Spatial Dynamics of Epidemic Models with Alle effect

Location: Laboratoire de Mathématiques Appliquées du Havre (LMAH), Université Le Havre Normandie.

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Summary: The last few years have been marked by upheavals in the global climatic and biological order, with an increase in extreme phenomena in 2022 (summer and winter heat, forest fires, etc.) in a context of emerging from the epidemic crisis. These changes have been accompanied by the appearance of several emerging pathogens of which the coronavirus responsible for COVID-19 is one of the most notorious in terms of its global impact, although others continue to cause concern (Zika, chikungunya, monkeypox...) or threaten to extend their endemic zone (dengue fever, malaria...). It therefore seems urgent to better understand the way in which these epidemics appear and spread. The object of mathematical epidemiology is precisely to develop tools to better understand the way in which pathogens spread in populations, in order to be subsequently applied in real situations.

As part of this thesis we will propose a new type of non-linear incidence which models an Allee effect on the infectious agent. The Allee effect (Allee 1938) corresponds to a positive relationship between the density of individuals and fitness, in other words to the fact that individuals reproduce more when the local density is important. This effect has been very little studied in the context of epidemic models, and makes it possible to take into account transmission modes in which the local density of infected contributes to increasing the probability of successful contamination, for example when the infected contaminate the external environment or when vectors accumulate pathogens during close contact. In this context, we can observe that the survival of the epidemic is conditional on the presence of a sufficient number of infected: if too few infected are present initially (below a critical threshold), the epidemic dies out without succeeding in invading the population.

We will study the spatial dynamics and the existence of traveling fronts for reaction-diffusion equations

$$\begin{cases} \partial_t S = d_S \Delta S + f(S) - \beta(I)\tau SI, & t > 0, x \in \mathbb{R}^n, \\ \partial_t I = d_I \Delta I + \beta(I)\tau SI - \gamma I, & t > 0, x \in \mathbb{R}^n, \\ S(t = 0, x) = S_0(x), I(t = 0, x) = I_0(x), & x \in \mathbb{R}^n, \end{cases} \tag{1}$$

where $f(S)$ describes the dynamics of the host population in the absence of pathogen (we will typically take $f(S) = \Lambda - \theta S$ or $f(S) = rS(1 - S)$ to describe non-trivial dynamics), $\beta(I)$ is the conditional probability of infection during a contact, $\tau > 0$ is the local contact rate between individuals, $d_S > 0$, $d_I > 0$ are the respective diffusion coefficients of susceptible and infected hosts, and $\gamma > 0$ is the exit rate of the infected.

Reaction-diffusion equations modeling the spread of pathogens in host populations have attracted much attention in recent years. Many studies describe in particular the spread of pathogens (Diekmann 1978; Hosono and Ilyas 1995; Ducrot and Magal 2009; Ducrot 2016; Griette and Raoul 2016; Ducrot 2021) for linear incidence rates or for non-linear rates having a property of systematic invasion from a certain threshold of susceptible hosts (i.e., invasion or non-invasion is only determined by the initial quantity of hosts susceptible and is independent of a positive quantity of infected). We propose a non-linear incidence rate model in which the invasion is non-systematic, i.e. when, even if the initial number of susceptible hosts is sufficient, an epidemic starting from too few of infected can go out. This dynamics is better fitted to represent the underlying natural phenomenon for which these extinctions are likely to occur (stochastic extinction). We will focus in particular on the threshold phenomena, the propagation dynamics and the existence of traveling waves for this model.

Profile of the candidate: The candidate must have a solid background in the analysis of partial differential equations (PDEs), dynamical systems, and a strong interest in applications in biology. Computer skills and in particular mastery of a programming language will be particularly appreciated.

To apply, contact Quentin Griette by email with a CV, short paragraph about your motivation and a recommendation letter.

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