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**Mary Therese Padberg\*** (padbergmt@gmail.com), **Isabel Darcy**, **Stephen Levene**, **Stefan Giovan** and **Rob Scharein**. *Determining Geometric Structures of Protein-Bound DNA using Modeling Software*. Preliminary report.

The complex relationship between proteins and DNA allows our cells to perform their various functions: gene expression, DNA replication, and regulation of cellular functions among them. In order for these processes to occur, proteins must first interact with DNA through a binding process. In this talk we focus on proteins that bind, cut, and religate (i.e. ‘reconnect’) DNA. When proteins bind to segments of DNA (creating protein-bound DNA) we assume the protein to be a ball and the DNA to be strings within the ball. Thus we can identify the protein-bound DNA as a mathematical tangle. This tangle type describes the topology of the DNA, whereas the geometry of the DNA is described by the spatial location of the DNA base pairs. Recent successes of laboratory experiments have allowed scientists to determine the tangle type of the protein-bound DNA. However, in many cases the limitations of available experiments have prevented us from determining a geometric structure for the protein-bound DNA segments whose topology is known. In this talk we will present new software, along with some preliminary results, that allows us to take a known topological structure of protein-bound DNA and find a potential geometric structure associated with it. (Received September 21, 2015)