HCPS) occurs when humans are exposed to the virus. Creating a model of hantavirus spread in mice will directly relate to the spread in humans, because the disease is spread through inhalation of mouse excreta. The disease does not spread from human to human, therefore, modeling of the human population is unnecessary.

Description of the Methods

Research

We did research on the habits and behaviors of the deer mouse , hantavirus's primary host. We also researched the effect of hantaviruses on the mice and whether or not it harms them. This is the information we found to be important to our models:

Roaming Range	~3000-4000 square meters
Female Sexual Maturity	49 days
Litter Size	5 babies

Mice per Acre	11
Predation	Many nocturnal predators
Intrerval Between Litters	At least 27 days
Life Expectancy	Usually less than a year
Virus Effect	There is no major effect

Modeling

We chose two different methods to model our project. One was agent-based modeling, and one was mathematical modeling. The mathematical model was not completed because of several computer errors.

Method 1: Agent-based

We made two agent-based models, one using Netlogo and one using Starlogo TNG.

Netlogo

One of our agent-based models was made using Netlogo. The mice in the model, which are the only agent, have energy, age and gender as variables. They gain and lose energy as they eat and move, and when their energy reaches zero they die. Their energy is also lost if they reproduce. They have a certain energy value, called idealhealth, which controls their eating. If they go above their idealhealth value, they stop eating until they go down

again. Our research indicates that this is how mice actually behave. The age variable keeps track of how old the mice are, and they die after one year. They cannot reproduce until their age is greater than .08 years (49 days). Their gender,which is either male or female, tells them whether they can reproduce or not. Since roughly half of them can reproduce, it helps keep the population down and makes the model more realistic. When a mouse reproduces it first checks to make sure it is old enough, and then checks to make sure it is a female. If it passes these checks, there is a probability that it will reproduce. After this it has 5 babies and loses a large amount of energy. Some of the mice begin infected by the disease, and they can infect other mice through contact. If a mouse is infected there is no recovery because they remain carriers for the rest of their life, and they do not die because the disease does not effect them. The mice die from a mortality rate, used to model predators. This mortality rate can be easily changed to control the population, but not kill them off.

There is also food, modeled as patches, which the mice eat. When the mice eat the food they gain some energy and the food goes away. The food

grows back at a “food regrowth rate”, which is set with a slider. The regrowth rate set a number which is counted down to 0, which is when the patch turns into food. When it turns to food the color is set to green instead of brown. There are four seasons in the model which change the regrowth rate. During two of the seasons it is a positive number and during the other two it is a negative number. When it is a negative number, the food dies when it reaches 0. This keeps the population down, but still needs some work.

Starlogo

The Starlogo model is coming along well, but still requires some work. The mice are either classified as “female” or “other”, and only the females breed. In the case of a collision between mice there is a certain chance that, if one of them is female, they will breed. This only happens, however, if the female has enough energy. The female produces 3 baby mice and there is a random chance that a baby will also be female. The food grows in groups, and only if the population of food drops below a certain number. The mice hunt for food within a certain radius. They lose energy from breeding and walking, and gain energy by eating. There is no disease at the moment, as we are still

trying to maintain a steady population. It will, however, be implemented soon.

Method 2: Mathematical

We were planning to make a SIR mathematical model using Java, but due to computer errors we could not complete it. SIR stands for Susceptible, Infected, and Recovered. An SIR model assumes that the population is well mixed, so every agent has the same chance of being infected, and recovered agents are completely immune from further infection. There are three equations that make up and SIR model, and they are as follows:

Where:

$$\frac{dS}{dt} = -rSI$$

S is Susceptible, most of the agents will be susceptible to start

r is the infection rate, individuals are infected are rate *r*

I is the Infected individuals

$$\frac{dI}{dt} = rSI - aI$$

a is the recovery rate for infected individuals

R is the recovered and immune individuals

$$\frac{dR}{dt} = aI$$

Results

In our Netlogo model there is a cyclic mouse population. The population fluctuates with food availability, which changes with seasons. The virus spreads and infects 30-60% of the population. It sometimes infects 100% too. The food regrowth rates can be varied to account for global warming, however we did not have time to include it.

In the Starlogo model when the mice breed, three mice are produced. The food in this model grows in groups around other food, and only if the food count drops below a certain number. The mice can hunt for food, “sniffing” food within a certain radius and changing direction to face it. The model does not yet have a stable population because the mice hunt too much and the food steadily declines. This model does not have results because there is no disease.

