Systems Biology

Project Proposal

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Topic: Mathematical Modelling of within-host viral dynamics of SARS-CoV-2 in humans. Implications for Immune response and Antiviral treatments.

A class of mathematical models that focus on the intra-host dynamics of the spread of infectious agents have been studied extensively in the context of HIV-AIDS and influenza, among others. These models, often using a set of coupled ordinary differential equations (ODEs), describe how the virus or the infective agent spreads within the host and the mechanisms within the host to resolve such infections. One of the key parameters tracked by such models is the viral load in the body of the patient. Mathematical models that track the viral kinetics in CoVID-19 patients have also been built recently. However, very few models exist so far that incorporate the interactions of the virally infected cells with different types of immune responses in the body. Such attempts can be powerful for understanding how the different clinical phenotypes appear as manifestations of underlying immune cell interactions with the infected cells.

Among different model structures to represent viral dynamics, the **target cell limited model** has served to represent several diseases such as HIV, Hepatitis, Ebola, and influenza among many others.

$$dU/dt = -\beta UV$$

$$dI/dt = \beta UV - \delta I$$

$$dV/dt = pI - cV.$$

U: Susceptible cells, I: Infected cells, V: Viral load

Furthermore, I wish to use the viral dynamics model to predict the effectiveness of unlicensed drugs that have different methods of action.

References:

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