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Using liquid crystal models to study DNA knotting in bacteriophages

Bacteriophages, viruses that propagate in bacteria, packed their genome in a protein container called capsid. Inside the capsid the viral genome is at a such high concentration and pressure that it is best described as a liquid crystal. This liquid crystal structure of DNA is characterized by ordered layers near the capsid and an isotropic phase at the center of the capsid.

Topological studies have shown that DNA extracted from P4 bacteriophages (P4 DNA) is knotted and the observed knots are very complex (i.e. high average crossing number). Interestingly, the distribution of knots of low average crossing number show an absence of the four crossing knot and a prevalence of the toroidal five crossing knot (5_1) over the twist crossing knot (5_2).

In this work we use cryo-electron microscopy to determine the layer organization of DNA in bacteriophage P4, and the continuum theory of liquid crystals to model its liquid crystal structure. The model shows that the experimentally observed structure is a minimizer of the proposed energy and that the experimental knot distribution can be reproduced by perturbing the minimizer. We therefore propose a new liquid crystal model based on cryoEM observations that is consistent with topological studies of P4 DNA.