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Cameron J Browne* (cameron.j.browne@vanderbilt.edu). *Within-host virus models with cell infection-age structure.*

Modeling of viruses, such as HIV, has been an extensive area of research over the past two decades. In order to describe the heterogeneities of the infected cell lifecycle, the standard ODE within-host virus model can be generalized by incorporating first order hyperbolic PDEs representative of infected cells stratified by infection-age. In this talk, I will discuss recent results in the analysis of these within-host virus models with cell infection-age structure. First, I consider the model with multiple virus strains. For each viral strain, a quantity called the reproduction number is defined. The main result is that the single-strain equilibrium corresponding to the virus strain with maximal reproduction number is a global attractor, i.e. competitive exclusion occurs. As an application of the model, HIV evolution is considered and simulations are conducted. In particular, we consider the effect of CTL (Cytotoxic T Lymphocyte) immune response acting at different times in the infected-cell lifecycle based on recent studies demonstrating superior viral clearance efficacy of certain CTL clones that recognize infected cells early in their lifecycle. Interestingly, explicit inclusion of early recognition CTLs can cause oscillatory dynamics. (Received January 30, 2015)