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Kinetic Modelling of Transcription Elongation DAIBHID O'MAOILEIDIGH, Rutgers University, VASISHT TADIGOTLA, Rutgers University, ANIRVAN SENGUPTA, Rutgers University, VITALY EPSHTEIN, New York University Medical Center, RICHARD EBRIGHT, Rutgers University, EVGENY NUDLER, New York University Medical Center, ANDREI RUCKENSTEIN, Rutgers University — Transcription is the first step in gene expression and it is at this stage that most of genetic regulation occurs. The enzyme RNA polymerase (RNAP) walks along DNA creating an RNA transcript at a highly non-uniform rate. We discuss how many non-intuitive features of the system may be experimentally and physically motivated and present first a model, which agrees qualitatively with a host of experimental evidence. We also examine intrinsic pauses where it is thought that the RNAP will move backwards along the DNA template without changing the length of the RNA transcript. We describe a simplified kinetic scheme for the recovery of intrinsic pauses with the same degree of predictive power as our thermodynamic model (presented separately). The separation of timescales between the movement of the RNAP and global changes in the RNA secondary structure is seen to be crucial for the function of RNAP. This is essentially a model of a Brownian ratchet where RNAP executes a 1D random walk in a sequence dependent potential over a range determined by the co-transcriptional RNA fold for each transcript length

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