TWO-LEVEL EVOLUTION OF CHRONIC VIRAL INFECTIONS AND THE EFFECT OF THE POPULATION-LEVEL CONTROL

Dmitry Gromov[*1] and
Ethan O. Romero-Severson[2]

[1]Faculty of Applied Mathematics and Control Processes,
Saint Petersburg State University, St. Petersburg, Russia

[2]Theoretical Biology and Biophysics Group,
Los Alamos National Laboratory, Los Alamos, New Mexico, USA

dv.gromov@gmail.com (*corresponding author),
eoromero@lanl.gov

In this contribution, we consider a two-level model model of the dynamics of a multiple strain infection. This research is motivated by a need for mathematical models that not only integrate within-host genetic diversity and genotypic (resp., phenotypic) evolution with epidemiological dynamics, but also consider the joint effects of therapeutic and prophylactic controls. We attempted to balance the complexity of the model to be usable as a data analysis tool with the desire to understand the mathematical and statistical properties of the model using analytical methods. Our model accounts for within-host evolution among multiple phenotypes characterized by variable contagiousness, resistance to prophylactic measures, and resistance to therapeutic measures. The used framework allows for new phenotypes to emerge in chronic infection and later spread within the population. In addition to the disease dynamics, we consider the epidemiological and evolutionary effects of both therapy for infected persons and chemo-prophylaxis-type measures for uninfected persons.

We thoroughly analyze the structural properties of the model and present a number of results aimed at facilitating parameter identification and validation of the model. In particular, we characterize and analyze the behavior of the basic reproduction number R_0 under different assumptions about the model structure and study how the endemic equilibrium state depends on the systems parameters. We also present a sensitivity analysis along the lines described in [1] and make suggestions aimed at improving the intervention strategies design for combating the disease.

References

[1] Gromov, D., Bulla, I., & Romero-Severson, E. O. (2019). *Systematic evaluation of the population-level effects of alternative treatment strategies on the basic reproduction number*. Journal of Theoretical Biology, 462:381–390. https://doi.org/10.1016/j.jtbi.2018.11.029.