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Numerical analysis of the instability and aggregation in a kinetic transport equation with internal state

Collective motion of chemotactic bacteria, such as E. Coli, stems from, at individual level, continuous reorientations by runs and tumbles. It has been established that the length of run is decided by a stiff response to the external chemical cue via the intracellular signal transduction pathway. This study numerically investigates the self-organized aggregation of chemotactic bacteria based on a kinetic transport equation with internal state coupled with a reaction-diffusion equation of chemical cues. We put the focus on the effect of the adaptation time in the intracellular dynamics on the self-organized aggregation both at the macroscopic and microscopic levels. We found that the aggregation profile is highly affected by the adaptation time. Especially, we uncovered a non-monotonic behavior of the peak aggregation density with respect to the adaptation time. This indicates that there exists an optimal adaptation time to perform a strong aggregation behavior. Remarkably, this non-monotonic behavior is observed only at the kinetic level when the adaptation time is moderately large compared to the tumbling frequency, but cannot be described at the continuum level, i.e., the Keller-Segel model, which is obtained by the asymptotic analysis of the kinetic model. We also discover a plateau-like aggregation profile when the adaptation time is very large. We illustrate the formation of the plateau-type aggregation by a microscopic characterization.