

CMMA Monthly Seminar

第 27 回 CMMA 月例セミナー

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Pathogens are beings that depend on other organisms to live. The host organism usually tries to protect himself from the infection and the pathogen has to find suitable responses to survive. One way to avoid the elimination is to evolve rapidly and evade the countermeasures developed by the host. Many pathogens are known to exhibit a high level of variability, which can be achieved for instance by a high genomic instability leading to fast mutation rates (e.g. RNA viruses: influenza, rabies, measles, etc...). Such a genetic variability is often left aside in mathematical models trying to predict or analyse the spatial spread of diseases. My research precisely aims at better integrating this evolutionary phenomenon into mathematical methods in epidemiology.

First, we consider a simple model in which only two phenotypes can be reached through mutations. This leads to a system of two KPP-type reaction-diffusion equations, which are coupled by mutation and competition. This allows us to analyse the spatial dynamics of the epidemics. This is a mathematical challenge, because of the lack of a comparison principle in our context. Then, variations and generalisations of our models are also discussed.

"Mathematical models for the spread of evolving diseases"

日時：2018 年 7 月 20 日（金） 16:30-17:30

場所：明治大学 中野キャンパス高層棟 6 階 研究セミナー室 3

主催：

文部科学省 共同利用・共同研究拠点
明治大学先端数理科学インスティテュート
現象数理学研究拠点 (CMMA)



■連絡先

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