TRAFFIC JAM GENERATES PHASE TRANSITION IN TRANSLATION

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The process by which proteins are made in the cell is called translation. In this process, huge molecular machines, called ribosomes, translate a sequence of nucleotides -a messenger RNA molecule- into a sequence of amino acids -a protein. This process can be modelled by particles in a lattice that hop from one site to the next with a certain probability. Each site of the lattice has associated a different hopping probability, since at each "site" of the mRNA molecule, the ribosome has to wait on average a different time interval to get the appropriate amino acid. Therefore, if one ribosome has to wait a long time at a certain site, a queue of ribosomes can form behind it, leading to a "traffic jam". In this talk, I will address how the configuration of slow sites influences the current of particles on the lattice, or equivalently, the current of ribosomes on the mRNA molecule. I will show that depending where the slow sites of the lattice are positioned, the current of particles can be subject to a first order phase transition. We analysed 500 mRNA sequences from yeast and found that we can classify them into two main groups, depending whether they experience a phase transition or not. Most importantly, these two groups of mRNA molecules translate into proteins with two very distinct biological functions. Therefore, our theory predicts a classification of mRNA sequences purely based on the dynamics of the ribosome tra□c, and this classification matches perfectly the biological function, providing thus the direct link between the phase transition and biological function. On the other hand, the advance of particles in many driven diffusion systems depends on the availability of resources in the surrounding environment. In the balance between supply and demand of such resources we are confronted with a regime in which, under limited resource availability, the flow is markedly reduced. In the context of mRNA translation this represents the finite availability of amino acid-tRNA molecules. In this limited resources regime a severe depletion of amino acid tRNAs is also observed. These dramatic effects are vital to our understanding of translation, and are likely to also be important for the many other applications of driven diffusion models.

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