Conclusions

Our mice have a cyclic population, and the infected mice follow the normal

population. If we add global warming we predict that hantavirus would be a larger problem, especially in the southwestern United States because of increased precipitation and food supply. The mouse population would increase because of the excess food supply, and hantavirus would have more vectors to spread through. However, the mice might not go near houses as much because they would not need the food from them, decreasing the risk to humans. Overall we think global warming would make hanta more prominent in humans.

Achievement

Our most significant achievement was making models of a hanta infected mouse population. These models can have global warming added to them later, even though they are not yet completed.

Works Cited

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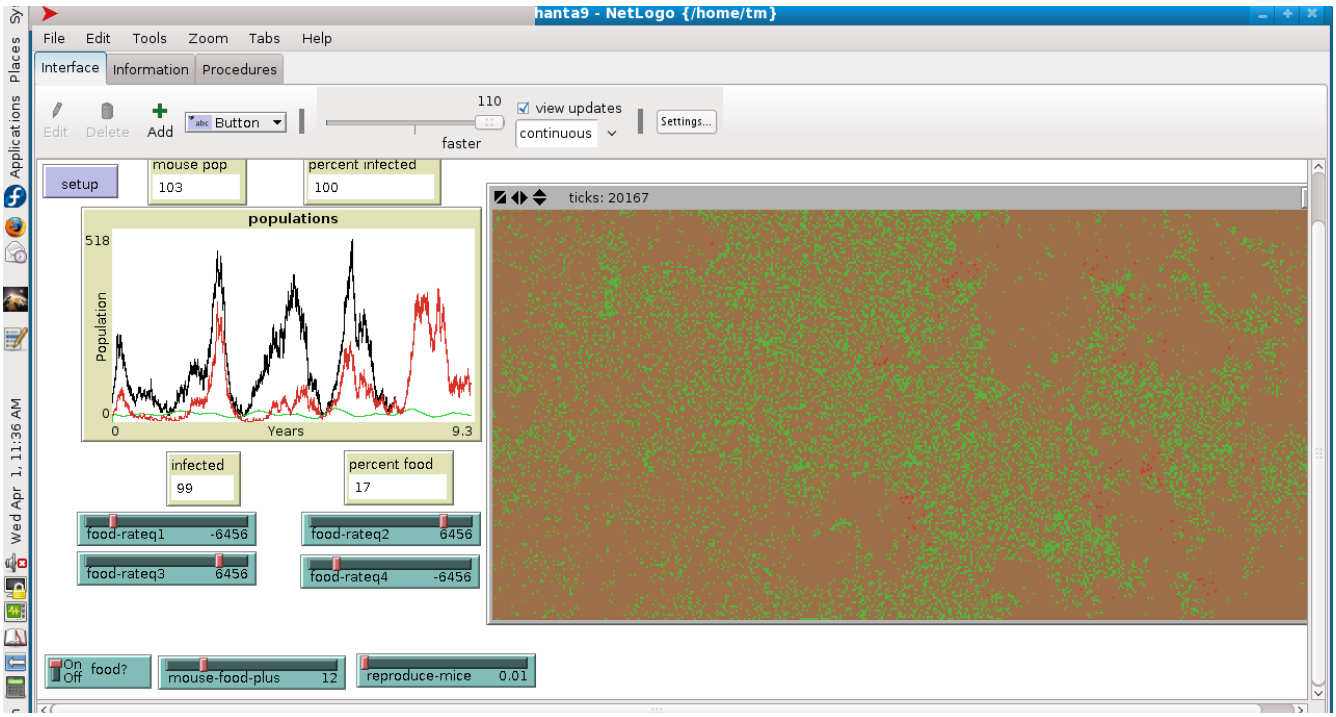
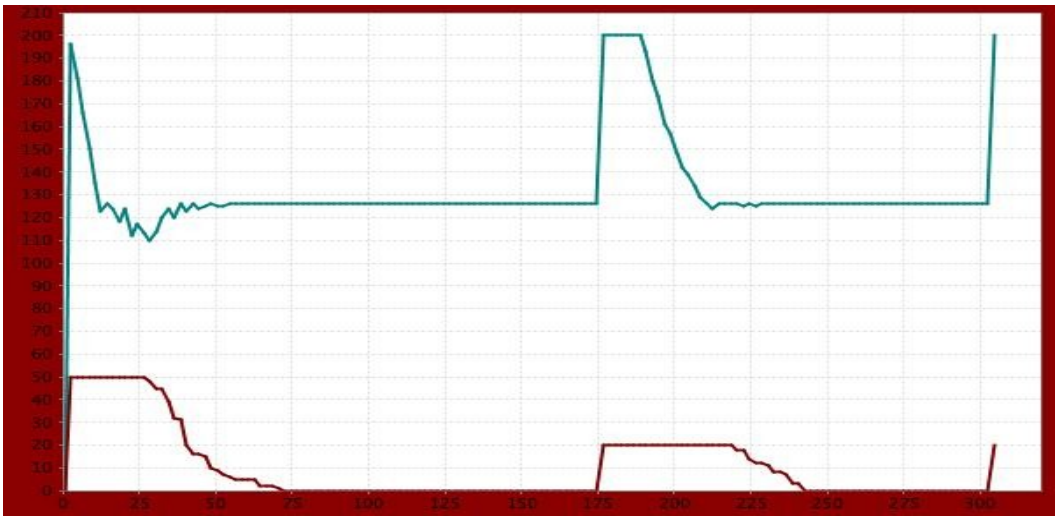
Netlogo Plot



