Adaptive Virus

New Mexico Super Computer Challenge
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Team 20
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Executive Summary

Viruses are constantly changing over time. During viral evolution the viruses genetic DNA changes due to the environment conditions of its host. The genetic material of the virus will have adapted to survive. The concept of the survival of the fittest can be coin to a virus ability to survive the numerous contacts it has had with various eukaryotic cells. Human cells are composed of eukaryotic cells and carry the genetic DNA. As prokaryotic cell, viruses are able to mobilize themselves through various organisms and surfaces.

The concept of implementing the use of a pseudo-virus in a control environment and developing a vaccine to combat the genetic adaptations of the pseudo-virus is the bases of our research. Viruses have evolved over several eras, the development of a pseudo-virus that will increase the survival of individuals and provide a treatment. Our result will indicate a realistic population of our society of healthy and unhealthy individual the probability of infection increasing throughout a population.

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Problem Statement

In the 2009 flu pandemic, the virus isolated from patients in the United States was found to be made of genetic elements from four different flu virus – North American swine influenza, North American avian influenza, human influenza and swine influenza virus typically found in Asia and Europe (Influenza A virus Subtype H1N1, 2009). Viruses have been around for millions of years and contributed to our evolutionary development. Due the vast number of viruses and its existence before living cell it has developed genetically over time. Since a virus is single cell organism known commonly as Prokaryotic cell, their DNA is but a single strand enclosed within the cell. Virus can infect all types of organisms from animals and plants to bacteria and archea (Virus), causing a continual viral genetic evolutionary development over time.

Unlike prions and viroids, viruses consist of two or three parts: all viruses have genes made from either DNA or RNA, long molecules that carry genetic information; cell have a protein coat that protects these genes; and some have a envelope of lipids that surrounds them when they are outside the cell (Viroids do not have a protein coat and pirions contain no DNA or RNA) (Virus). The origin of virus in evolution is still unclear. The structure of virus is a simple single cell envelope by capsid which is made up of a protein coat that protects the fragile DNA. The capsid protects the viral DNA from physical, chemical and enzymatic damages. Viruses vary from simple helical and icosahedral shapes to more complex structures (Virus). The protein subunits in a virus capsid are multiply redundant, i.e. present in many copies per particle. Damage to one or more subunits may render that particular subunit non-functional, but does not destroy the infectivity of the whole particle (Cann, 2007). Furthermore, the outer surface of the virus is responsible for recognition of the host cell. Initially, this takes the form of binding of a specific

virus-attachment to a cellular receptor molecule. However, the capsid has a role to play in initiating infection by delivering the genome (DNA) from its protective shell in a form in which it can interact with the host cell (Cann, 2007).

To form an infectious particle, a virus must overcome two fundamental problems: 1) to assemble the particle utilizing only the information available from the component which make up the particle itself (capsid and genome), and 2) virus particle form regular geometric shapes, even though the proteins from which are made are irregular shaped (Cann, 2007). Virus are able to solve these problems in the rules of symmetry. In 1957, Fraenkel-Conrat & Williams showed that when mixtures of purified tobacco mosaic virus (TMV) RNA & coat protein were incubated together, virus particles formed. The discovery that virus particles could form spontaneously from purified subunits without any extraneous information indicated that the particle was in the free energy minimum state and was therefore the favored structure of the component. This stability is an important feature of the virus particle.

Viruses are found wherever there is life and have probably existed since living cell first evolved. Three different theories have been proposed to explain the origin of viruses.

- The first, the Regressive Theory, proposes that viruses arise from free-living organisms like bacteria that have progressively lost genetic information--- to the point where they become intracellular parasites dependent upon their hosts to supply the function they have lost (Orgin of Virus).
- The second theory, the Cellular origin hypothesis, proposes that some viruses may have evolved from bits of DAN or RNA that "escaped from the genes of a larger organism. The escaped DNA could have come from plasmids (pieces of naked DNA

that can move between cells) or transposons (molecules of DNA that replicates and move around to different positions within the gene of the cell) (Virus).

- The third theory, proposes that viruses originated and evolved along with most primitive molecules that first contained self-replicating abilities. While some of the molecules were eventually collected into unites of organization and duplication termed cells, other molecules were packed onto virus particles that coevolved with cells and parasitized them (Orgin of Virus).

