

Modeling early evolution of human immunodeficiency virus

Kelly Hennessey, St. Olaf College, Northfield, MN, USA and NIMBioS: National Institute for Mathematical and Biological Synthesis, Knoxville, TN, USA

Vedaste Mutambuka, University of Arkansas, Little Rock, AR and NIMBioS, Knoxville, TN, USA

Anthony Rhoads, McKendree University, Lebanon, IL and NIMBioS, Knoxville, TN, USA

Vitaly Ganusov, Department of Microbiology, University of Tennessee and NIMBioS, Knoxville, TN, USA

Calistus Ngonghala, NIMBioS, Knoxville, TN, USA

HIV establishes a life-long chronic infection in vast majority of infected individuals despite strong antiviral responses elicited by the host. High mutation rate of HIV is thought to be one explanation for the ability of the virus to avoid host's immune response yet whether the observed rates of mutation are sufficient to explain rapid appearance of viral variants escaping recognition by T cell immunity is unclear. During this project we will formulate models of HIV evolution and investigate the role of mutation and recombination in early diversification of HIV in patients.

**This is an Undergraduate Poster