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Abstract: I carry on the study of natural networks (genetic, chemical and immune) evolving according to two levels of change called dynamics and metadynamics. The dynamics is the evolution in time of the concentration of the units currently present in the networks: the genetic, the molecular or the immune species. Their concentration evolves as a function of their network interaction with the other units. However, this evolution is also a function of their "exogenous" fitness so that the fitter units should in principle grow faster than the others. The metadynamics is the only way for innovation, and amounts to the generation of new units on the basis of the genetic or chemical materials constituting the units existing so far in the network. This metadynamics, indirectly subject to the exogenous pressure, tends to selectively favor units that are easier to produce from the existing ones. For instance, the genetic recombination of two species could occur between species presenting particular similar properties and thus generating new species merging these properties. This metadynamics also greatly influences the concentration of the units present in the network. The paper will experimentally show, on chemical, genetic and immune networks, that the interaction between these two levels of change, together with the intricate balance between the "exogenous" and the "network endogenous" selective drift, can induce a hard-to-predict concentration profile, subject to discontinuous changes.

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Abstract: Technology advances allow integrating on a single chip entire system, including memories and peripherals. The test of these devices is becoming a major issue for manufacturing industries. This paper presents a methodology for inducing test-programs similar to genetic programming. However, it includes the ability to explicitly specify registers and resorts to directed acyclic graphs instead of trees. Moreover, it exploits a database containing the assembly-level semantic associated to each graph node. This approach is extremely efficient and versatile: candidate solutions are translated into source-code programs allowing millions of evaluations per second. The proposed approach is extremely versatile: the macro library allows easily changing target processor and environment. The approach was verified on three processors with different instruction sets, different formalisms and different conventions. A complete set of experiments on a test function are also reported for the SPARC processor.

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Abstract: We present a novel approach for 3d-scene interpretation with numerous applications, for instance in robotics. The models are rendered using

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Abstract: Recent advances in biotechnology offer the ability to measure the levels of expression of thousands of genes in parallel. Analysis of such data can provide understanding and insight into gene function and regulatory mechanisms, and open a new gate to tissue classification. Since the first work of Golub et al in cancer classification based on gene expression profile rather than on morphological appearance of the tumor, there are several endeavors have been made on this direction. However, these tasks are made more difficult due to the noisy nature of array data and the overwhelming number of genes. In this paper, we propose a solution to the problem of gene selection using a multiobjective evolutionary algorithm (MOEA). Results from experiments with benchmarking data sets are also given.

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- Abstract:** For many interesting design problems the solution is most naturally represented as a type of graph. This paper proposes that the problem of evolving spring-mass models for a set of design challenges makes an excellent test-bed for evaluating the performance of various graph encoding schemes. We describe how the problem is set up, and intro-duce a planar graph coding scheme. Results demonstrate that the planar graph encoding scheme significantly out-performs a simple direct encoding scheme on a height-challenge design problem.
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Abstract: Protein three-dimensional structure determination is one of the most important problems in molecular biology. Nuclear Magnetic Resonance (NMR) spectroscopy is one of the promising techniques capable of determining the three-dimensional structures of proteins at atomic resolution. In determining protein structures by using NMR spectroscopy, Nuclear Overhauser Effect (NOE) signal assignment is the most laborious and time-consuming process. Attempts to automate the NOE signal assignment have failed so far. In this paper, we propose a new automatic assignment method of NOE signals based on a real-coded genetic algorithm and examine its effectiveness by applying it to determining the structure of a aa aa -helix, which is a well-known common substructure of proteins, and a protein called HMG2B.

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Abstract: Cultural Algorithms are self-adaptive models that support the collective evolution process through the employment of a population and a belief space. Here, the Cultural approach is applied to derive a generalized set of beliefs from successive populations of parameter configurations from an agent-based simulation of transactions within a durable goods market. The maintenance of this information allows for the guided evolution of the agent-based system over successive simulations. In order to more effectively evaluate parameter configurations, Software Engineering techniques of white and black box testing are applied. In this paper, a methodology for the use of Cultural Algorithms to optimize strategies in agent-based models is presented. This approach is demonstrated in an application used to model pricing strategies in the context of an agent-based model under a simulated real-world market scenario and a heterogeneous population.

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Abstract: Clustering is a hard combinatorial problem and is defined as the unsupervised classification of patterns. The formation of clusters is based on

the principle of maximizing the similarity between objects of the same cluster while simultaneously minimizing the similarity between objects belonging to distinct clusters. This paper presents a tool for database clustering using a rule-based genetic algorithm (RBCGA). RBCGA evolves individuals consisting of a fixed set of clustering rules, where each rule includes d non-binary intervals, one for each feature. The investigations attempt to alleviate certain drawbacks related to the classical minimization of square-error criterion by suggesting a flexible fitness function which takes into consideration, cluster asymmetry, density, coverage and homogeneity.

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Abstract: discusses issues that arise when a redundant genotype-phenotype mapping is used in the context of a real-world application. Previous studies have suggested that a redundant mapping, which introduces neutrality into the search space, can provide a beneficial role. Many of the studies to date have concentrated on relatively abstract search spaces. In this paper we consider these issues in the context of a specific real-world application. We show that redundancy can indeed be useful, but that it must be carefully introduced with due consideration to details of the application being considered, and its associated search space. Although the details of the redundant encoding are specific to the application, we seek to deduce some heuristics that are likely to prove useful for designing genetic encodings for other problems to facilitate search for fitter phenotypes.

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Abstract: This survey covers the broad area of evolutionary computation applications to optimization, model identification, and control in power systems [1]. Due to space limitation, all reviewed papers have been selected since 1996, from the IEEE Transactions only. A total of 85 articles are listed in this survey. It shows the development of the area and identifies the current trends. The following techniques are considered under the scope of evolutionary computation: evolutionary algorithms (e.g., genetic algorithms, evolution strategies, evolutionary programming, and genetic programming), simulated annealing, tabu search, and particle swarm optimization.

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Abstract: Genetic Programming (GP) has been emerged as a promising approach to deal with classification task in data mining. This work extends the tree representation of GP to evolve multiple comprehensible IF-THEN classification rules. In the paper, we introduce a concept mapping technique for fitness evaluation of individuals. A covering algorithm that employs an artificial immune system-like memory vector is utilized to produce multiple rules as well as to remove redundant rules. The proposed GP classifier is validated upon nine benchmark datasets and the simulation results confirm the viability and effectiveness of the GP approach for solving data mining problems in a wide spectrum of application domains.

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Abstract: In this paper, a new technique that uses an especially tailored genetic algorithm is proposed for attitude determination via the GPS carrier phase observables. The technique overcomes restrictions due to computational overheads incurred by existing techniques such as the Ambiguity Function Method. We present experimental results which show that the algorithm is able to efficiently search the complex search space imposed by the problem in addition to being immune to cycle slips compared to other conventional methods.

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