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Dorothy Buck* (d.buck@imperial.ac.uk), Dept of Mathematics, Imperial College London, London, SW7 2AZ, England, and **Ken Baker**. *The Classification of Rational Tangle Adjacencies, with Applications to Complex Nucleoprotein Assemblies.*

Many proteins cleave and ligate DNA molecules in precisely orchestrated ways. Modelling these reactions has often relied on the underlying DNA molecule being covalently closed, so these cut-and-seal mechanisms can be tracked by corresponding changes in the knot type of the DNA axis. However, in the (common) case when the DNA molecule is linear, or the enzyme action does not manifest itself as a change in knot type, or the knots types are not ‘standard’, these knot theoretic models are less germane.

Here we give a taxonomy of local DNA axis configurations. We endow this classification with a distance: that determines how many enzyme reactions of a particular type (corresponding to steps of a specified size) are needed to proceed from one local conformation to another. We discuss a variety of applications of this categorization, including type-II topoisomerase, site-specific recombinase, and transposase-mediated reactions. (Received September 15, 2010)