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Abstract

This paper relates to the optimisation of structural design using Genetic Algorithms (GAs) and presents an improved method for determining the fitness of genetic codes that represent possible design solutions.

Two significant problems that often hinder design optimisation using genetic algorithms are expensive fitness evaluation and high epistasis. Expensive fitness evaluation results in slow evolution and occurs when it is computationally expensive to test the effectiveness of possible design solutions using an objective function. High epistasis occurs when certain genes lose their significance or value when other genes change. Consequently, when a fit genetic code has an important gene changed this can have a dramatic effect on the fitness of that genetic code. Often the reduction in fitness results in failure of the genetic code being selected for reproduction and inclusion in the next generation. This loss of evolved genetic information can result in the solution taking considerable time to discover.

Most attempts at overcoming expensive fitness evaluations involve saving the fitness evaluations in a file or memory so they can subsequently be looked up, instead of being evaluated again, if the same genetic code occurs more than once in the same population, or again in a latter generation (Gantovnik et al. 2003). Although saving fitness evaluations for latter reference can provide a cost saving, many fitness evaluations still have to be done, making some problems unviable for GAs, particularly if the genetic code is large and the objective function expensive.

Reducing high epistasis is usually done by representing the problem in a different manner or with different parameters. Sometimes, placing dependant genes next to each other in the genetic code can assist in preventing these genes becoming separated by the crossover operation. However, design problems with high epistasis generally remain difficult to solve with GAs or by other means.

This paper seeks to overcome these two fundamental problems with GAs by training a neural network to recognise fitness and using the neural network to classify the fitness of genetic codes. Training the neural network is done during each generation by using training patterns comprised of genetic codes and their fitness which is obtained from the fitness function or memory. Although, this still requires fitness evaluations to be done, our experiments have shown that only a subset of the population is needed to train the neural network to classify fitness sufficiently for evolution to progress. This can result in a considerable cost saving when it is expensive and time consuming to perform fitness evaluations.

Although the neural network can only produce an approximate estimate of the fitness of genetic codes, based on its architecture and training, its ability to generalise enables substantial portions of fit gene strings to be identified and appropriately awarded fitness even if the whole genetic code has not occurred before. Furthermore, when important genes change in genetic codes, which may influence the significance of other genes in the genetic code, this does not have such a dramatic effect on the genetic code's classified fitness and allows significant fit gene strings to remain represented in the population despite high epistasis.

We provide experimental results involving a classical design optimisation of a 10 bar indeterminate steel truss with genetic algorithms (Atrek 1984; Turkkan 2003). We compare a traditional GA with the same GA equipped with a neural network for generalising and classifying the fitness of genetic codes. Our results show that the GA equipped with the neural network is able to find the solution in significantly fewer generations than the traditional GA and with considerably less fitness evaluations.

Keywords: Genetic algorithm, neural network, epistasis, fitness classifier, structural optimisation, truss

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