

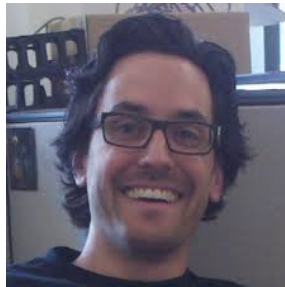


181 Longwood Avenue
Boston, Massachusetts 02115-5804

Department of Medicine
Channing Division of Network Medicine

Channing Network Science Seminar

October 31, 2014, 3pm @ 5th-floor Conference Room



Speaker: Daniel Larremore, Ph.D
Harvard School of Public Health
Center for Communicable Disease Dynamics
Dept. of Epidemiology

Title: A complex networks approach to understanding genetic recombination in malaria antigens

Abstract: Malaria parasites evade the human immune system by sequentially expressing diverse proteins on the surface of infected red blood cells. The diversity of these camouflage proteins comes from rapid genetic recombination that shuffles the genes that encode the proteins. Unfortunately, this shuffling precludes the use of traditional sequence analysis techniques, such as multiple alignments, and phylogenetic trees. We therefore take a new approach by mapping sequences to a complex network in which each vertex represents a single sequence and constraints on recombination reveal themselves in the community structure of the network. We validate this map and the networks it produces on synthetic sequences, before applying it to multiple different locations in the malaria immune evasion genes. We find that different pieces of the immune evasion proteins are under different types of evolutionary selection, with implications for theoreticians and clinicians alike. We then apply these techniques to a large set of sequences from both human- and ape-infecting malaria parasites, revealing that the observed genetic states of 6 distinct malaria species have arisen from a common set of initial sequence content dating back prior to the most recent common ancestor of the entire ape-infecting Plasmodium subgenus.

hosted by: Yang-Yu Liu