

Project Summary

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Globally, the human immunodeficiency virus (HIV) is extraordinarily variable and this amazing diversity poses a major obstacle to AIDS vaccine development. Moreover this diversity (strains belonging to the same subtype can differ by up to 20%) is continually growing. Although the scale of the HIV pandemic makes action imperative, there is still much to learn about this virus and many questions about it still need to be answered before an effective vaccine strain can be developed.

One of these questions is: How many viruses are initially transmitted when there is contact between an infected organism and a healthy one? The motivation for this question is that, if we know the number of viruses that infect an organism and can retrace their DNA sequences, we will then be able to overcome some of the diversity present between the children of these viruses and can thus develop powerful weapons against them. One of the difficulties that arise when one is trying to answer this question is that, when replicating, the HIV virus can be subject to a number of different mutations, some of which can substantially change the DNA sequence of the virus. And thus, when given a DNA sequence it is hard to know whether it is a result of recombination between two viruses, a new virus or maybe, a series of convergences.

I am working with Tanmoy Bhattacharya and Bette Korber on trying to detect recombination using statistical methods and data collected from infected patients that show us the DNA sequences of the viruses present in the organism at a given time (approximately one month after the infection occurred).