1163-92-1375   **Brenton LeMesurier*** (`lemesurierb@cofc.edu`) and **Alexander Kasman** (`kasmana@cofc.edu`). *Mathematical modeling of DNA transcription bubbles.* Preliminary report.

In 1990, Englander et al proposed the sine-Gordon equation (sGE) as a basic mathematical model of the DNA transcription bubble. sGE is an integrable PDE having exact solutions in the form of kink solitons. However, the derivation of this continuous model relies on many dubious approximations and assumptions. In particular, it assumes uniformity of the bases along the DNA strands and symmetry of the two helices.

Numerous authors have proposed and studied refinements over the intervening decades. This talk describes some of those modeling efforts, with an emphasis on the effects of symmetry-breaking and the implications of the sequence-dependent dynamics. The good news is that some useful core aspects of the sine-Gordon approximation persist. It still has coherent kink solutions whose dynamics are of possible relevance to DNA transcription bubbles, and shows some interesting effects of codon non-uniformity. (Received September 15, 2020)