1041-92-210 **Stephen D Levene*** (sdlevene@utdallas.edu), Departments of Molecular and Cell Biology, and Physics, 800 W. Campbell Road, Richardson, TX 75080, and **Andreas Hanke** (hanke@phys.utb.edu), Department of Physics and Astronomy, 80 Fort Brown, Brownsville, TX 78520. *DNA Looping in Topologically Constrained Domains.* Preliminary report.

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 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 describe an enhanced Monte Carlo model of superhelical DNA molecules that accounts for sequence-specific effects such as intrinsic bends or regions of altered flexibility, thereby significantly extending previous models of superhelical structure based on isotropic wormlike-chain behavior. This approach was used to compute the effective local concentration of loop ends, the generalization of the J factor in DNA cyclization, within topologically constrained domains. Applications to DNA site-specific recombination and the roles played by architectural DNA-bending proteins in recombination are discussed. (Received August 11, 2008)