A communicable disease is carried by microorganism and transmitted through people, animals, surfaces, foods, or air. Communicable diseases rely on fluid exchange, contaminated substances, or close contact to travel from an infected carrier to a healthy individual (Mithra, 2010). Parasites, bacteria and viruses all qualify as pathogens, nicknamed "germs" and can cause a communicable disease, Their method of transmission, period of dormancy, ease of contagiousness, and relative danger can differ drastically from one disease to the next (Mithra, 2010). Examples of common human disease caused by viruses include the common cold, influenza, chickenpox and cold sores. Many serious disease such ebola, AIDS, Avain influenza and SARS are caused by viruses (The Medical News)

Although viruses cause disruption of healthy homeostasis, resulting in disease, they may exist relatively harmlessly within an organism (The Medical News). As viruses mature through their lifespan, they are able to replicate their genetic materials and the genetic material of the host. Causing an increase in immunity to the virus as it re-infects other organisms. The genetic adaptation of the virus to adapt to it environments has given rise to various new viruses in the process.

Each year in the United States on average, 5% to 20% of the population gets the flu; on average, more than 200,000 people are hospitalized from flu-related complications, and; about 36,000 people die from flu-related causes. Some people, such as older people, young children, and people with certain health conditions, are at high risk for serious flu complications (Center for Disease Control Center, 2009). Influenza virus may be transmitted among humans in three ways: (1) by direct contact with infected individuals; (2) by contact with contaminated objects (called fomites, such as toys, doorknobs); and (3) by inhalation of virus-laden aerosols. The contribution of each mode to overall transmission of influenza is not known. However, CDC recommendations to control influenza virus transmission in health care settings include measures that minimize spread by aerosol and fomite mechanisms (Racanielle, 2009). The mode of viral transmission is an important process for viral survival in any prokaryotic and eukaryotic organism.

A pandemic is a worldwide epidemic. The 1918 flu pandemic, commonly referred to as the Spanish flu, was a category 5 influenza pandemic caused by an unusually severe and deadly influenza A virus (The Medical News). Within a 10 year span the Spanish Flu killed approximately 40-50 million people. The Spanish flu is an example of a virus adapting to it environment and developing new genetic make-up and becoming and new virus to content with. The recent pandemic of H1NI a byproduct of the Spanish flu is prime example of it being a subunit of influenza which over time has become viral infection.

 How many individuals will be become infect with a pseudo virus, and will this virus be altered and adaptive to the environment of its host. Although, the problem of can be studied on a worldwide population. We would like to address the problem in a small community. The validity

of a small community would compare to a larger community. The initial problem of viral infection is the time frame of infection and the rate of immunity related to the outcome of the population of the community. The concept of a pseudo virus deals the concept of an unknown virus that would adapt to it environment over time and genetically be altered. We feel this is important due the fact that a virus can be altered in a laboratory or can be altered via the community contact of the virus.

Method

The method that we employed was the NetLogo Virus Model. This model simulates the transmission of perpetuation of a virus in a human population. Ecological Biologist have suggested a number of factors which may influence the survival of a directly transmitted virus within a population (Wilensky, 1998).

In November of 2009, Mr. Nick Bennet and Mr. Jon Gonzales provided a small workshop to assist our group with a better understanding and implementation of our project. We envision and different model using Netlog TNG but was dissuaded to use the NetLogo as it was easier to work with.

As we worked with the model we generated our model similar to the Netlogo Virus model and utilized the same button and application. This provided a better understanding of the how the model came together and how each button applied to the model. During the process of applying various buttons and setting up the model was difficult to work with. As we were making various applications we would return to the model and redefine the role of each button.

The initial community population of 300 individuals was set for a small subset. The small population provides the research to visually distinguish the difference in rate of infection and immunity of the population. The duration of infection varied between two to ten weeks. During these weeks individuals become ill or developed and immunity to the virus. The virus is indentified by colored individuals. These individuals came in contact with each other. Individual who are colored white when they encountered an infected individual, they would turn red, depending on its susceptibility and immunity. This same individual would develop and maintain the virus for the duration of time set, and then either die- if unhealthy- or live-healthy- and would then turn to the corresponding color.

Each slider has a specific purpose. "Infectiousness" slider is how high the virus can be contracted. Ninety-nine percent infection means the probability of contracting the virus is very high. "Population-fitness" slider is how healthy the population is and can reduce or increases its chances of contracting the virus. "Duration" slider is how long an individual maintains the virus. "People" slider is the initial population within the program. "Vaccinated" slider is the percent of the population that will receive the vaccine- just a probability.

