Quantifying factors influencing influenza virus evolution

University of Cambridge supervisor: Dr Colin Russell, Cambridge Infectious Diseases (CID) (car44@cam.ac.uk)

A*STAR Singapore supervisor: Dr Sebastian Maurer-Stroh, Bioinformatics Institute (sebastianms@bii.a-star.edu.sg)

Influenza viruses are a serious public health threat through seasonal epidemics and occasional pandemics and a cause of major economic burden. Global surveillance and research efforts are in place to collect and analyze samples and several thousand new influenza genome sequences are added to the databases every year. Together with the already existing pool of data this represents a valuable collection to study various aspects of virus evolution. Classical and advanced phylogenetics methods provide us with the relationships among the viruses and their origins and together with studies on antigenic changes we can get a broad view of the evolutionary dynamics of the virus (Barr et al., 2010; Russell et al., 2008). The fitness of a strain and risk to spread depends on many factors which include host-dependent adaptation mutations for receptor interactions (Maurer-Stroh et al., 2014; Russell et al., 2012), replication efficiency (Fonville et al., 2013) and viral fusion (Maurer-Stroh et al., 2010). Taken together one can identify the factors influencing influenza virus evolution but quantifying and predicting them using computational methods remains a grand but interesting challenge (Russell et al., 2014) which will be attempted during this project using computational and partially experimental approaches.

Both Cambridge and Singapore supervisors have already worked and published together in the field (Russell et al., 2014) and their expertise is highly complementary which makes this project very well suited for this scheme.


