

COBRE/DEPT. OF TROPICAL MEDICINE SEMINAR

RNA Virus Evolution: Tracing Quasi-Species of HIV-1 and Predicting Influenza Viruses

One of the hallmarks of many RNA viruses is their rapid evolution which enables them to evade host immune responses. Continuous immune escape facilitates chronic infection by HIV-1, while antigenic drift allows seasonal influenza viruses to repeatedly infect the same host. We have sequenced the changing HIV-1 population in about 10 serial samples in 11 patients and achieve a sequencing depths of >1000 covering the entire genome. Using this data set, we quantify how HIV-1 explores sequence space and evades immune responses. Similarly, influenza A/H3N2 changes its antigenic properties every few years and the seasonal influenza vaccine needs frequent updating. I will present a computational approach to anticipate the strains dominating future seasons.

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