Size-structured population models with coagulation and fragmentation

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Fragmentation-coagulation equations, combined with transport terms, have been used to describe a wide range of phenomena. Pure fragmentation, and the reverse coagulation, processes appear in many branches of natural sciences ranging from physics, through chemistry, engineering, biology, to ecology. In many cases, however, these two processes are complemented by events which change the total mass/size of the system. For instance, in solid drugs break-up in organisms or solvents external processes, such as dissolution, cause the exposed surface of particles to recede, resulting in the loss of mass of the system, and simultaneously widen the surface pores of the particle leading to their break-up. On the other hand, in biological applications, the fragmentation-coagulation models describe blood cell agglutination and separation, algae aggregation, evolution of prions, or animal grouping. However, the clusters of living organisms can grow due to natural birth processes, causing the total mass/size of the system to change.

In this talk we present a theory of such problems covering also the case of strong fragmentation. In particular we identify classes of problems admitting global in time classical solutions as well as situations in which the solutions blow up in a finite time.