Traditional epidemiological models consist of compartmentalizing hosts into susceptible, exposed, infected, recovered (SEIR), and variations of this paradigm (e.g. SIR, SIR/SI, etc.). These models are challenged when the within-host dynamics of disease is taken into account with aspects such as: (i) Simultaneous Infection: Simultaneous presence of several distinct pathogen genomes, from the same or multiple species, thus causing individual to belong to multiple compartments simultaneously. (ii) Antigenic diversity and variation: Antigenic variation, defined as the ability of a pathogen to change antigens presented to the immune system during an infection, and antigenic diversity, defined as antigenic differences between pathogens in a population, are central to the pathogen’s ability to 1) infect previously exposed hosts, and 2) maintain a long-term infection in the face of the immune response. Immune evasion facilitated by this variability is a critical factor in the dynamics of pathogen growth, and therefore, transmission. This talk explores an alternate mechanistic formulation of epidemiological dynamics based upon studying the influence of within-host dynamics in environmental transmission. A basic propagation number is calculated that could guide public health policy. (Received September 26, 2013)