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Agent-based models: examples from bacterial aggregation and epidemic models

Agent-based models are widely used in numerous applications. They have an advantage of being easy to formulate and to implement on a computer. On the other hand, to get any mathematical insight (motivated by, but going beyond computer simulations) often requires looking at the continuum limit where the number of agents becomes large. In this talk I give two examples.

1. Consider the following model of bacterial motion. Bacteria moves at random, except that with some "switching rate", the bacteria will choose a random neighbour within its "sensing radius" and reorient itself towards it. For sufficiently large switching rate, aggregation patterns (clumps of bacteria) can form. Under reasonable assumptions, the continuum limit of this model results in a nonlinear fourth-order PDE. The resulting PDE gives further insights, including the clump profile and stability.
2. We present a simple model of disease spread that incorporates spatial variability in population density. Starting from first-principles ABM model, we derive a novel PDE with state-dependent diffusion. Consistent with observations, this model exhibit higher infection rates in the areas of higher population density. The model also exhibits an infection wave whose speed varies with population density. In addition, we demonstrate possibility of super-diffusive propagation of infection, whereby an infection can "jump" across areas of low population density towards the areas of high population density. Finally, a case study of coronavirus spread in Nova Scotia is presented with qualitatively similar features as our model, including density-dependent infection rates and infection that jumps across main population centers.