1058-92-211 **Stephen D Levene*** (sdlevene@utdallas.edu), Departments of Molecular and Cell Biology, and Physics, University of Texas at Dallas, Richardson, TX 75080. *Mechanics and Energetics of DNA Loops in Complex Nucleoprotein Assemblies.*

Formation of DNA loops mediated by proteins bound at distant sites along a single molecule is an essential mechanistic aspect of many biological processes including gene regulation, DNA replication, and recombination. These processes are closely coupled to the topological state of DNA domains through supercoiling, knotting, and linking. Moreover, DNA looping is facilitated by an abundance of architectural proteins in cells such as HU, IHF, and HMGs, which bend the intervening DNA between cognate protein-binding sites. The complex interplay between DNA topology, expression of architectural DNA-bending proteins, and the regulation of DNA transactions remains poorly understood. We discuss numerical approaches for computing the free energies of DNA loop formation that account for intrinsic DNA properties such as bends or regions of altered flexibility, as well as global properties such as supercoiling. The objective of these approaches is to obtain the effective local concentration of loop ends, the generalization of the J factor in DNA cyclization, for topologically defined domains of complex nucleoprotein structures. Applications to lac-repressor-mediated gene regulation and the effects of architectural DNA-bending proteins on loop-mediated regulation will be discussed. (Received February 15, 2010)