

1099-92-201      **Isabel K Darcy\*** ([idarcymath@gmail.com](mailto:idarcymath@gmail.com)), 14 MLH, Mathematics Department, Iowa City, IA 52242, and **Annette Honken** ([annette-honken@uiowa.edu](mailto:annette-honken@uiowa.edu)), 14 MLH, Mathematics Department, Iowa City, IA 52242. *Topological Distances on DNA Knots and Links*.

Topoisomerases and recombinases are two classes of proteins which can knot circular DNA. Type II topoisomerases are proteins which cut one double-stranded DNA segment, allowing a second DNA segment to pass through before resealing the break. This is mathematically modeled by changing a crossing. Recombinases break two segments of DNA, exchanging the DNA ends before resealing the breaks. This action can be mathematically modeled by smoothing a crossing. Distances between knots have been defined based upon the minimum number of times these proteins must act to convert one knot into another knot. Methods for calculating these distances will be discussed. Applications and ways to visualize and analyze these distances via graphs and KnotPlot will be discussed. (Received February 08, 2014)