

DNA knotting in spooling like conformations in bacteriophages

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A number of idealized models have been proposed to explain the long range organization of the DNA in bacteriophages. However, none of these models account for the distributions of complex knots found when examining DNA extracted from bacteriophage P4 capsids. Furthermore, these models do not consider possible chirality biases in the arrangement of the DNA molecule inside the capsid. In this talk, we address these two issues by proposing a randomized version of spooling models. We present analytical and numerical results for the properties of the random polygons (knots) generated using this model and relate them to our previous experimental results.