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Probabilistic modeling of antibody kinetics post infection and vaccination

Rayanne A. Luke^{1,2}, Prajakta Bedekar^{2,3}, Anthony Kearsley²

¹Department of Mathematical Sciences,
George Mason University, USA
rluke@gmu.edu

²Applied and Computational Mathematics Division,
National Institute of Standards and Technology, USA
anthony.kearsley@nist.gov

³Department of Applied Mathematics and Statistics,
Johns Hopkins University, USA
pbedeka1@jh.edu

Modeling the deterioration of antibody levels is essential to understanding the time-dependent response to infections or vaccinations. Important questions remain despite significant experimental studies. The influence of the order of events and time elapsed between infection and vaccination on the kinetics of “hybrid immunity” is not well understood. Moreover, disease or vaccination prevalence in the population and time-dependence on a personal scale simultaneously influence the immune response.

A rigorous mathematical characterization may inform public health decision making. Thus, we design a time-inhomogeneous Markov chain model for event-to-event transitions coupled with a probabilistic framework for post-event antibody kinetics. This approach is ideal to model sequences of infections and vaccinations, or personal trajectories in a population, and predict missed events. Further, this framework extends beyond the capability of a susceptible-infected-recovered (SIR) characterization, which models disease transmission but cannot track the distribution of antibody response of a population across time. In contrast, we provide such probabilistic information.

We present ideas from our recent work [1] and a promising extension that allows multiple immune events. To illustrate, we apply our mathematical machinery to longitudinal severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) data from individuals reporting infection and vaccination events. Our work is an important step towards a comprehensive understanding of antibody kinetics that could lead to an effective way to analyze the protective power of natural immunity or vaccination and provide booster timing recommendations.

Keywords: antibody testing, diagnostics, Markov chain models, time-dependence

References

- [1] P. Bedekar, R. A. Luke, A. J. Kearsley, Prevalence Estimation Methods for Time-Dependent Antibody Kinetics of Infected and Vaccinated Individuals: A Markov Chain Approach, *Bulletin of Mathematical Biology*, 87:26, 2025.