Abstract Submitted
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Chiral symmetry breaking in model bacterial suspensions: mechanism and system size dependence[1] ROBIN SELINGER, Kent State University, REBEKKA BREIER, Max Planck Institute for Dynamics and Self-Organization, Gottingen, Germany, GIOVANNI CICCOTTI, University of Rome "La Sapienza" and University College Dublin, STEPHAN HERMINGHAUS, MARCO MAZZA, Max Planck Institute for Dynamics and Self-Organization, Gottingen, Germany — We investigate the mechanism by which chiral structures spontaneously emerge in a model bacterial suspension with achiral interactions. Simulation studies demonstrate that the probability to nucleate a chiral velocity profile depends strongly on system size. To understand this dependence, we consider a classical 1-d rotor model with nearest-neighbor Lebwohl-Lasher interactions and periodic boundary conditions. In a dynamics simulation with a Langevin thermostat, we repeatedly quench the 1-d rotor model from high T to near T=0. In each trial we find either a metastable final state with one or more half twists, or else the untwisted ground state. We find that for a given quench rate, the mean square number of twists grows linearly with system size. For short chains, the untwisted ground state is the most probable outcome, but for chains beyond a threshold length, the most probable final state has exactly one half twist. We discuss the implications for understanding chiral symmetry breaking in bacterial suspensions.

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