Applications of Bioinformatics and Systems Biology to Study Infectious Diseases

廖玉潔
國家衛生研究院群體健康科學研究所

Abstract

Infectious diseases are caused by infective agents including bacteria, fungi and viruses, resulting in worldwide infectious epidemics. To prevent or slow down the transmission of infectious diseases, researchers have been devoted to study the evolutions and metabolic functions of infectious pathogens based on the genomic and phenotypic information. Since influenza viruses cause substantial medical and social burdens, we aim to conduct bioinformatics approaches to influenza surveillance. We have developed bioinformatics models for predicting antigenic variants of influenza A/H3N2 virus, and provided an analytical tool for influenza virus surveillance. Besides, we found the contrasting substitution patterns between HA proteins of avian and human influenza viruses, implication for monitoring human influenza epidemics. In addition to study influenza viruses, we aim to study the metabolic network for Klebsiella pneumoniae by using a systems biology approach. We have reconstructed a genome-scale metabolic network for Kp. MGH 78578. With the metabolic network reconstruction, we can perform in silico knockout simulations for identifying potential drug targets.