Lastly, the territories are color coded, as to show boundaries within a "person's" life on a daily basis. Since not every person will be traveling all across the board. White (gray) people are immune, green is susceptible, red is sick, and blue is the total amount of people within the world.

Results

We ran four trail versions of the virus model. Each trail provides different results and in which we discuss the outcome for each trail. Each trail had an initial population of 300 individuals. The duration of infection varied between two to ten weeks. During these weeks,

individuals become ill or developed immunity to the virus. In addition, the individuals were able to reproduce- if healthy- and able to die from the sickness. One major variable introduced to this program was the initiation of patches set in different colors, as to show a "normal" person usual routine, since they might not be roaming the whole county. The virus is indentified by red individuals, as immune were gray, susceptible were green and the total number of individuals were blue.

I. Trail 1: During this trail, the infection rate increased to approximately 302 infected individual with the virus. Fifty percent of the individual were healthy and none were vaccinated. However, during a eight week time frame, the virus infected percent of the population. We can assume from these results that if a pseudo-virus, with a 99% infection rate and with our population of people being only 50% healthy- most like our community. Then we predicted that a new and advanced virus, without a vaccine can and will most likely affect the entire initial population plus some of the newborns, and lasting for around 40-50 months.

Trail 1:

99% infection

50% fit

8 weeks

0% vaccines
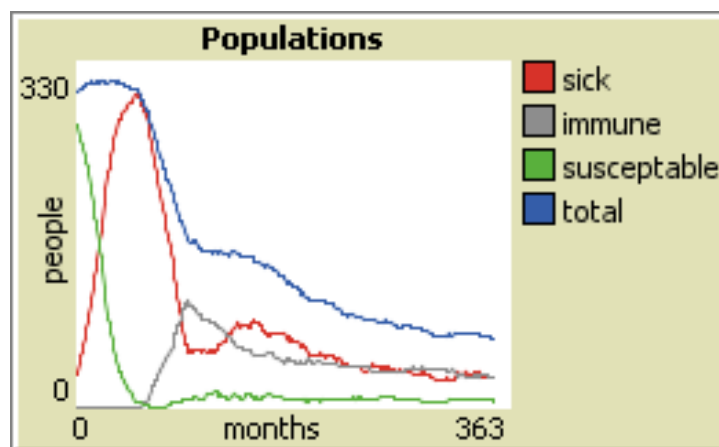
II.   Trail 2: During this trail, the infection rate increased to approximately 184 infected individual with the virus. Fifty percent of the individual were healthy and 100% were vaccinated. However, during a ten-week period, the virus infected around 60% of the population. We predicted for this result, if a virus with advanced genes and yet very affective, with the population as it is now, half of population will be infected over a long time of 60 months. So the faster we produce a vaccine and administer it to everyone the more people will be immune from it, given how un-healthy our population is now.
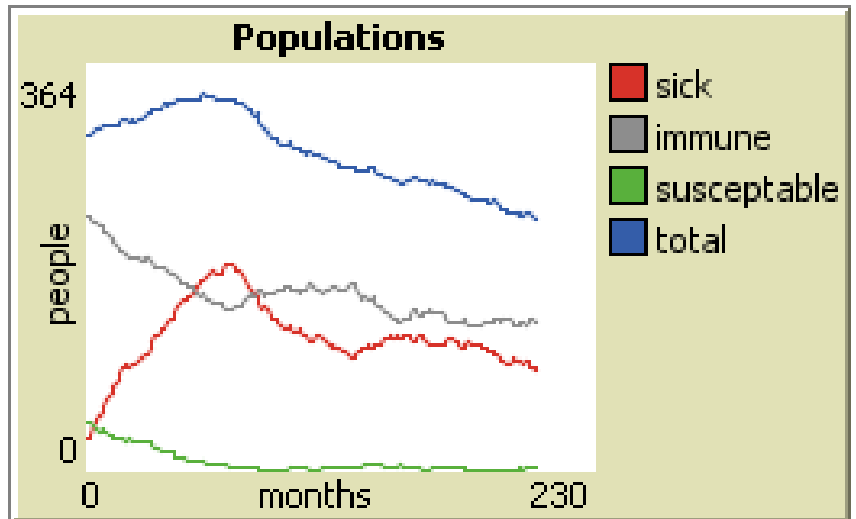
Trail 2:

