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Abstract for an Invited Paper  
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### **Natural Selection in Large Populations**

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I will discuss theoretical and experimental approaches to the evolutionary dynamics and population genetics of natural selection in large populations. In these populations, many mutations are often present simultaneously, and because recombination is limited, selection cannot act on them all independently. Rather, it can only affect whole combinations of mutations linked together on the same chromosome. Methods common in theoretical population genetics have been of limited utility in analyzing this coupling between the fates of different mutations. In the past few years it has become increasingly clear that this is a crucial gap in our understanding, as sequence data has begun to show that selection appears to act pervasively on many linked sites in a wide range of populations, including viruses, microbes, *Drosophila*, and humans. I will describe approaches that combine analytical tools drawn from statistical physics and dynamical systems with traditional methods in theoretical population genetics to address this problem, and describe how experiments in budding yeast can help us directly observe these evolutionary dynamics.