Research Program :: Ariel Cintrón-Arias

"Increasingly in recent decades, however, mathematics has become pervasive in biology, taking many different forms: statistics in experimental design; pattern seeking in bioinformatics; models in evolution, ecology, and epidemiology; and much else" Sir Robert M. May

The following areas of applied mathematics are of particular interest to me: nonlinear dynamics; mathematical modeling and simulation; and parameter estimation.

Moreover, I am interested in mathematical formulations (deterministic and stochastic) that describe time-evolution of contact processes including, population models for single species (e.g. logistic) and population models for interacting species (e.g. predator-prey systems, transmission dynamics of infectious diseases, within-host dynamics). Some modeling approaches of my interest are those that employ: ordinary differential equations; continuous-time Markov chains; discrete-time dynamical systems; network growth models.

In a broad sense, mathematical descriptions of dynamical systems must be validated against real datasets before these descriptions can be implemented for prediction, forecasting or data analysis. Model validation involves: inverse problem theory, statistical inference, sensitivity analysis, and asymptotic statistical theory, to mention a few. I am interested in estimation methodologies that include: ordinary and generalized least squares; Markov chain Monte Carlo methods; and genetic algorithms.

Below, descriptions of my most recent projects are included. These projects involve modeling and computer simulation, as well as parameter estimation. Some pre-prints are also attached.

Sensitivity Analysis and Parameter Selection
We discuss methods for a priori selection of parameters to be estimated in inverse problem formulations for dynamical systems with numerous state variables and even larger number of parameters. We illustrate the ideas with an in-host model for HIV dynamics, which has been successfully validated with clinical data, and a model for the reaction of the cardiovascular systems to an ergometric workload.

Evolutionary Games and Social Landscapes
We revisit the formulation of Prisoner's Dilemma, an evolutionary game, for well-mixed populations of players. Populations with social landscapes have structure. Under some conditions (ratio of benefit to cost exceeding average number of connections per individual), this social structure supports the persistence of altruism. This is a reverse feature from the well-mixed scenario where all cooperators go extinct. Samples of social-network real datasets are used to illustrate with Monte Carlo simulations the outcome of repeated Prisoner's Dilemma.

Backward Bifurcation on an SEIRS Model with Vaccination
A compartmental model with vaccination is studied here. Bifurcation and sensitivity analyses are carried out. The role of the vaccination compartment and parameters is reflected in a backward bifurcation: the type of bifurcation that supports sub-critical equilibria and hysteresis.

Seasonality of Influenza Revisited
Influenza, a seasonal viral disease in countries with temperate climates, causes a significant morbidity and mortality burden on the population. Here we use 2009 A(H1N1) data that span a summer school holiday and more than two full seasons in the Northern Hemisphere, and winter and a school holiday in the Southern Hemisphere. We explore the underlying causes of seasonality of influenza. We estimate parameters of an age-structured deterministic model with seasonal transmission rate and reduction in social contact rates during periodic school closures.