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Personalized virus-load curves for acute viral infections

We introduce an explicit function that describes virus-load curves on a patient-specific level. This function is based on simple and intuitive model parameters. We validate our model on data from mice influenza A, human rhinovirus data, human influenza A data, and monkey and human SARS-CoV-2 data. We find wide distributions for the model parameters, reflecting large variability in the disease outcomes between individuals. Further, we compare the virus load function to the commonly used ODE model of Baccam, Smith and others. Our explicit formula gives an alternative way to estimate exponential growth and decay rates. The virus-load function offers a new way to analyse patient specific virus load data. (joint work with C. Contreras and J. Newby)