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Role of boundary constrains in DNA looping problem. ALEXEI TKACHENKO, University of Michigan — We present a theoretical study of the effects of boundary constrains on DNA looping. The developed Effective Hamiltonian description enables one to calculate the looping probability density (so called J-factor), in a much simpler way than by traditional methods. Our approach is applicable to a variety of in-vitro and in-vivo problems, ranging from DNA cyclization, to protein-mediated DNA looping. In particular, it will be demonstrated that the existing controversy between various DNA cyclization experiments can be attributed to the variation in the boundary conditions.

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