

Unraveling within-host signatures of dengue infection at the population level

Ryan Nikin-Beers¹ Julie Blackwood² Lauren Childs³ Stanca Ciupe³

¹ *University of Florida, Gainesville, FL, US, 32611* rnikinbeers@ufl.edu

² *Williams College, 880 Main St, Williamstown, MA, US, 01267*

³ *Virginia Polytechnic Institute and State University, Blacksburg, VA, US 24061*

Dengue virus causes worldwide concern with nearly 100 million infected cases reported annually. The within-host dynamics differ between primary and secondary infections, where secondary infections with a different virus serotype typically produce higher viral loads and induce more severe disease. We build upon the variable within-host virus dynamics during infections resulting in mild dengue fever and severe dengue hemorrhagic fever. We couple these within-host virus dynamics to a population-level model through a system of partial differential equations. The resulting multiscale model examines the dynamics of between-host infections in the presence of two circulating virus strains that involves feedback from the within-host and between-host interactions. We analytically determine the relationship between the model parameters and the characteristics of the model's solutions, and find an analytical threshold under which infections persist in the population. Furthermore, we develop and implement a full numerical scheme for our model, allowing the simulation of population dynamics under variable parameter conditions.