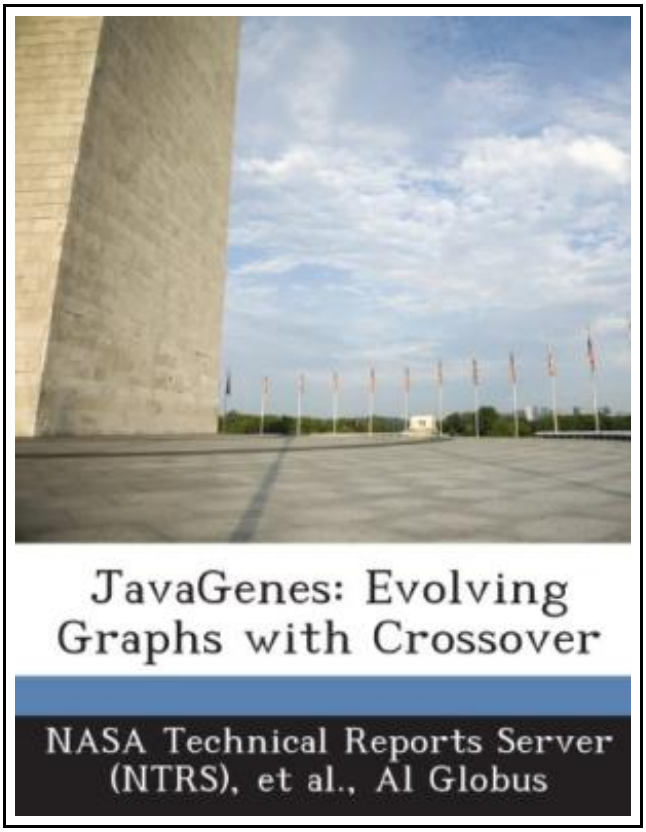
Javagenes: Evolving Graphs with Crossover



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JAVAGENES: EVOLVING GRAPHS WITH CROSSOVER

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BiblioGov. Paperback. Book Condition: New. This item is printed on demand. Paperback. 28 pages. Dimensions: 9.7in. x 7.4in. x 0.1in.Genetic algorithms usually use string or tree representations. We have developed a novel crossover operator for a directed and undirected graph representation, and used this operator to evolve molecules and circuits. Unlike strings or trees, a single point in the representation cannot divide every possible graph into two parts, because graphs may contain cycles. Thus, the crossover operator is non-trivial. A steady-state, tournament selection genetic algorithm code (JavaGenes) was written to implement and test the graph crossover operator. All runs were executed by cycle-scavagging on networked workstations using the Condor batch processing system. The JavaGenes code has evolved pharmaceutical drug molecules and simple digital circuits. Results to date suggest that JavaGenes can evolve moderate sized drug molecules and very small circuits in reasonable time. The algorithm has greater difficulty with somewhat larger circuits, suggesting that directed graphs (circuits) are more difficult to evolve than undirected graphs (molecules), although necessary differences in the crossover operator may also explain the results. In principle, JavaGenes should be able to evolve other graph-representable systems, such as transportation networks, metabolic pathways, and computer networks. However, large graphs evolve significantly slower than smaller graphs, presumably because the space-of-all-graphs explodes combinatorially with graph size. Since the representation strongly affects genetic algorithm performance, adding graphs to the evolutionary programmers bag-of-tricks should be beneficial. Also, since graph evolution operates directly on the phenotype, the genotype-phenotype translation step, common in genetic algorithm work, is eliminated. This item ships from La Vergne,TN. Paperback.

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