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Effects of mobile membrane proteins on the structure and dynamics of lipid rafts JUN FAN, MARIA SAMMALKORPI, Mechanical and Aerospace Engineering, MIKKO HAATAJA, Mechanical and Aerospace Engineering, Princeton Institute for the Science and Technology of Materials, Program in Applied and Computational Mathematic — Compositional lipid domains (“lipid rafts”), which reside in the plasma membrane, are thought to facilitate many important cellular processes, including signal transduction and viral entry. Experimentally, raft dynamics have been probed mainly indirectly through observations of raft-associated membrane proteins, and the interpretation of the data relies heavily on assumptions about raft shape and viscosity. Previously, we have shown that strong interactions between rafts and immobile protein clusters may induce the formation of spatially extended raft aggregates [J. Fan et al., PRL 100, 178102 (2008)], thus complicating the interpretation of experimental data. In this work we correlate the dynamics of membrane proteins with the underlying time-dependent raft domain structure via a hybrid continuum-particle simulation scheme, and develop strategies for extracting quantitative information about raft dynamics from observations of the membrane proteins alone.

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