**Inference of HIV-1 Transmission Clusters: from phylogenetic clusters to contact network**

Increase of human immunodeficiency virus (HIV) epidemics among men who have sex with men (MSM) is a growing concern in the era of highly active antiretroviral therapy (HAART). Transmission clusters play a crucial role in fueling HIV-1 epidemics and understanding clusters is necessary prior to planning a health intervention to curb the spread of HIV in this group. The availability of HIV genotyping data has made the use of phylogenetic clustering common. Phylogenetic models aim to estimate the ancestral relationships between DNA sequences. In doing so, they help in the detection of HIV transmission clusters, but what phylogenies can reveal about the contact network underlying an HIV epidemic is still unclear. The present work investigates the link between phylogenetic clusters and sexual contact networks. Specifically, we compared standard distance-based hierarchical clustering algorithms with maximum likelihood-based computationally intensive methods, based on a sample of HIV DNA sequences from 1224 men from the MSM population in Montreal, Quebec, Canada. We noted a very close correspondence between clusters resulting from each approach, suggesting that transmission clusters could rely on simple clustering algorithms.

We also simulated contact network structures and HIV transmission over these networks. We obtained simulated DNA samples and partitioned them with a distance-based clustering algorithm. Returned clusters were projected back onto the network graph and we evaluate properties of these sub-networks, leading to the conclusion that estimated phylogenetic clusters do not map uniformly on the contact network graph.