Modeling Viral Evolution and Epidemic Simulation Using Genetic Algorithms

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The rapid mutation of COVID-19 has made the pandemic prolonged, requiring flexible implementation of virus mutation, immunity, and anti-pandemic policies. However, traditional mathematical approaches have had difficulty implementing these. In this study, Genetic Algorithm was introduced to simulate virus mutation and to understand the changes in viral traits and human immunity. The simulation involve random movements of humans, with social distancing measures implemented when the number of infected individuals exceeded 5%. The virus is defined by two traits: the infection rate between humans and the virus attack, represented by character strings and floating-point genes, respectively. The progression of the disease is calculated through the "life system," based on the competition between the virus attack and the human recovery rate. The viruses were classified into subspecies based on genetic similarity. The simulation results showed that the increase in the number of infected individuals changed several times, and through analysis of the changes in traits per species, it was concluded that an increase in infection rate and a decrease in virus attack within the body were favorable variations for the survival of the virus. Simulation results were compared with the daily new confirmed COVID-19 cases in Sweden, demonstrating accuracy of the simulation. This simulation is more realistic and adaptable in terms of the implementation of mutations and immunity compared to existing spread models. It is expected that by analyzing the effectiveness of quarantine policies, the damage caused by infectious diseases could be reduced drastically.

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