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Heterogeneous responses to viral infection: Insights from mathematical modeling of yellow fever vaccine

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Abstract

Most of our knowledge of within host disease dynamics and immune response comes from studies performed in mice or other laboratory animals. These biological models have some natural advantages: genetic similarity, identical medical history and synchronized time of infection. Removing confounding variables has helped reveal many of the important processes underlying infection and immunity. However, studies in inbred mice can also be limiting precisely because they lack diversity. Many mathematical models, making very different assumptions about the underlying biology can be fit to the same data. Although these models make similar predictions about for a single individual, they may make quite different predictions about the difference that appear in population of individuals. Therefore, we will likely benefit from fitting these models to human data, and not just because of the increased clinical relevance. The yellow fever vaccine establishes a short term infection in patients and thus represents an ethical way to study viral dynamics and immune response in humans. We find that we cannot distinguish between different models when we fit to the mean data alone, but only when we consider the differences between patients.