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Abstract: We describe a genetic segmentation algorithm for image data streams and video. This algorithm operates on segments of a string representation. It is similar to both classical genetic algorithms that operate on bits of a string and genetic grouping algorithms that operate on subsets of a set. It employs a segment fair crossover operation. For evaluating segmentations, we define similarity adjacency functions, which are extremely expensive to optimize with traditional methods. The evolutionary nature of genetic algorithms offers a further advantage by enabling incremental segmentation. Applications include browsing and summarizing video and collections of visually rich documents, plus a way of adapting to user access patterns.

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> **Abstract:** Many newly discovered genes are of unknown function. DNA microarrays are a method for determining the expression levels of all genes in an organism for which a complete genome sequence is available. By comparing the expression changes under different conditions it should be possible to assign functions to these genes. However, many hundreds of thousands of data points may be produced over a series of experiments. Genetic programming provided simple explanatory rules for gene function from such datasets, where previous approaches had not succeeded.

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> **Abstract:** This paper investigates fitness sharing in genetic programming. Implicit fitness sharing is applied to populations of programs. Three treatments are compared: raw fitness, pure fitness sharing, and a gradual change from fitness sharing to raw fitness. The 6- and 11-multiplexer problems are

compared. Using the same population sizes, fitness sharing shows a large improvement in the error rate for both problems. Further experiments compare the treatments on learning recursive list membership functions; again, there are dramatic improvements in error rate. Conversely, fitness sharing runs achieve comparable results to raw fitness using populations two to three times smaller. Measures of population diversity suggest that the results are due to preservation of diversity and avoidance of premature convergence by the fitness sharing runs

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Abstract: Nuclear materials safeguard efforts necessitate the use of non-destructive methods to determine the attributes of fissile samples enclosed in special, non-accessible containers. To this end, a large variety of methods has been developed. Usually, a given set of statistics of the stochastic neutron-photon coupled field, such as sourcedetector, detector-detector cross correlation functions, and multiplicities are measured over a range of known samples to develop calibration algorithms. In this manner, the attributes of unknown samples can be inferred by the use of the calibration results. The sample identification problem, in its most general setting, is then to determine the relationship between the observed features of the measurement and the sample attributes and to combine them for the construction of an optimal identification algorithm. The goal of this paper is to compare a combination of genetic algorithms and neural networks (NN) with genetic programming (GP) for this purpose. To this end, the time-dependent MCNP-DSP Monte Carlo code has been used to simulate the neutron-photon interrogation of sets of uranium metal samples by a 252Cf-source. The resulting sets of source-detector correlation functions, R12(?) as a function of the time delay, ? , served as a data-base for the training and testing of the algorithms.

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> **Abstract:** In earlier work we predicted program size would grow in the limit at a quadratic rate and up to fifty generations we measured bloat O(generations**(1.2-1.5)). On two simple benchmarks we test the prediction of bloat O(generations**2.0) up to generation 600. In continuous problems the limit of quadratic growth is reached but convergence in the discrete case limits growth in size. Measurements indicate subtree crossover ceases to be disruptive with large programs (1,000,000) and the population effectively converges (even though variety is near unity). Depending upon implementation, we predict run time O(number of generations**(2.0-3.0)) and memory O(number of generations**(1.0-2.0)).

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