Abstract Submitted
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Stochastic lattice simulation of competing nucleoproteins binding to single-stranded DNA[1] S.M. ALI TABEI, University of Northern Iowa — Homologous recombination (HR) is one of the most enigmatic processes in DNA metabolism and is a fundamental driver of evolution. Its central step involves the search for homology between two DNA molecules and the subsequent exchange of the DNA strands. We developed a dynamic Monte Carlo model to study the competition and dynamics of nucleoproteins binding/unbinding to single stranded DNA. In addition, we have developed a computational toolbox to identify and categorize different kinetic scenarios from single-molecule data.

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