

# **Predicting the Prevalence of Chagas' Disease using a Parasite-Host-Human Mathematical Model and Simulation**

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## **Introduction**

Despite dramatic medical advances over the last century, including the widespread use of antibiotics and vaccinations, Chagas' Disease continues to run rampant in Central and South America. Current estimates suggest that 16-18 million people are currently infected and another 120 million remain at risk [1]. Furthermore, there is no vaccine for this disease and the two drug treatments, however 50 percent effective during the acute phase, are not often used due to their substantial toxicity [2]. Lacking an effective way to control the disease, researchers have directed their efforts toward modeling the diffusion of *Trypanosoma cruzi* - the causal agent of Chagas' disease - in order to disrupt the transmission of the disease.

The idea of modeling biological systems mathematically is a well-established concept. In the 1920's, Alfred Lotka and Vito Volterra presented a basic mathematical model that demonstrated how the population of a predator and its prey relate to each other in an oscillatory fashion [3]. Since then, population models have become increasingly sophisticated, including ones that incorporate time delays and can even depict the conflict between a parasite and human antibodies [4]. As experimental research seeks to control spread of Chagas', the need to know just how severe it will become in a specific population becomes increasingly more important.

## **Methods**

My proposed BBSI project would look to extend current research in order to model the prevalence of Chagas' disease within a population. Using a system of coupled nonlinear ordinary differential equations, we hope to find relationships between the many varied contributing factors to this disease and predict what will result from various modulations of single and combinations of these factors--no project has yet to combine all of these variables into a comprehensive model. Furthermore, since many of the modeling calculations will be made via computer, I seek to simulate the equations in a C++ program so that one may more clearly enter and modify variables to see how they relate to one another and the entire system.

## **Possible results and their implications**

Through determining prevalence of Chagas' disease, it may be possible for populations to assess their own risk as well as predict effectiveness of preventative efforts. Furthermore, knowing how factors relate will allow for the analysis of cost-effective ways to combat the illness. A well-constructed model and simulation could also serve as groundwork for modeling other parasite-host systems.

## **References**

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