Exploring Multi-type Branching Processes
Recapitulating the results of Antia 2003

Objective

We are interested in exploring the probability of emergence of zoonotic virus in a population immune to a cross-reactive relative of the virus, particularly as the portion of the population immune decreases over time. As chains of human-human transmission increase, the the zoonotic virus faces selective pressure and opportunity to evolve a higher R_0 in its new host.

These ideas were initially explored in Antia, Regoes, Koella, & Bergstrom (2003), wherein the probability of disease emergence as a function of 1) mutation rate, 2) number of mutations required for specialization to the new host, and 3) fitness of intermediate mutations, were modeled using a muti-type branching process framework.

The goal of this document is to develop and plot the same models present in Antia et al. (2003).

References

Antia, R., Regoes, R. R., Koella, J. C., & Bergstrom, C. T. (2003). Role of evolution in the emergence of infectious diseases. *Nature*, *426*, 655–658. https://doi.org/10.1038/nature02 177