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Unveiling adaptation using high-resolution lineage tracking JAMIE BLUNDELL, SASHA LEVY, DANIEL FISHER, DMITRI PETROV, GAVIN SHERLOCK, Stanford University — Human diseases such as cancer and microbial infections are adaptive processes inside the human body with enormous population sizes: between $10^6 - 10^{12}$ cells. In spite of this our understanding of adaptation in large populations is limited. The key problem is the difficulty in identifying anything more than a handful of rare, large-effect beneficial mutations. The development and use of molecular barcodes allows us to uniquely tag hundreds of thousands of cells and enable us to track tens of thousands of adaptive mutations in large yeast populations. We use this system to test some of the key theories on which our understanding of adaptation in large populations is based. We (i) measure the fitness distribution in an evolving population at different times, (ii) identify when an appreciable fraction of clones in the population have at most a single adaptive mutation and isolate a large number of clones with independent single adaptive mutations, and (iii) use this clone collection to determine the distribution of fitness effects of single beneficial mutations.

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