Meeting: 1001, Evanston, Illinois, SS 15A, Special Session on Mathematical Problems in Robotics

1001-43-128 **Gregory S. Chirikjian*** (gregc@jhu.edu), Dept. of Mechanical Engineering, 3400 N. Charles St., Baltimore, MD 21218. *Mathematical and Computational Models in Robotics and Structural Biology.*

Many similar issues exist in the computational modeling of chain-like molecules and highly articulated robot arms. This talk reviews methods of noncommutative harmonic analysis developed by the speaker for computing the entropy of polymers and the propagation of error in robotic manipulators. It is shown how Fourier analysis on the group of rigid-body motions as well as minimization of functions on this group can be useful tools in these calculations, as well as in image registration and encoding of spherical motion.

In the second part of the talk, kinematic models of large biomolecules are discussed. In many biomolecular systems, function is related to structure through motion and conformational change. Methods for coarse-grained mechanics-based analysis of biological macromolecules is a reasonable approach to developing insights into the structural motions that are relevant to function. In this part of the presentation, motions of a number of large biological macromolecules that have been modeled by the presenter, his students, and collaborators are reviewed. These include the maturation of the HK97 virus, normal mode analysis of the GROEL/GROES, and theoretical models of DNA conformational statistics. (Received August 19, 2004)