Abstract

Drug resistance in infectious diseases is a significant global concern. Within this talk, we present two new mathematical models of drug resistance in infectious diseases.

We will present first the modeling process, in which we develop the mathematical models that describe the dynamics of vector-borne diseases with medical treatment, for both non-structured and structured populations.

In the theoretical part, we analyse two systems of differential equations. Specially for investigation of the integro-partial differential equations, we extend the method of characteristics and the idea of the Banach fixed point theorem.

In the numerical study, we present parameter estimation and simulation for the non-structured model, with a data set taken from Burkina Faso, Africa. For the structured population model, we propose a constructive algorithm and discuss potential data as well as open challenges.

For application, we need to consider different practical settings. With a good data set, the simulations can improve treatment control, especially for malaria. The models also suggest the necessity of experimental works to reach a more precise understanding.