The traditional skein relation for the Alexander polynomial involves an oriented knot, $K_+$, with a distinguished positive crossing; a knot $K_-$, obtained by changing the distinguished positive crossing of $K_+$ to a negative crossing; and a link $K_0$, the orientation preserving resolution of the distinguished crossing. We refer to $(K_+, K_-, K_0)$ as the oriented skein triple.

Topoisomerases are proteins that break one segment of DNA allowing a DNA segment to pass through before resealing the break. Effectively, the action of these proteins can be modeled as $K_- \Leftrightarrow K_+$. Recombinases are proteins that cut two segments of DNA and recombine them in some manner. While recombinase local action varies, most are mathematically equivalent to a resolution, i.e. $K_\pm \Leftrightarrow K_0$. The oriented triple is now viewed as $K_- = \text{circular DNA substrate}$, $K_+ = \text{product of topoisomerase action}$, $K_0 = \text{product of recombinase action}$.

The theorem stated in this work gives a relationship between two 2-bridge knots, $K_+$ and $K_-$, that differ by a crossing change and a link, $K_0$ created from the oriented resolution of that crossing. We apply this to difference topology experiments using topoisomerase proteins to study SMC proteins. (Received September 04, 2012)