

THE UNIVERSITY



OF HONG KONG

*Institute of Mathematical Research
Department of Mathematics*

Special PDE Seminar

Aggregation-Diffusion Equations for Collective Behaviour in the Sciences

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Abstract

Many phenomena in the life sciences, ranging from the microscopic to macroscopic level, exhibit surprisingly similar structures. Behaviour at the microscopic level, including ion channel transport, chemotaxis, and angiogenesis, and behaviour at the macroscopic level, including herding of animal populations, motion of human crowds, and bacteria orientation, are both largely driven by long-range attractive forces, due to electrical, chemical or social interactions, and short-range repulsion, due to dissipation or finite size effects. Various modelling approaches at the agent-based level, from cellular automata to Brownian particles, have been used to describe these phenomena. An alternative way to pass from microscopic models to continuum descriptions requires the analysis of the mean-field limit, as the number of agents becomes large. All these approaches lead to a continuum kinematic equation for the evolution of the density of individuals known as the aggregation-diffusion equation. This equation models the evolution of the density of individuals of a population, that move driven by the balances of forces: on one hand, the diffusive term models diffusion of the population, where individuals escape high concentration of individuals, and on the other hand, the aggregation forces due to the drifts modelling attraction/repulsion at a distance. The aggregation-diffusion equation can also be understood as the steepest-descent curve (gradient flow) of free energies coming from statistical physics. Significant effort has been devoted to the subtle mechanism of balance between aggregation and diffusion.

In some extreme cases, the minimisation of the free energy leads to partial concentration of the mass. Aggregation-diffusion equations are present in a wealth of applications across science and engineering. Of particular relevance is mathematical biology, with an emphasis on cell population models. The aggregation terms, either in scalar or in system form, is often used to model the motion of cells as they concentrate or separate from a target or interact through chemical cues. The diffusion effects described above are consistent with population pressure effects, whereby groups of cells naturally spread away from areas of high concentration. This talk will give an overview of the state of the art in the understanding of aggregation-diffusion equations, and their applications in mathematical biology.

Date: October 2, 2024 (Wednesday)
Time: 3:30 – 4:30pm
Venue: KKL106, KK Leung Building, HKU

All are welcome