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Computational Approaches to Viral Evolution and Rational Vaccine Design

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Viral pandemics, including HIV, are a major health concern across the world. Experimental techniques available today have uncovered a great wealth of information about how these viruses infect, grow, and cause disease; as well as how our body attempts to defend itself against them. Nevertheless, due to the high variability and fast evolution of many of these viruses, the traditional method of developing vaccines by presenting a heuristically chosen strain to the body fails and an effective intervention strategy still eludes us. A large amount of carefully curated genomic data on a number of these viruses are now available, often annotated with disease and immunological context. The availability of parallel computers has now made it possible to carry out a systematic analysis of this data within an evolutionary framework. I will describe, as an example, how computations on such data has allowed us to understand the origins and diversification of HIV, the causative agent of AIDS. On the practical side, computations on the same data is now being used to inform choice or design of optimal vaccine strains.