99% infection,

50% healthy

10 week duration

100 vaccinated

III.   Trail 3: During this trail, the infection rate increased to approximately 134 infected individual over a total of 20 months with the virus. Ninety percent of the individual were healthy and fifty percent were vaccinated. But during a three week time frame, the virus infected a small percent of the population, due to the fact that there were so many individuals who were healthy. We also see that over the time the virus remains constant giving us the explanation that the vaccines do not work as well since the virus is adapting and evolving.
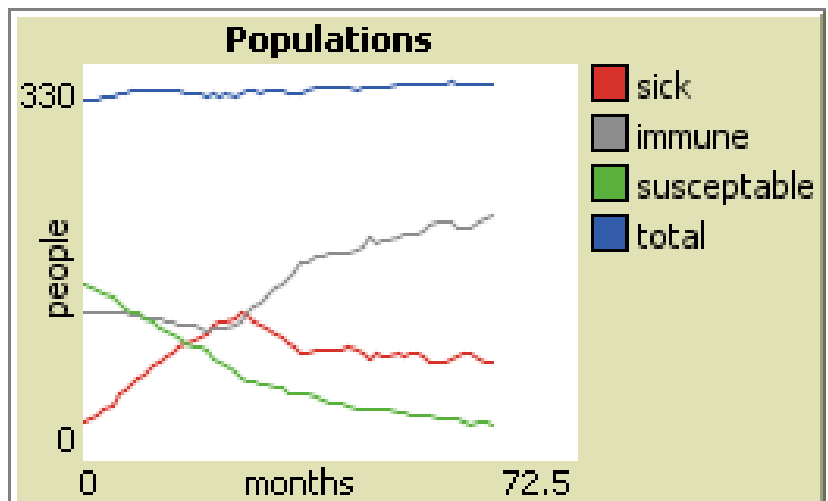
Trail 3:

99% infection

90% fitness

3 weeks

50 % vaccinated

IV.   Trail 4: During this trail, the infection rate increased to approximately 70 infected individual with the virus. 99 % of the individual were healthy and 100% were vaccinated. But during a 2 week time frame, the virus infected not even a quarter of the population. This outcome reminds us of the H1N1 outbreak. The infection was not horribly infectious, and most the population was healthy. The virus ran for a while and now is calming down since the vaccines have been administered yet continues to evolve in our present day environment.
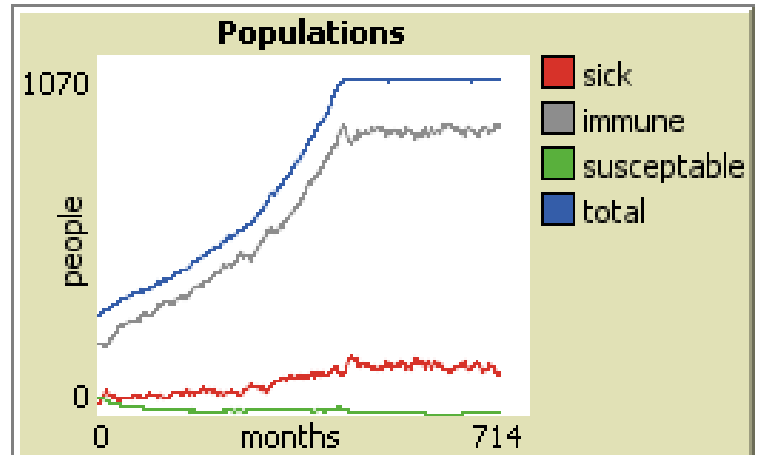
Trail 4:

50% infection

99% healthy

2 weeks

100% vaccinated

Conclusion

The second theory, the Cellular origin hypothesis, proposes that some viruses may have evolved from bits of DAN or RNA that "escaped from the genes of a larger organism. The escaped DNA could have come from plasmids (pieces of naked DNA that can move between cells) or transposons (molecules of DNA that replicates and move around to different positions within the gene of the cell) (Virus). Based on our analysis of the infection and immunity rate the number of individual who became ill would eventually die. But if the individuals who were vaccinated with our pseudo-virus the chances of survival greatly increase their chance of survival.

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Achievements

- The completion of our project is a great accomplishment for our team. It taught all of us to work hard and that persistence pays off. We encountered many challenging obstacles through the duration of our project, but our perseverance and cohesiveness allowed for us to complete our project.

- Obstacles we encountered are:

    o Changing the title of our project and the focus.

    o Scheduling conflicts between sports and school activities. After school jobs and college courses in the evenings.

    o Losing a member of our team and refocusing our energy on completing the task at hand.

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