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From Condensed Matter Theory to Complex Biological Structures

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Condensed matter theory has given us many successful examples of the combination of analytic theory and numerical modeling in treating microscale and nanoscale physical phenomena. The methods of condensed-matter theory are increasingly being applied to biological problems. We will describe recent work modeling the growth of actin networks in biological cells. Actin, an abundant intracellular protein, polymerizes into semiflexible filaments which are important for many processes, including cell motion and shape changes. The growth of the filaments is regulated by intracellular proteins that can, for example, cap the growing ends of filaments, cause new branches to grow on existing filaments, or sever filaments. These activities generate a dynamic actin filament network at the cell edge. The filaments' growth can generate forces large enough to move the cell and change its shape. The talk will describe Brownian-dynamics simulations of the growth of single filaments against an obstacle, and stochastic-growth modeling of the growth of the actin network. The single-filament growth simulations show that even filaments attached to an obstacle can grow and push it forward, at rates comparable to free-filament growth rates. This result is consistent with experimental observations of filament-obstacle attachments. The network-growth simulations use a minimal stochastic growth model including capping, branching, and severing. Simulation studies of this model yield a network structure quite similar to that seen by electron microscopy. Surprisingly, the growth velocity of the network is almost independent of the opposing force. Analytic theory shows that this effect is due to the autocatalytic nature of the branching route to filament generation. Studies of the polymerization dynamics of this model reveal a "branching explosion" in which large clusters of branched filaments form at short times, but the filaments are nearly unbranched at long times.