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Messenger RNA sequence and the translation process –a particle transport perspective¹ JIAJIA DONG, BEATE SCHMITTMANN, ROYCE K.P. ZIA, Virginia Tech — The translation process in bacteria has been under intensive study. A key question concerns the quantitative effect of different elongation rates, associated with different codons, on the overall translation efficiency. Starting with a simple particle transport model, the totally asymmetric simple exclusion process (TASEP), we incorporate the essential components of the translation process: Ribosomes, cognate tRNA concentrations, and messenger RNA (mRNA) templates correspond to particles, hopping rates, and the underlying lattice, respectively. Using simulations and mean-field approximations to obtain the stationary currents (the protein production rates) associated with different mRNA sequences, we are especially interested in the effect of slow codons, i.e., codons which are associated with rare tRNAs and are therefore translated very slowly. As the first step, we look at a "designed sequence" with one and two slow codons and quantify the marked impact of their spatial distribution to the currents. Extending the results to several mRNA sequences taken from real genes, we argue that an *effective translation rate* including the information from the vicinity of each codon needs to be taken into consideration when seeking an efficient strategy to optimize the protein production.

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