

ALISON HILL

<http://www.people.fas.harvard.edu/~alhill/>

Using HIV sequence diversity to better understand the infection

The HIV virus evolves rapidly and high levels of diversity are seen within individual hosts and across the globe. This capacity for adaptation facilitates escape from immune responses and the evolution of drug resistance. Here I will discuss two examples of how we are using HIV sequence diversity to better understand the infection. Firstly, I'll discuss how we can map out HIV fitness landscapes using various sources of experimental data, and then use this to build in silico simulations of response to antiretroviral drugs. These models can help us understand what properties of therapy contribute to success and help us predict the outcome of new treatment strategies. Secondly, I'll discuss how we are using viral genetic diversity to understand how latent virus persists in infected cells despite decades of therapy. Our results suggest that the dynamic nature of this persistence is a potential avenue for new potentially curative therapies.