1105-57-144 **Annette Marie Honken*** (annette-honken@uiowa.edu), Department of Mathematics, University of Iowa, 14 Maclean Hall, Iowa City, IA 52242. *Mapping Distance One Neighborhoods within Knot Distance Graphs.* Preliminary report.

DNA can become knotted during biological processes such as recombination and replication. Type II topoisomerases are proteins tasked with keeping DNA unknotted. They act on double-stranded circular DNA by breaking the backbone of the DNA, allowing another segment of DNA to pass through, and re-sealing the break. Thus, a crossing change on a knot models the action of this protein on DNA. The distance between two knots, $K_1$ and $K_2$, is defined to be the minimum number of crossing changes required to obtain $K_1$ from $K_2$ or vice versa. Hence, to focus on the action of the type II topoisomerase on DNA, we look at knots of distance one.

We create a graph of this information by letting the set of vertices be knots and placing an edge between two vertices if the two knots represented by these vertices are of distance one. A neighborhood of a vertex, $v$, is the set of vertices with which $v$ is incident via an edge. Using graph theoretical and topological tools, we examine graphs of knot distances and define a mapping of distance one neighborhoods. How this relates to Dehn surgery on the double-branched cover of a knot will be briefly mentioned. (Received September 22, 2014)