Abstract for SURF UVM Spring 2010: Naomi Pollica

Systems Modeling of Chagas disease in Guatemala Using STELLA

Chagas disease is the most serious infectious disease in the Americas. My research focuses on the endemic country Guatemala, where ecotopes, population distribution, and disease transmittance is diverse. Transmitted through Triatomine blood-feeding insects called *T. dimidiata* and other blood-feeding insects that defecate while feeding, Chagas disease causes megacolon, megaesophagous, and heart disease. There is no vaccine, and disease control efforts focus on prevention (such as spraying to reduce the insect population) rather than treatment. Using STELLA to implement a disease model of human, insect, domestic and peridomestic animal populations, and environmental factors as a closed system in Bolivia, we are able to explore how Chagas disease spreads and how various prevention methods affect the spreading. Initial parameters were gathered from existing literature such as the CIA Fact Book and academic articles pertaining to Chagas Disease in Latin American populations. In addition, using data accumulated from bloodmeal analysis of specimens of *T. dimidiata* from Guatemala, we were able to observe the feeding preferences and the distribution of genetic differences of *T. dimidiata*. The data from our finished model will be compared to published findings from Argentina, and our results will further the investigation of how to best control the spread of Chagas disease.