1108-92-78   **Isabel K. Darcy*** (`idarcymath@gmail.com`), MLH 14, Mathematics Department, University of Iowa, Iowa City, IA 52242. *Tangle analysis of protein-DNA complexes.*

Just like local knots can occur in long extension cords, such knots can also appear in DNA. DNA can be be either linear or circular. Some proteins will cut DNA and change the DNA configuration before resealing the DNA. Thus, if the DNA is circular, the DNA can become knotted. Protein-DNA complexes were first mathematically modeled using tangles in Ernst and Sumners seminal paper, Ä calculus for rational tangles: applications to DNA recombination" (Math Proc Camb Phil Soc, 1990). A tangle consists of arcs properly embedded in a ball. In order to model protein-bound DNA, the protein is modeled by the ball while the segments of DNA bound by the protein can be thought of as arcs embedded within the protein ball. This is a very simple model of protein-DNA binding, but from this simple model, much information can be gained. The main idea is that when modeling protein-DNA reactions, one would like to know how to draw the DNA. For example, are there any crossings trapped by the protein complex? How do the DNA strands exit the complex? Is there significant bending? Tangle analysis cannot determine the exact geometry of the protein-bound DNA, but it can determine the overall entanglement of this DNA, after which other techniques may be used to more precisely determine the geometry. (Received December 29, 2014)