Starlogo Plot



Netlogo Code

```
breed [mice mouse]
patches-own [countdown]
turtles-own [ energy age col gender infected ]
globals [d x y year max-age ave-lit season-change half-year fourth-year three-fourth-year]

to setup
  ca
  set year 2190 ;; ticks per year(4 moves per day)
  set three-fourth-year 1641
```

```
  set half-year 1094
  set fourth-year 547
  set max-age 1
  set ave-lit 5
  setup-mice
  set season-change 0 ;;one quarter  of yr=547 ticks
  ask patches [ set pcolor brown ]
  if food? [
   ask patches [
    set countdown random abs food-rateq1
    set pcolor one-of [ green brown brown brown brown]
    ]

   ]
end

to setup-mice
set-default-shape mice "mouse side"
create-mice initial-number-mouse
[
set color black
set size 1
set age random-float 1
setxy random-xcor random-ycor
set energy idealhealth
;set col 1
set gender one-of [ 1 2 ]
set infected one-of [0 0 1]
if infected = 1 [set color red ]
]
update-plot
end

to go
if not any? turtles [stop]
ask mice [
move
set x -10
set y 10
;if col = 1 [
;dist
;]
;if d >= 5 [
;facexy -10 10
;fd 1]
if food? [
eat-food
set energy energy - 1
]
get-old
death
reproduce
;move-out
infect
]
if food? [ask patches[grow-food ] ]
;;set season-change season-change + 1
sesan-change
```

```
tick
update-plot
end

to move
fd 1
rt random 360
end

to update-plot
set-current-plot "populations"
set-current-plot-pen "mouse"
plotxy ticks / year count mice
set-current-plot-pen "food"
plotxy ticks / year count patches with [pcolor = green] / count patches * 100
set-current-plot-pen "infected-mouse"
plotxy ticks / year count mice with [infected = 1]
end

to grow-food
  if (pcolor = brown) and (food-regrowth-time >= 0) [
    if countdown <= 0 [
      set pcolor green
      set countdown random food-regrowth-time
    ]
    set countdown countdown - 1
  ]
;  if pcolor = green and food-regrowth-time < 0 [
;    if countdown <= 0 [
;      set pcolor brown
;      set countdown random abs food-regrowth-time
;    ]
;    set countdown countdown - 1
;  ]
  ;;set countdown countdown - 1
end

to eat-food
if energy < idealhealth [
if pcolor = green [
set pcolor brown
set energy energy + mouse-food-plus
]
]
end

to death
  if energy < 0 [die]
  if age >= max-age [die]
  if ticks >= 2 * year [
  if random-float 1 <= mortality-rate [die]
  ]
end

;to dist
;set d sqrt((xcor - x) ^ 2 + (ycor - y) ^ 2)
;end
```

```
to reproduce
if random-float 2 < reproduce-mice and age > .08 and gender = 2 [
energy-decrease
hatch ave-lit [ set age 0]
]
end

to get-old
set age age + (1 / year)
end

to sesan-change
if season-change >= year [ set season-change 0 ]
if season-change = three-fourth-year [ set food-regrowth-time food-rateq4 ]
if season-change = half-year [ set food-regrowth-time food-rateq3 ]
if season-change = fourth-year [ set food-regrowth-time food-rateq2 ]
if season-change = 0 [ set food-regrowth-time food-rateq1 ]
set season-change season-change + 1
end

;to move-out
;if energy <= 100 [
;set col 0
; ]
;end

to energy-decrease
set energy energy / divisor
end

to infect
  if any? turtles-here with [infected = 1]
     [if random-float 1 < .01 [ set infected 1 set color red ]
     ]
  if random-float 1 < .00001 [ set infected 1 set color red ]
end
```