EXPLORING THE COMPLEXITY OF A PROPOSED RECURSIVE MEASURE OF RECOMBINATIONAL DISTANCE

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Abstract

When studying evolutionary systems, either from the natural world or artificially constructed using simulated populations, researchers must be able to quantify the genotypic differences that are observed. With the simple genetic algorithm employing both a unary mutation operator and a binary recombination operator to maintain variation in the population, it is exceedingly difficult to quantify the distance between elements of the chromosome space with an approach that is truly representative of the distance that would need to be traversed by the evolutionary mechanism. Although evaluation function dependence and the binary arity of the recombination operator both contribute to this difficulty, it is possible to redefine the function of recombination in such a way as to facilitate the computation of a more representative measurement of the distance the genetic algorithm would need to traverse to create a specific chromosome from a given population. The recursive approach presented here entails the definition of unary recombination operators and ultimately results in a technique for calculating the recombinational distance between chromosomes with a time complexity that is improved logarithmically over a simplistic approach.