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Ergodic protein dynamics underlie the universal shape of protein distribution in populations NAAMA BRENNER, EREZ BRAUN, Technion-Israel Institute of Technology, JAMES ROTELLA, HANNA SALMAN, University of Pittsburgh, NAAMA BRENNER COLLABORATION, EREZ COLLABORATION, JAMES ROTELLA AND HANNA SALMAN COLLABORATION — We have previously shown that protein fluctuations in cell populations exhibit a universal distribution shape under a broad range of biological realizations. Here we report new results based on continuous measurement in individual bacteria for over ~ 70 generations, which show that single-cell protein trajectories sample the available states with the same distribution shape as the population, i.e. protein fluctuations are ergodic. Analysis of temporal trajectories reveals that one effective random variable, sampled once each cell cycle, suffices to reconstruct the distribution from the trajectory. This in turn implies that cellular microscopic processes are strongly buffered and population-level protein distributions are insensitive to details of the intracellular dynamics. Probing them thus requires searching for novel universality-breaking experimental perturbations.

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