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Evolution of Mutation Rate in Asexual Populations SCOTT WYLIE, HERBERT LEVINE, Center for Theoretical Biological Physics, UCSD, DAVID KESSLER, Bar-Ilan University — Several evolution experiments with E. coli document the spontaneous emergence and eventual fixation of so called "mutator" alleles that increase the genomic mutation rate by the order of 100-fold. Variations in mutation rates are due to polymorphisms in the molecular machinery that copies and checks the genome for errors. These polymorphisms are coded in the genome and thus heritable. Like any heritable trait, elevated mutation rates are subject to natural selection and evolution. However, unlike other traits, mutation rate does not directly affect the rate at which an organism reproduces, i.e. its fitness. Rather, it affects the statistical distribution of the offspring's fitness. This fitness distribution, in turn, leads via "hitchhiking" to a change in the frequency of the mutator allele, i.e. evolution of the mutation rate itself. In our work we simulate a birth-death process that approximates simple asexual populations and we measure the fixation probability of rare mutators. We then develop an approximate analytic model of the population dynamics, the results of which agree reasonably well with simulation. In particular, we are able to analytically predict the "effective fitness" of mutators and the conditions under which they are expected to emerge.

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