Vaccination Efficacy for Zoonoses with Varying Spillover R_0

Recapitulating the results of Antia 2003

Objective

The goal of this document is to develop a multi-type branching process model to investigate the impact of vaccination on the probability of emergence of emergence of a zoonotic disease in a population.

In this document, we will consider the simplest case of pathogen evolution, where the pathogen is a single mutation away from evolving an $R_0 >= 1$, which is sufficient for the pathogen to achieve sustained human-human transmission.

Model outline

We base the following on a model presented in Antia, Regoes, Koella, & Bergstrom (2003), which predicts the probability of disease emergence for Zoonotic variants as a function of their abilities to transmit after spillover (inital R_0), rates of of mutation, and mutational distance (number of mutations) from an $R_0 >= 1$.

Predictions are made by calculating the extinction probabilities of chains of transmission initiated by a spillover variant using a multi-type branching process framework.

For a better understanding of this model, please refer to `code/exploratory/AntiaNat2003_models.qmd`.

Effect of population immunity on emergence probability

We adapt the above model to observe how the probability of emergence changes as a function of the fraction of the population immune to infection. We refer to this change in probability as $\Delta P.emergence$

We first assume that vaccination provides complete immunity, such that 25% vaccinated means 25% less likely to infect and generate offspring cases. Ultimately:

$$\Delta P.emergence = P.emergence(R_{0,WT}) - P.emergence(f_v R_{0,WT}),$$

where $R_{0,WT}$ is the R_0 of the spillover variant in an unvaccinated population and f_v is the fraction of the population vaccinated.

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/nature02177