Human immunodeficiency virus (HIV) evolves rapidly within infected individuals, accumulating mutations that allow the virus to escape targeting by the host immune system and thereby preventing effective immune control of infection. In this talk I will show how we can use techniques from statistical physics to infer information about the fitness landscapes of HIV proteins from sequence data, providing insight into HIV evolution and mutational escape from immune control. I will discuss experimental tests of these proposed fitness landscapes and applications of this technique in understanding intra-host viral evolution. Additionally, I will show some analogies between sets of collectively coupled mutations in HIV and Hopfield neural networks.