

GENETIC ALGORITHM IN HDV EVOLUTION ANALYSIS

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Abstract

Genetic algorithms are used to search large spaces for solutions. Pioneered for applications including artificial intelligence by Holland [1] in 1975, they are inspired from the renowned work of Darwin [2] on the origin of species. At the core, as defined by Holland [1], the genetic algorithms have three operators: selection, crossover and mutation. Many different implementations were already researched for each of these, like k-means selection [6], roulette-wheel selection [7], uniform or two point crossovers [8] or mutations like uniform, insert and DMGA [9].

Genetic algorithms have vast applications worldwide. A successful example could be the antenna that flew on March 22, 2006 on ST5 NASA and that was evolved using a genetic algorithm, described by Hornby et al. [3]. Multiple potential uses are analyzed by Sindhu et al. [4] in domains like Bioinformatics, Phylogenetics, Software Testing, Agriculture, Chemistry and Pharmaceuticals. Hard problems in evolution and phylogenetic tree analysis, problems in agro-economic systems and other derived approaches are presented by BOLBOACĂ et al. [5]. Tobias et al. [10] describe the use of the genetic algorithms for determining strain designs for the overproduction of succinate, ethanol, lactate and glutamate.

This work is concentrated on using genetic algorithms for the analysis and potentially prediction of the evolution of a specific virus, namely hepatitis delta virus. As it is stated by Deny et al. [11], the understanding of the history of the HDV might help predict its evolution, as currently HDV might infect 15-20 million people worldwide who are also infected with HBV. Being the smallest virus currently known [12], hepatitis delta virus is the best choice in starting studying the applicability of genetic algorithms for Darwinian evolution analysis of viruses. Starting from a list of strains and an outgroup, we are interested in the *in silico* evolution of the outgroup to the selected strains and afterwards in the possibility to use the algorithm in the prediction of possible future strains of evolution. The success of this work might present important interest in the development of efficient viral treatments, like, for example, the neural networks and rough set techniques that are used in the prediction of virus mutation for the same reason [13].

Keywords: genetic algorithm; virus; evolution

Domain: computer science

Section: Elaboration of the doctoral thesis

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