

Experimental evolution studies provide powerful tools for analyzing populations adapting to a selection pressure. The availability of inexpensive genome sequencing has led to an increase in evolve-and-resequence experiments aimed at generating time series genomic data. The time-series genomic data provides a molecular view of evolution in action. However, existing statistical methods do not adequately model intrinsic characteristics of these datasets. In this paper, we present a novel method, CLEAR, to analyze time-series genomic data. CLEAR estimates population size as well as selection parameters to find the genomic regions responding to the selection pressure.