Emergence of more contagious COVID-19 variants from the interaction of viruses and policy interventions

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Abstract

At the end of 2020, policy responses to the SARS-CoV-2 outbreak have been shaken by the emergence of virus variants. The emergence of these more contagious, more severe, or even vaccine-resistant strains have challenged worldwide policy interventions. Anticipating the emergence of these mutations to plan ahead adequate policies, and understanding how human behaviors may affect the evolution of viruses by coevolution, are key challenges. This article hopes to provide a simple, starting illustration to these important, complex dynamics. We present a dual genetic algorithm model in which viruses fighting for survival and policy measures aiming at minimising infection rates in the population competitively evolve. Simulation runs reproduce the emergence of more contagious variants, and identifies the evolution of policy responses as a determinant cause of this phenomenon. This evolution opens new possibilities to visualise the impact of governments interventions not only on outbreak dynamics, but also on its evolution, to improve the efficacy of policies.

Introduction

The recent awareness on the emergence of variants has transformed the trajectory and impact of the SARS-CoV-2 outbreak. As early as June 2020, the initial COVID-19 strain identified in China was replaced as the dominant variant by the D614G mutation, found to have increased infectivity and transmission (\textit{WHO} (2020a)). On November 5 2020, a new strain of SARS-CoV-2 was reported in Denmark (\textit{WHO} (2020b)), linked with the mink industry, found to moderately decrease the sensitivity of the disease to neutralising antibodies. On 14 December 2020, the United Kingdom reported a new variant VOC 202012/01, with increased transmissibility, ICU occupation and mortality (\textit{WHO} (2020b); \textit{Wallace} and \textit{Ackland} (2021); \textit{Iacobucci} (2021)). On 18 December 2020, the variant 501Y.V2 was detected in South Africa, after rapidly displacing other virus lineages in the region. 501Y.V2 was associated with a higher viral load, which may cause increased transmissibility (\textit{WHO} (2020b)), and found to undermine the efficacy of vaccines (\textit{Mahase} (2021)). Policy interventions against COVID-19 are changing objects as well, that can be seen as evolving towards greater efficacy through experimentation, learning and communication. As the virus mutates, so do the policy interventions, in a competitive evolution process. The large search spaces involved, the focus on individual viruses and hosts and the choice of a genetic representation make GAs adequate to illustrate this competitive adaptation (\textit{Holland} (1992); \textit{Lohn} et al. (2002); Vie (2021)). It is common in coevolution that greater ecological pressures can increase the fitness of the populations involved (Rosin and Belew (1997)). We are here examining this phenomenon with COVID-19 variants, evaluating the impact of policy interventions evolution over the evolution of the viruses.

Model

Starting from initial conditions constituted by i) a population distribution of SARS-CoV-2 variants with identified genome sequences and traits and ii) a distribution of the current policy measures, we can simulate the evolution of viruses and policy actions as two coevolving GAs.\footnote{All data and simulation code is available at \url{https://github.com/aymericvie/Covid19_coevolution}}

We assume that viruses do not have any fitness function to maximise. Each virus is characterised by a reproduction rate $r$, composed of a base rate $b$, and the sum of the impacts of its mutations. The virus genome is represented as the bit string $A = [a_1, a_2, \ldots, a_v]$ and the mutation impacts by the vector $M = [\mu_1, \mu_2, \ldots, \mu_v]$. In initialisation, all viruses have no active mutations ($A = \emptyset$). Depending on $M$, mutations can increase the virus reproduction rate, others be innocuous or decrease it. At each period of time, each individual virus genome replicates itself by infecting new individuals according to its reproduction rate $r$, reduced by policies’ effects. Each replication can trigger binary mutations that (dis)activate specific mutations in the virus genome.

Policy interventions in the model are composed of 46 different non-pharmaceutical interventions, which effects on the virus reproduction rate have been identified (\textit{Haug} et al. (2020), from lockdowns to targeted closures. The effects are recorded by the effect vector $E = [e_1, e_2, \ldots, e_{46}]$. Policies represented as the bit string $P = [p_1, p_2, \ldots, p_{46}]$ are
initialised with no active measure ($P = 0$), and aim at minimising the effective virus reproduction rate $r_e$. By fitness-proportionate selection, uniform crossover and random binary mutations, policies can activate different measures, increasing their efficacy. Policies reduce the effective reproduction rate of the viruses, controlling the outbreak.

$$r_e = b_v + \sum_{i=1}^{46} a_i \mu_i - \sum_{j=1}^{46} p_j c_j$$

(1)

Results over single runs

Under coevolution, virus adaptation towards more infectious variants is considerably faster than when the virus evolves against a static policy. Although unguided by an objective, viruses evolve more efficiently facing a strong policy opposition (coevolution) than when the policies stay inactive (virus-only evolution). The average virus reproduction rate rises considerably more (up to 3.1) under coevolution than under virus-only evolution, in which this increase is low, and stays close to the natural reproduction rate of 2.63 (Mahase (2020)). Despite fewer hosts, selection in the virus population becomes more efficient under coevolution.

More contagious strains become dominant much faster in the virus population under coevolution. Figure 1d displays the fraction of viruses in the virus population containing the mutation gene granting the highest increase in reproduction rate. Not driven by diversity and population size, but by a higher efficiency of evolution, this fraction is considerably higher under coevolution than virus-only evolution. Figure 1c shows that the number of different variants in the population rises up to 800 under virus-only evolution, but only to 200 under coevolution. This difference is explained by the relatively large number of cases obtained under unconstrained virus-only evolution. As this extreme variant becomes dominant, the coevolution simulation run reproduced a variant-induced second wave of infections similar to the impact of VOC 202012/01 in the UK (Figure 1b). Both relaxing measures for political or economical motives, and emergence of variants, can thus trigger multiple waves.

Seeing more infectious virus variants becoming dominant may signify that the policy measures are effective. When policies are not evolving, more infectious variants are slower to become dominant in the population. While seeing stronger variants becoming quickly dominant is a struggle, it can be seen as the sign that the current measures are putting stress on the virus: they are efficient in pushing weaker strains to extinction. Future work from this perspective could attempt strive to include more realistic epidemiological models such as a SIR model, and to include vaccines as a policy measure, allowing viruses to obtain a vaccine-resistant trait by mutations and observing how the evolution of vaccine policies shapes the emergence of vaccine-resistant strains of SARS-CoV-2.

Figure 1: Key results from the coevolution dual genetic algorithm
References


Mahase, E. (2021). Covid-19: Novavax vaccine efficacy is 86% against uk variant and 60% against south african variant.


