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How Large Asexual Populations Adapt

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We often think of beneficial mutations as being rare, and of adaptation as a sequence of selected substitutions: a beneficial mutation occurs, spreads through a population in a selective sweep, then later another beneficial mutation occurs, and so on. This simple picture is the basis for much of our intuition about adaptive evolution, and underlies a number of practical techniques for analyzing sequence data. Yet many large and mostly asexual populations – including a wide variety of unicellular organisms and viruses – live in a very different world. In these populations, beneficial mutations are common, and frequently interfere or cooperate with one another as they all attempt to sweep simultaneously. This radically changes the way these populations adapt: rather than an orderly sequence of selective sweeps, evolution is a constant swarm of competing and interfering mutations. I will describe some aspects of these dynamics, including why large asexual populations cannot evolve very quickly and the character of the diversity they maintain. I will explain how this changes our expectations of sequence data, how sex can help a population adapt, and the potential role of “mutator” phenotypes with abnormally high mutation rates. Finally, I will discuss comparisons of these predictions with evolution experiments in laboratory yeast populations.