1098-74-159 **Robert S Manning*** (rmanning@haverford.edu), Department of Mathematics and Statistics, Haverford College, 370 Lancaster Ave., Haverford, PA 19041. *Monte Carlo simulations within a rigid base model of DNA with comparison to experimental measurements of persistence length and cyclization.* Preliminary report.

We present Monte Carlo simulations within a DNA model (developed by the laboratory of John Maddocks) that assumes the DNA bases are rigid with the two bases in a basepair allowed to move relative to each other. The parameters for shape and flexibility of a given DNA molecule depend on its sequence via parameters extracted by Maddocks and collaborators from a large ensemble of molecular dynamics simulations.

The Monte Carlo simulations allow us to extract estimates of the *persistence length*, a characteristic length-scale for bending often measured experimentally. Averaging over many random sequences, our model predicts a persistence length in good agreement with the generally accepted value for DNA. In addition, we compare our model's predictions for sequence-dependent persistence lengths to experiments designed to explore this same effect.

The Monte Carlo simulations also allow comparison to the *cyclization J-factor*, an experimental measurement related to the likelihood that a DNA molecule forms a loop. We show results for how our model's predicted $J$-factors depend on DNA length and on the specific basepair sequence for some sequences studied experimentally. (Received January 23, 2014)