Mathematical Models of Artificial Genetic Representations with Neutrality

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Kimura's neutral theory of molecular evolution [1] addresses the fact that most mutations at the genotypic level are not expressed in the phenotype, and suggests that random genetic drift is of great importance in natural evolution. Sets of genotypes connected by such neutral mutations form potentially large *neutral networks* [2] within which natural selection cannot play a direct role. However, it is understood that the accumulation of neutral mutations may potentiate the occurrence of beneficial mutations at a later stage.

Studies of neutrality in genotype-phenotype mappings have been conducted both in biology and in evolutionary computation [3]. In particular, Fonseca and Correia [4] proposed a family of uniformly redundant binary representations based on error-control codes. Such representations can exhibit various degrees of redundancy, neutrality, and other properties believed to influence the performance of evolutionary algorithms, such as connectivity, locality, and synonymity [5], and have allowed this influence to be studied experimentally to some extent [6].

In this work, a mathematical framework for the study and characterisation of Fonseca and Correia's representations is developed, leading to the definition of suitable equivalence classes and to the partitioning of the representation space with respect to neutral network structure and connectivity. The practical implications of the proposed framework are also discussed.

Keywords: Mathematical models; genetic representations; neutral networks; evolutionary computation.
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