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Modeling the competition between aggregation and diffusion of proteins on curved lipid bilayers[1] ARIJIT MAHAPATRA, DAVID SAINTILLAN, PADMINI RANGAMANI, University of California, San Diego — Membrane bending is an extensively studied problem from modeling and experimental perspectives because of the wide implications of curvature generation in cell biology. Many of the curvature generating aspects in membranes can be attributed to interactions between proteins and membranes. Recently we have shown that a high membrane curvature region prevents the diffusion of proteins creating an apparent aggregation effect. Here, we focus on the role of explicit aggregation of proteins on the surface of the membrane in the presence of membrane bending and diffusion. Aggregation of proteins on the membrane surface has been implicated in many biophysical phenomena and pathological states such as Alzheimer's disease. We develop a comprehensive framework that includes lipid flow, membrane bending energy, the entropy of proteins distribution, and an explicit aggregation potential. We first derive the governing equations and compare this framework to the Cahn-Hillard formalism to find the regimes in which the proteins form patterns on the membrane. We demonstrate the utility of this model using numerical simulations of various experimental scenarios to predict how aggregation and diffusion, coupled with curvature generation can alter the energy landscape of membrane-protein interactions.

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