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THE ITERATIVE PROCESS OF QUANTITATIVE MODELING OF INFECTION DYNAMICS IN RENAL TRANSPLANT RECIPIENTS

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Mathematical models play a significant role in providing a numerical and analytical perspective to biological models. When formulating these mathematical models to improve our understanding of biological processes, it is not always possible to find all parameter values in literature. In such cases, and in the presence of data, inverse problems are performed to estimate these unknown parameters. Statistical error models used during inverse problem formulations help quantify the uncertainty and variability that arises with using experimental data. This process of applying mathematical and statistical techniques for modeling physical processes is an iterative one that often leads to new insights following every new iteration. There is a relatively

recent research effort in modeling the mechanisms of solid organ transplants, specifically kidney transplants. We present mathematical and statistical models to illustrate the iterative process of modeling for renal transplant recipients infected by BK virus. Using a second order difference-based method to eliminate statistical error model misspecification, we show how modified residuals from the inverse problem can be used to detect discrepancies in mathematical model formulation. Moreover, we illustrate the iterative process of modeling biological processes by improving the current mathematical model to be more biologically accurate.

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