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Modeling cell growth dynamics with a diffusion model of protein evolution KONSTANTIN ZELDOVICH, KELLY THAYER, UMass Medical School — Mesoscopic models of protein evolution, where mutations are represented as a diffusion process in protein stability space, gave important insight into the constraints on evolution imposed by protein thermodynamics in simple organisms such as bacteria or viruses. For example, the distribution of protein stablities and an absolute mutation rate limit directly follow from this model. Here, we propose a novel model, where the biomass growth rate of an individual cell is dependent on the stabilities of the cell's proteins, and the cell divides as soon as it reaches a critical biomass. Simulations of the model reveal that it reproduces all the features of the earlier models, including the mutation speed limit and the protein stability distribution, but adds a new dynamical dimension, a statistical description of the cell interdivision times which is extremely close to the experimental data. We analyze the dependence of the distribution of interdivision times on the mutation load and number of protein in the cell, and find that elevated mutation rates result in a broader distribution of interdivision times. Thus, we find that elevated mutation rates yield a disproportionately high fraction of very slow dividing cells, which may be a very important generic mechanism of non-adaptive resistance to mutagens.

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