Influenza epidemics occur when novel strains emerge without warning, whereas HIV epidemics are now chronic and well established in populations. In this talk, I will focus on the temporal dynamics of influenza and geospatial patterns of HIV epidemics. For influenza, I will present a multi-strain/multi-host model that I have developed to track the spread of inter-species strains among birds, pigs and humans. I will show how this model explains the dynamics of emerging super-strains of influenza. These new strains emerge when genetic recombination occurs between avian and human strains in co-infected pigs; therefore, pigs act as “mixing vessels”. My analysis will show how specific subtypes (e.g., H1N1) can cause an epidemic then virtually disappear for decades before reemerging. For HIV, I will discuss the epidemic in Lesotho, a small sub-Saharan African nation with one of the world’s most severe epidemics. In this country, it is estimated that approximately one in four adults are infected. Notably, the majority of infected individuals in this country have not been diagnosed (i.e., the epidemic is mainly “hidden”). Currently, individuals need to be tested to be diagnosed. However, I have determined, by using geospatial analysis of GPS data, the number and geographic location of all HIV infected individuals. I will then show how I have used my results to determine geographic targeting strategies that optimize treatment programs.