A Generalized Theory of DNA Looping and Cyclization DAVID
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University of Michigan — We have developed a semi-analytic method for calculating
the Stockmayer Jacobson J-factor for protein mediated DNA loops. The formation
of DNA loops on the order of a few persistence lengths is a key component in
many biological regulatory functions. The binding of LacI protein within the Lac
Operon of E.coli serves as the canonical example for loop regulated transcription.
We use a non-linear rod model to determine the equilibrium shape of the inter-
operator DNA loop under prescribed binding constraints while taking sequence-
dependent curvature and elasticity into account. Then we construct a Hamiltonian
that describes thermal fluctuations about the open and looped equilibrium states,
yielding the entropic and enthalpic costs of loop formation. Our work demonstrates
that even for short sequences of the order one persistence length, entropic terms
contribute substantially to the J factor. We also show that entropic considerations
are able to determine the most favorable binding topology. The J factor can be used
to compare the relative loop lifetimes of various DNA sequences, making it a useful
tool in sequence design. A corollary of this work is the computation of an effective
torsional persistence length, which demonstrates how torsion bending coupling in a
constrained geometry affects the conversion of writhe to twist.

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