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"Double Bubble" and other trouble with DNA looping

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DNA looping is essential for such biological processes as regulation of gene expression and DNA packaging into nucleosomes. Classical theory of looping, based on the elastic description of DNA, was proposed more than two decades ago by Shimada and Yamakawa. However, a number of puzzles related to the problem remain largely unresolved to date. For instance, DNA loops in nature tend to be significantly shorter than the optimal once predicted theoretically, and the looping probability appears to be much larger. Even in vitro experiments conflict with each other and with the theory. In my talk, I will review a number of mechanisms which may be responsible for these discrepancies, and which add complexity to the overall problem. I will briefly discuss possible roles of bending-induced and protein-induced structural defects (such as kinks and bubbles), as well as effects of boundary constraints. I will then focus on two phenomena: the effect of sequence disorder, and the loop formation in a supercoiled DNA. The former results in the lack of self-averaging of looping probabilities. The supercoiling may explain the smaller optimal loop size observed in vivo.