

A Simple Model for Human Immunodeficiency Virus Based on Erlang's Method of Stages

Samuel Swanson

Abstract

The purpose of this talk is to select a model for HIV that uses few parameters while fitting the worldwide prevalence and death data. We consider a set of models based on Erlang's method of stages, including some with and some without social distancing. The use of stages is supported by biological studies which suggest that HIV passes through stages in each individual. To perform model selection, we compute R_0 and use it to estimate initial values of the parameters in this model. We run thousands of iterations of a Nelder-Mead simplex search algorithm to determine the optimal values of parameters for each model and the error associated with each model in order to select the most likely model. We then perform identifiability analysis and determine that the "true values" of the parameters for this model are uniquely determinable based on the data points.