

Complex Networks and Agent-Based Models of HIV Epidemic
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Understanding the dynamics of infectious disease is important in epidemiology in order to understand and prevent the progression and spreading of infectious diseases. For many viral infections social interactions as well as genetic diversity of the transmitted viral agent among individuals dictate the dynamics of infectious disease spreading in a population. Therefore, the infection transmission can be investigated at different spatio-temporal scales, from molecular to epidemiological levels.

One particular example is the human immunodeficiency virus (HIV) infection that causes the acute immunodeficiency syndrome (AIDS). HIV infection and AIDS have so far caused the death of millions of people worldwide and have turned out to one of the most severe infectious diseases of our time. Regarding HIV epidemic a wide range of data has been gathered, from genome sequencing and blood samples to social interactions and sexual contacts of infected individuals. Based on these data, many models have been developed to investigate the complexity of HIV dynamics, immune response and drug therapy.

In this thesis, we look into HIV-1 data present at different scales (from molecular and cellular to epidemiological scales). We build data-driven models and perform network analysis in order to understand the dynamics of HIV at different scales. At cellular scale, we propose a computational model of HIV intracellular replication where infected cells undergo a single cycle of virus replication. A novel method is also introduced to reconstruct HIV transmission networks based on patient's genetic, demographic and clinical data. The method is based on real patients data and considers epidemiological factors as well as viral genome data for network construction. We argue that combining data from different scales is required for a more realistic description of complex systems behavior such as transmission of infectious disease and HIV epidemic.