

Modélisation mathématique et simulation de la dynamique spatiale de populations de campagnols dans l'est de la France

November 4, 2020

Abstract

In this talk, I present the different PDE models to describe the evolution of the density of the population of voles, which are particularly monitored in Eastern France for many years. The first model consists of a scalar PDE depending on time, age, and space supplemented with a non-local boundary condition. The flux is linear with a constant coefficient in the direction of age but contains a non-local term in the directions of space. Moreover, the equation contains a second order term in the spatial variables only. Existence and stability of weak entropy solutions for this model are demonstrated by using, respectively, the Panov's theorem of the multidimensional compensated and a doubling of the variables type argument. Next, inspired by a Multi Agent model proposed by Marilleau-Lang-Giraudoux, where the spatial dynamics of juveniles is decoupled from local evolution in each plot, a directed graph is introduced where its nodes are the plots. In each node, the evolution of the colony is described by a transport equation with two variables, time and age, and the movements of dispersion, in space, are represented by the passages from one node to the other. The numerical simulations of this approach reproduce the qualitative characteristics of the spatial dynamics observed in nature. Furthermore, concerning the interaction between voles and its predators, I introduce a predator-prey system consisting of a hyperbolic equation for predators and a parabolic-hyperbolic equation for preys, where the prey's equation is analogous to the first model of the vole populations. The drift term in the predators' equation depends nonlocally on the density of prey and the two equations are also coupled via classical source terms of Lotka-Volterra type. The proof of existence of entropy admissible solution is based on compensated compactness technique and Helly theorem. Uniqueness and stability are obtained by doubling of variables method.

In the last part, I will present the models describing the evolution and interaction of the salmonella pathogens in the gut of farm animals. An ODE model for the evolution of the pathogen concentration is constructed. In the case of a large population of the bacterium, a PDE model is considered. Existence and uniqueness of the solutions are obtained by using the theory of strongly continuous semigroups. The convergence to a stationary state and many numerical simulations are also studied.