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Multi-scale models of infectious disease dynamics and validating with data

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The bidirectional feedback induced through population and individual-level infectious disease and host immune dynamics requires development of innovative multi-scale models. In this talk, I will introduce structured nonlinear partial differential equation models linking immunology and epidemiology, along with novel stability analysis and computational tools for simulating ODE-PDE hybrid systems to understand the nonlinear dynamics and apply them to biological data. Applying the modeling framework to dengue virus, we first demonstrate how intermediate levels of antibodies enhance infection severity within a host, and scale up to population wide antibody level distributions evolving through multiple infections by distinct strains and waning immunity. Then, to test the theoretical results, we fit primary and secondary dengue infection data to provide evidence of antibody dependent enhancement. These results have critical implications for optimal vaccination policy, and the modeling framework is currently being applied to examine the emergence of COVID-19 variants.

References

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