

Abstract Submitted
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Backtracking and error correction in DNA transcription MARGARITIS VOLIOTIS, School of Computing and Department of Applied Mathematics, University of Leeds, NETTA COHEN, School of Computing, University of Leeds, CARMEN MOLINA-PARIS, Department of Applied Mathematics, University of Leeds, TANNIEMOLA LIVERPOOL, Department of Mathematics, University of Bristol — Genetic information is encoded in the nucleotide sequence of the DNA. This sequence contains the instruction code of the cell - determining protein structure and function, and hence cell function and fate. The viability and endurance of organisms crucially depend on the fidelity with which genetic information is transcribed/translated (during mRNA and protein production) and replicated (during DNA replication). However, thermodynamics introduces significant fluctuations which would incur massive error rates if efficient proofreading mechanisms were not in place. Here, we examine a putative mechanism for error correction during DNA transcription, which relies on backtracking of the RNA polymerase (RNAP). We develop an error correction model that incorporates RNAP translocation, backtracking pauses and mRNA cleavage. We calculate the error rate as a function of the relevant rates (translocation, cleavage, backtracking and polymerization) and show that its theoretical limit is equivalent to that accomplished by a multiple-step kinetic proofreading mechanism.

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