Latin America's Next Top Model:

Predicting Chagas Prevalence

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Introduction

For over 9,000 years [1], Chagas' Disease has been taking its toll on the Southern Cone region of Latin America. The causal agent, protozoan parasite *Trypanosoma cruzi*, currently afflicts 16-18 million people [2]. Little progress has been made to curtail its spread to the over 120 million people in danger of infection [3].

Models of how parasites and hosts interact have given insight into the behavior of the parasite and infected hosts [4-8]. Plague models also offer insight, but like Chagas' Disease are limited due to the complexity of the disease [9-11]. As new populations become exposed and new conditions affect old numbers, calculating the prevalence of this disease becomes increasingly insightful. A functional model will always help determine which factors are most important to consider from any standpoint, be it humanitarian, medical, economic or otherwise.

Methods

Both a dynamic model and a computer simulation are implemented in predicting disease prevalence. A dynamic model can be created to model the interactions between the affected bug, human and mammal populations. Once a system of differential equations was established, the first step in analyzing the equations is to find steady states, i.e. where all differential equations equal zero. With a solution it is possible to linearize nonlinear equations and use linear algebra to study what behavior will occur near the various steady-state values.

Due to the difficulty of solving dynamic systems in the abstract form, the program Maple was implemented in solving these equations numerically when given initial conditions. Maple can also plot behavior of the system, giving visual aids in analysis.

Created in NetLogo 3.1.1, a simulation has been written in hopes of recreating real-life scenarios *in silico*. To create such a replication, the behavior of hosts and vectors must be known well enough to emulate, which goes hand-in-hand with the efforts of creating a dynamical systems model. Simulations can be tested for accuracy by comparing its results to real-life data. When finely tuned, it can then be used to suggest outcomes of changing conditions within the system.

Results

The first solution considered was the trivial solution, both for its ease of use and its ease of discovery. Eigenvalues discovered for this scenario imply that the net reproductive rates are responsible for the behavior of the system in the null state. We can conclude that the values will always be real, but their signs depend entirely on birth and death rates of the populations, causing behavior to vary as these values do. The numeric solving methods used in Maple have successfully shown behavior of the system given initial conditions, but are limited by the quality of input available.

The simulation has been used to spread the disease among populations and plots the populations given initial conditions, but also lacks. It is no more sophisticated than the system of equations from which it was based.

Discussion and Future Plans

In analyzing the system, only the trivial solution has been considered. Although interesting behavior does occur at this result, considering when all populations are dead is

not so interesting. Finding steady-state solutions for a nonlinear system of equations can provide valuable insight for more intriguing settings. Due to their difficulty of discovery, this will require further research and development of analytic capability.

The power of Maple is clearly evident in its ability to solve the complex system and plot variables. These preliminary results, however computed correctly, indicate behavior that is not observed in nature. Without refinements to both the equations and coefficients, the system cannot currently display accurate data nor be used to discover more interesting types of behavior within the system. Much of this discord can be attributed to the assumptions used in creating the model, which will need to be modified or removed entirely to improve accuracy. Furthermore, although the coefficients used in sample plots are reasonable, they are by no means accurate. Gathering information to accurately approximate these coefficients is crucial to making this model precise.

As mentioned before, the agents in the simulation do indeed emulate the transmission of a disease. Such a simulation may provide valuable insight into the system's behavior rapidly and cheaply, disclosing information that would not otherwise be easy to discover. Like the system of equations, the quality of the output is only as good as the input. The refinements in the equations will likewise need to be reflected in the code for the simulation. Also, the program bears its share of bugs and will need to be more fully tested and debugged to ensure that it is working properly.

Once the model and simulation are refined and accurate, many potential uses for these are evident. Vaccination and other control strategies may be based off of these models. Economic impacts of the disease such as person-years of labor and QALYs (Quality-Adjusted Life Years) lost, health care costs could be predicted rapidly, cheaply

and accurately. This knowledge could help combat Chagas' Disease not only in areas

currently exposed but for populations threatened by disease migration.

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