Lourdes Esteva FACULTAD DE CIENCIAS, UNAM e-mail: lesteva@lya.fciencias.unam.mx Gustavo Cruz-Pacheco INSTITUTO DE INVESTIGACIONES EN MATEMÁTICAS APLICADAS Y EN SISTEMAS, UNAM e-mail: cruz@mym.iimas.unam.mx Cristobal Vargas DEPARTAMENTO DE CONTROL AUTOMÁTICO, CINVESTAV-IPN e-mail: cvargas@ctrl.cinvestav.mx

## Modelling transmission of Chagas' disease

Chagas disease, also known as American trypanosomiasis, is a potentially lifethreatening illness caused by the protozoan parasite, Trypanosoma cruzi (T. cruzi) which is found mainly in Latin America. The main mode of transmission of Chagas disease in endemic areas is through the bite of an insect vector called a triatomine bug. The disease may also be spread through blood transfusion and organ transplantation, ingestion of food contaminated with parasites, and from a mother to her fetus. Control measures are limited since vaccines to prevent the disease are not available, and drugs are effective only in the acute and early chronic phase of infection, but have adverse effects. Control measures include insecticides to kill the vector, screening blood donors, and treatment to patients in the acute phase. Recently, a controversial strategy, Zooprophylaxis, has been proposed for the control of vector transmitted diseases. This technique refers to the control of vector-borne diseases by attracting vectors to domestic animals in which the pathogen cannot amplify (a dead-end host).

In order to assess the efficiency of the different control measures for Chagas disease, in this work we develop a mathematical model considering four populations: humans, vectors, and susceptible and no susceptible domestic animals to Chagas infection. We obtain the basic reproductive number of the disease, and through it we evaluate the impact of the control measures.