

Mathematical Models of Viral Infections

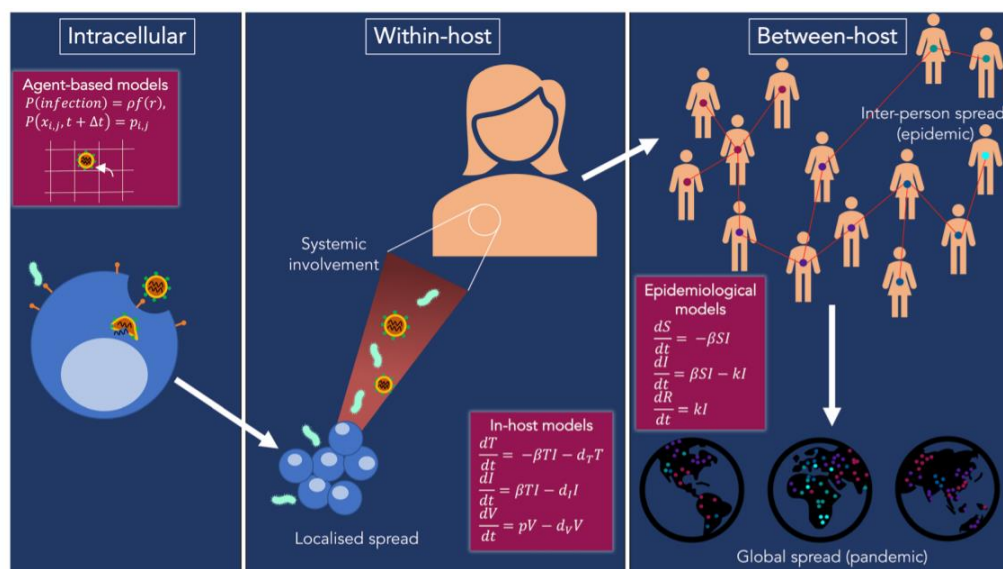
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Mathematical models are powerful tools in the study of several viral infections, such as Hepatitis viruses (HBV and HCV), SARS, and HIV. These models can be categorized into two main classes according to the studied aspect of the infection. The first concentrates on the epidemiological aspect of the infection. A population where the infection has spread is divided into groups according to their infection status (i.e.: susceptible individuals, exposed individuals, recovered individuals, protective individuals or vaccinated individuals). The dynamics of the infection among them is analyzed based on the epidemic's characteristics. Usually, this class of models is used to study viral infections regionally, which helps researchers to understand the spread rates of these infections and gives a sight for decision makers.

The second class of models concentrates on the cellular level of the infection. In these models, the state variables are the host cells (healthy cells and infected cells), the viral particles, the immune system and the treatments. Through simulating several infection cases using the mathematical models, researchers develop a better understanding of the cellular processes of the viral infection. These simulations give them the chance to study cases that are difficult to test in labs due to the high cost or the ethical constrains of *in vivo* tests.

Here in KCST, we plan to work on projects where engineering techniques are utilized to provide efficient control strategies to treat viral infections. These control mechanisms propose a customized treatment plans based on patients' measurements and give an estimation of the required treatment efficacy for each case.



Jenner, A. L., Aogo, R. A., Davis, C. L., Smith, A. M., & Craig, M. (2020). Leveraging Computational Modeling to Understand Infectious Diseases. *Current Pathobiology Reports*, 1-13.