

Codon Bias, DNA transcription forks, and Kink-Solitons

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The transcription of DNA into messenger RNA (and eventually into protein) involves the motion of the transcription fork – a short region in which the two strands separate – along the chromosome in a specified direction. This motion clearly has superficial similarity to the motion of solitons, localized nonlinear wave phenomena that behave like particles. In fact, Salerno has proposed a model in which the transcription fork takes the form of a kink-soliton of the discrete Sine-Gordon equation. An interesting aspect of this model is that the dynamics depend explicitly upon the DNA sequence. Prior research by Salerno and others has shown, for instance, that the sequences at the start of coding regions have the property that they will force a stationary soliton profile to begin traveling in the right direction.

Here we consider the question of the effect that the sequence will have on the continued motion of that soliton through the coding region. It is shown, through numerical solution of mathematical models, that the choice of codon for an amino acid or the presence of a non-coding intron can either allow or prevent the transcription fork from completing its task. This suggests the possibility of a previously unrecognized role for nonlinear dynamics in codon selection.

In this work in progress, we consider successively more complex and accurate mathematical models of DNA strands, to assess the robustness of the phenomenon seen in the simplest discrete Sine-Gordon models, and to determine how much detail the mathematical models must include in order to give scientifically relevant results.