TANGLE ANALYSIS OF MU TRANSPOSASE

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Abstract:

Proteins which bind DNA have been modeled using tangles. A tangle consists of arcs embedded in a 3-dimensional ball. A protein can be modeled as a 3-dimensional ball, and DNA segments bound by the protein can be thought of as arcs embedded in the 3-dimensional protein ball.

2-string tangles have been used to study proteins such as topoisomerases and recombinases which bind two segments of DNA, cut, change DNA conformation, and rejoin the DNA ends. These proteins will knot circular DNA. By analyzing the knotted and catenated products of recombinase experiments on circular DNA, tangle analysis can determine the topological conformation of DNA bound by these proteins.

In this talk, we will discuss how n-string tangle analysis can be applied to study any protein which stably binds n segments of DNA.