Abstract

# Stochastic Nucleation in Biology
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The binding of individual components to form composite structures is a ubiquitous phenomenon within the sciences. Within heterogeneous nucleation, clusters form around exogenous tructures such as impurities or boundaries, while in homogeneous nucleation identical particles cluster upon direct contact. Particle nucleation and growth have been extensively studied, often
assuming infinitely large numbers of monomers and unbounded cluster sizes. These ssumptions led to mass-action, mean field descriptions such as the well known Becker Doering equations. In cellular biology, however, nucleation events often take place in confined spaces, with a finite number of components, so that discrete and stochastic effects must be included. In this talk we examine finite sized homogeneous nucleation by considering a fully stochastic master equation, solved via Monte-Carlo simulations and via analytical insight. We find striking differences between the mean cluster sizes obtained from our discrete, stochastic treatment and those predicted by mean field treatments. We also consider heterogeneous nucleation stochastic treatments, first passage time results and possible applications to prion unfolding and clustering dynamics.