

SAMPLING LARGE RANDOM KNOTS IN A CONFINED SPACE

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Abstract

DNA knots formed under extreme conditions of condensation, as in bacteriophage P4, are difficult to analyze experimentally and theoretically. In this paper, we propose to use the uniform random polygon model as a supplementary method to the existing methods for generating random knots in confinement. The uniform random polygon model allows us to sample knots with large crossing numbers and also to generate large diagrammatically prime knot diagrams. We show numerically that uniform random polygons sample knots with large minimum crossing numbers and certain complicated knot invariants (as those observed experimentally). We do this in terms of the knot determinants or colorings. Our numerical results suggest that the average determinant of a uniform random polygon of n vertices grows faster than $O(e^{n^2})$. We also investigate the complexity of prime knot diagrams. We show rigorously that the probability that a randomly selected 2-D uniform random polygon of n vertices is almost diagrammatically prime goes to one as n goes to infinity. Furthermore, the average number of crossings in such a diagram is at the order of $O(n^2)$. Therefore, the 2-dimensional uniform random polygons offer an effective way in sampling large (prime) knots, which can be useful in various applications.

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