CELLULAR PATTERN FORMATION

Abstract

by

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This thesis studies the formation and evolution of cellular patterns in foams and living organisms using the extended large-Q Potts model. Specific problems include grain growth, foam drainage, foam rheology, and patterning and cell sorting in the mound phase of the slime mode *Dictyostelium discoideum*.

In a wide range of cellular materials, surface-energy-driven diffusion leads to boundary motion which causes some grains to expend and others to shrink. Two-dimensional large-Q Potts model simulation of the evolution of a disordered cluster developed from a hexagonal grain array with a defect shows that abnormal grain growth can occur without strong anisotropy of surface energy. The grains at the boundary of the disordered cluster reach a special scaling state with no scale change.

In three-dimensional liquid foams, drainage occurs due to gravity. Large-Q Potts model simulations, extended to include gravity in three dimensions, agree with both experimental and analytical results for various kinds of foam drainage, and also predict new phenomena.

Foams exhibit a unique rheological transition from solid-like to fluid-like. Simulations using the large-Q Potts model, extended to apply shear to a two-dimensional foam, show three different types of hysteresis in foam's stress-strain relationship, which correspond to the elastic, viscoelastic and viscous fluid properties. This wide-ranging mechanical response depends on the structure and dynamics of local topo-

logical rearrangement of foam cells.

Biological tissues resemble foams and the large-Q Potts model can also simulate sorting in biological cell aggregates. In *Dictyostelium* mound, two types of cells are initially randomly distributed. In time, one cell type sorts to form a tip. Simulations show that both differential adhesion and chemotaxis are required for sorted tip formation. With only differential adhesion, no tip forms. With only chemotaxis, a tip forms containing both cell types. Thus simulations can provide a method to determine the processes necessary for biological patterning.