1058-92-281 **Mariel Vazquez*** (mariel@math.sfsu.edu), Mathematics Department, San Francisco State University, 1600 Holloway Avenue, San Francisco, CA 94132, and **Javier Arsuaga** (jarsuaga@math.sfsu.edu) and **Robert Scharein** (scharein@shaw.ca). *DNA unknotting, topoisomerases and bacteriophages.*

Type II topoisomerases simplify DNA knots and links efficiently by performing strand-passage on DNA strands. Experimental studies have shown that these enzymes simplify the topology of DNA very efficiently, however the key to this efficiency is yet to be revealed. Motivated by these experimental observations, we study random transitions of knotted polygonal chains of fixed length. We use Monte Carlo computer simulations and computational knot theory methods to model strand-passage, with and without topological biases. Unknotting patterns can assist knot identification. We propose to apply these methods in the study of the DNA knots extracted from bacteriophage P4 capsids. (Received February 16, 2010)