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Abstract: Bi-Directional Reflectance Distribution Functions are used in many fields including computer animation modelling, military defence (radar, lidar, etc.), and others. This paper explores a variety of approaches to modelling BRDFs using different evolutionary computing (EC) techniques. We concentrate on genetic programming (GP) and in hybrid GP approaches, obtaining very close correspondence between models and data. The problem of obtaining parameters that make particular BRDF models fit to laboratory-measured reflectance data is a classic symbolic regression problem. The goal of this approach is to discover the equations that model laboratory-measured data according to several criteria of fitness. These criteria involve closeness of fit, simplicity or complexity of the model (parsimony), form of the result, and speed of discovery. As expected, free form, unconstrained GP gave the best results in terms of minimising measurement errors. However, it also yielded the most complex model forms. Certain constrained approaches proved to be far superior in terms of speed of discovery. Furthermore, application of mild parsimony pressure resulted in not only simpler expressions, but also improved results by yielding small differences between the models and the corresponding laboratory measurements.

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Abstract: There are estimated to be on the order of 1000000 single nucleotide polymorphisms (SNPs) existing as standing variation in the human genome. Certain combinations of these SNPs can interact in complex ways to predispose individuals for a variety of common diseases, even though individual SNPs may have no ill effects. Detecting these epistatic combinations is a computationally daunting task. Trying to use individual or growing subsets of SNPs as building blocks for detection of larger combinations of purely epistatic SNPs (e.g., via genetic algorithms or genetic programming) is no better than random search, since there is no predictive power in subsets of the correct set of epistatically interacting SNPs. Here, we explore the potential for hill-climbing from the other direction; that is, from large sets of candidate SNPs to smaller ones. This approach was inspired by Kauffman's "random chemistry"approach to detecting small autocatalytic sets of molecules from within large sets. Preliminary results from synthetic data sets show that the resulting algorithm can detect epistatic pairs from up to 1000 candidate SNPs in O(log N) fitness evaluations, although success rate degrades as heritability declines. The results presented herein are offered as proof of concept for the random chemistry approach.

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Abstract: Many methods of generating behaviour sequences of agents by evolution have been reported. A new evolutionary computation method named Genetic Network Programming (GNP) has also been developed recently along with these trends. In this paper, a new method for evolving GNP considering Breadth and Depth is proposed.The performance of the proposed method is shown from simulations using garbage collector problem.

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Abstract: The process of developing genetic algorithms, genetic programs or training neural networks is a time consuming task. When the target device is an autonomous mobile robot, this development is often performed using software simulation. Software simulations are a cost effective tool and provide researchers with the ability to test out multiple algorithms quickly and efficiently. However, the end result is that the optimised algorithm(s) must be implemented and tested on an actual robot to evaluate performance in the real world. Significant cost can be associated with this final step. In this paper we propose to leverage Radio Frequency Identification (RFID) and a low-cost RFID capable mobile robot with the intent of creating basic foraging behaviour. Additionally, we will present experimental results that demonstrate the effectiveness of using Genetic Programming (GP) and a low-cost RFID capable robot to create foraging behaviour by presenting our experimental results.

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Abstract: Gene Expression Programming (GEP) is a new evolutionary algorithm that incorporates both the idea of simple, linear chromosomes of fixed length used in Genetic Algorithms (GAs) and the structure of different sizes and shapes used in Genetic Programming (GP). As with other genetic programming algorithms, GEP has difficulty finding appropriate numeric constants for terminal nodes in the expression trees. In this paper, we describe a new approach of constant generation using Differential Evolution (DE), which is a simple real-valued GA that has proven to be robust and efficient on parameter optimisation problems. Our experimental results on two symbolic regression problems show that the approach significantly improves the performance of the GEP algorithm. The proposed approach can be easily extended to other Genetic Programming variants.