

# COMPUTATIONAL MODELING OF THE INTERACTION OF THE *T. CRUZI* PARASITE WITH HOST CELLS

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## Introduction

Chagas' Disease, caused by infection with the *Trypanosoma cruzi* parasite, is deadly and wide spread, with 16-18 million people infected and another 120 million at risk for infection [1]. Unfortunately, very little is known about the parasite that could be used in treatment and prevention. The goal of the Virtual Parasite Project (VPP) is to design a computer program that provides insight into the parasite-host dynamics of the *T. cruzi* parasite with its host by modeling the biophysical interactions [2]. A good part of the simulation can be based on the actual physics of the parasite's movement. However, modeling all of the simulation in this way would be very inefficient. Some parts can be just as accurately handled by a rule-based swarming program that executes commands based on a set of conditions (i.e. "if A, then do B").

Modeling artificial life that interacts with its environment according to set rules is not new. Craig Reynolds [3], for example, modeled a flock of birds flying together and avoiding obstacles using only a few basic instructions in 1987. More research has been completed since that original publication, especially in the area of basing the rules of interactions and visual representation of the creatures on real-world physics [4].

However, the focus of previous research projects has been on behaviors that have already been thoroughly studied and therefore could be accurately modeled using the

physics combined with the experimental knowledge of the system. In the case of the *T. cruzi* parasite, very little is known about the mechanisms that control and facilitate its binding with and infection of a host cell.

## **Methods**

This BBSI project seeks to expand upon the existing *in silico* model of *T. cruzi* parasites, paying special attention to their interaction with the host cell and the factors that influence whether or not each parasite infects the host cell. The existing program is written in C++/FORTRAN and provides for some basic, randomized movements of the *T. cruzi* swarm. However, it does not address any of the binding/invasion components of the microparasitic infection. More accurate biophysical models of the *T. cruzi* parasite's swarming behavior in blood or fluid have also been developed since the program's beginnings. Because of this, more up to date mathematical and linguistic swarming rules must be added. In addition, a host cell invasion module will be defined with the aim of mimicking as closely as possible what is seen in the wet lab. A graphical simulator that renders the results of the code in three-dimensions will be used to check how closely the results match what is known of the behavior of the parasites.

## **Possible results and their implications**

The accuracy of the simulation will be determined by comparing the infection rate of the virtual parasite simulations with the infectivity of various strains as measured by the wet lab. An accurate invasion model could lead to insights on how to stop the invasion process and prevent infection.

## References

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