1086-VD-329 **Mary Therese Padberg***, The University of Iowa, 14 MacLean Hall, Iowa City, IA 52242, and **Isabel Darcy**, **Stefan Giovan**, **Stephen Levene** and **Rob Scharein**. *The Twisted Tale of Protein-Bound DNA.* Preliminary report.

Knowing how DNA interacts with proteins is vital for understanding basic biological functions such as replication and transcription. Thus, discovering the shape that DNA conforms to when bound by proteins (protein-bound DNA) is an important topic. Geometric structures for some protein-bound DNA complexes can be found using laboratory techniques. For most complexes, however, these techniques often fail. When this happens we can experimentally determine the general shape of the complex, or its topology (e.g. a square and a circle represent the same topological object because you can deform one into the other without introducing any breaks). Since two things can be vastly different geometrically but have the same topology, we cannot rely on topology alone. In order to understand the structure of protein-bound DNA at a scientifically useful level we need to know its geometry. In this talk we discuss how to geometrically describe the structure of DNA. We introduce preliminary software which can be used to determine likely geometries consistent with known protein-bound DNA topologies. We will discuss the flexibility of this software to accept user modifications in order to model the complex under variable conditions. This talk is aimed toward a general audience. (Received August 21, 2012)