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### Convergence in viral populations

One of the most intriguing puzzles in biology is the degree to which evolution is repeatable. The repeatability of evolution or parallel evolution has been studied in a variety of model systems, including viruses. In viruses, due to their short genome and high mutation rates, convergent evolution leads to identical mutations that fix in independently evolving populations. We mainly study two viruses, HIV-1 and phage  $\phi$ X174. Our analyses are performed on sequences isolated from HIV-1 infected patients as well as evolution experiments where HIV-1 grows on T-cell lines and  $\phi$ X174 evolving in a naïve *E. coli* C culture. Our analyses demonstrate that convergent evolution allows the inference of selection pressures in independent populations. These selection pressures can already be inferred early on in the experiment by measuring viral sequence diversity. Sequence diversity in turn is highly predictive of which mutations fix later on in the experiment.