

WITHIN-HOST MODELS UNRAVELLING THE DYNAMICS OF DENGUE REINFECTIONS

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Caused by four serotypes, dengue fever is a major public health concern worldwide. Current modeling efforts have mostly focused on primary and heterologous secondary infections, assuming that lifelong immunity prevents reinfections by the same serotype. However, recent findings challenge this assumption, prompting a reevaluation of dengue immunity dynamics.

In this study, we develop a within-host modeling framework to explore different scenarios of dengue infections. Unlike previous studies, we go beyond a deterministic framework, considering individual immunological variability. Both deterministic and stochastic models are calibrated using empirical data on viral load and antibodies immunoglobulin M and immunoglobulin G (IgM and IgG) concentrations for all dengue serotypes, incorporating confidence intervals derived from stochastic realizations.

With good agreement between the mean of the stochastic realizations and the mean-field solution for each model, our approach not only successfully captures primary and heterologous secondary infection dynamics facilitated by antibody-dependent enhancement (ADE) but also provides, for the first time, insights into homotypic reinfection dynamics. Our study discusses the relevance of homotypic reinfections in dengue transmission at the population level, highlighting potential implications for disease prevention and control strategies.

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