Simulating the Evolutionary Response of a Viral Pandemic to Behaviour Change

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Abstract

The progression of the global SARS-CoV-2 pandemic has been characterised by the emergence of novel 'variants of concern' (VOCs), which have altered transmission rates and immune escape capabilities. While numerous studies have used agent-based simulation to model the transmission and spread of the virus within populations, few have examined the impact of altered human behaviour in response to the evolution of the virus. Here we demonstrate a prototype simulation in which a simulated virus continually evolves as the agent population alters its behaviour in response to the perceived threat posed by the virus. Both mutations influencing intra-host and inter-host evolution are simulated. The model shows that evolution can dramatically reduce the effect of individual behaviour and policies on the spread of a pandemic. In particular only a small proportion of non-compliance with policies is sufficient to render countermeasures ineffective and lead to the spread of highly infectious variants.

Introduction

The SARS-CoV-2 pandemic has highlighted the need for greater understanding of the dynamics of viral evolution. As the pandemic has progressed, the virus has continually evolved, occasionally producing more highly evolved variants that have seeded new epidemic waves (the variants of concern, or VOCs), the origins of which are still poorly understood (Shrestha et al., 2022; Berkhout and Herrera-Carrillo, 2022). As SARS-CoV-2, as exemplfied by Omicron, is highly adapted to humans, current variants are persisting by accommodating further antigenic drift(Wiegand et al., 2022). The emergence of new VOCs with increased virulence could present a significant public health threat (Markov et al., 2022; Carabelli et al., 2023).

Throughout the pandemic, agent-based modelling has been used widely to simulate viral spread and the impact of public health interventions (Dignum, 2021; Kerr et al., 2021). However, few of these models have simulated the emergence of new VOCs over time. Further, the potential impact of within-host evolution has been largely ignored, though SARS-CoV-2 has shown significant within-host diversity (Tonkin-Hill et al., 2021; Lythgoe et al., 2021). Zhang et al. (2022) demonstrated an abstract model of intra- and inter-host evolution in relation to SARS-CoV-2, but individual behaviours were not simulated; Mellacher (2022) presents a more detailed evolutionary model, but again individual behavioural responses are not represented.

In this paper we present a proof-of-concept agent-based model that simulates the interaction between human behavioural change and viral evolution in a pandemic scenario. We include mutations impacting intra-host and inter-host evolution, specifically,mutationsable to generate changes in antigenicity and infectivity. Changes in behaviour, both voluntary and imposed by policy, affect transmission and subsequently impact the evolutionary dynamics.

Methods

Our model is an agent-based simulation implemented in Julia. The source code is available on GitHub at `https://github.com/mhinsch/covol/releases/tag/Alife_2023`.

Environment

The simulated environment consists of an abstracted urban area containing buildings of four types: residential; commercial; leisure; and schools. Public transport links are generated that connect two random areas of the map together, allowing agents to move around the map. Agents are always present at either a building or on public transport.

Agent properties and behaviours

Each simulation run starts with a population of 20k agents. Agent properties include: their age; locations of their home and place of work (or school); preferred places of leisure; their family (agents living in the same household); and their friends (randomly selected). Each agent follows a daily schedule, in which they leave their home in the morning at a randomised time, travel to their place of work or school by public transport or independently, and return home in the afternoon. On weekends agents have a given probability of travelling to leisure centres.

An agent's response to the simulated epidemic varies according to their individual level of virus awareness, which

increases when they or their friends or family are infected. High levels of virus awareness will cause the agent to voluntarily self-isolate. Government policies on self-isolation, masking and lockdown are followed according to each agent's 'obstinacy'; agents with higher obstinacy are more likely to ignore government guidance.

Viral transmission, infection and mutation

At the beginning of each simulation run 100 randomly selected agents are infected with the same random virus. During every simulation time step, every building or public transport link containing infectious agents is checked for encounters. If an uninfected agent encounters an infected agent, they may become infected. Their new viral population inherits the infectivity and antigenic properties of the transmitting agent's viral population. Agents have a simple 'immune system' which produces antibodies for previous variants it has seen; the 'immune reaction' is stronger if the newly infecting variant matches the current available antibodies, and decreases otherwise as mutations accumulate. If the overall immune reaction passes a certain threshold the infection is cleared.

Viral genomes are represented as a list of numbers. After each reproductive cycle of 10h, the virus population in each infected individual can undergo mutation. Only point mutations can occur, and the probability of mutation is assumed constant per base pair. Mutations affect the infectivity of the virus as well as the 'antigen' subsequently presented to the simulated immune system.

Health behaviours and policies

The simulation includes an abstracted government which can set public health policies in response to the epidemic. Policies are simple behavioural rules: self-isolation for sick agents; mask mandates; and full lockdown. Policies are implemented in response to the proportion of infected/symptomatic agents in the population; if the proportion is higher than a given threshold, the government increases its alert level (and decreases it otherwise). If the alert level passes corresponding thresholds, self-isolation, masking, and lockdown policies can be implemented. Agents follow these rules according to their individual 'obstinacy'.

Results

We find that generally the interactions between individual behaviour, government policy and virus spread and evolution can lead to unexpected virus population dynamics, in particular if reactions to infection levels are not immediate.

In terms of outcomes, stricter policies, more cautious individual behaviour as well as higher compliance lead to a reduction in overall number of infections. However, compared to a scenario without evolution, letting the pathogen evolve amplifies the effects of policies as well as behaviour. Without evolution, population immunity leads to moderate

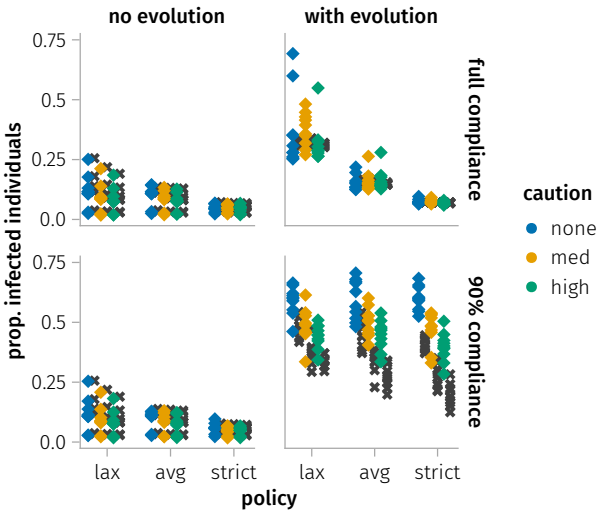

Figure 1: Final (diamonds) and average (crosses) proportion of infected individuals over two years of simulated time (10 replicates).

to low infection levels in the long term, even if policies are not strict and people take more risks (see Fig. 1). With evolution, only a strict policy is able to contain the spread of the virus, and only if there is full compliance. If a small proportion of individuals do not follow the guidelines, highly infectious VOCs evolve, a substantial proportion of the population is infected at all times and the number of infections does not reach equilibrium even after two years. This happens even if policies are strict and individual-level caution is high.

Conclusions

Our results demonstrate that the presence of evolution in a pathogen population substantially alters the outcome and effectiveness of mitigation strategies and behavioural changes. Especially in the light of recent events this strongly suggests that the interaction between pathogen evolution and human behaviour cannot be ignored when trying to understand or predict the spread of an infectious disease.

Future iterations of the model will enhance the viral evolution processes, simulated immune responses and behavioural aspects, and will be calibrated specifically to examine mechanisms that lead to the emergence of new variants in SARS-CoV-2 (e.g. Choi et al., 2020).

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