A Genetic Algorithm for Improved Shellsort Sequences

Robert S. Roos **Tiffany Bennett** **Jennifer Hannon** **Elizabeth Zehner**

Department of Computer Science
Allegheny College
Meadville, PA 16335
`rroos@allegheny.edu`

Abstract

A genetic algorithm is used to find shellsort increment sequences that give good average-case performance on sequences of bounded size. Our approach applies a local improvement by removing a set of common factors from each increment sequence.

1 INTRODUCTION

A complete analysis of the average case behavior of shellsort has remained an unsolved problem in the theory of algorithms for forty years (Sedgewick, 1996). This work seeks to evolve increment sequences that sort in less time than known sequences. The authors know of only one other attempt to apply genetic algorithms to the generation of shellsort sequences (Simpson and Yachavaram, 1999).

2 METHOD

We use a steady-state genetic algorithm that tries to minimize the clock time needed to sort a particular file of one million elements. We permit at most one multiple of two and at most one multiple of three in any increment sequence. Our population size is 50; the number of generations is 100.

Crossover selection is according to fitness rank and is performed once in each generation. Mutation, consisting of adding a random integer to a randomly selected increment, is applied after a crossover, giving an effective mutation rate of .02.

On files of size half a million and one million, our sequence, {1, 8, 23, 131, 149, 155, 877, 2585, 5267, 13229, 72985, 91433}, outperformed the sequence of Simpson and Yachavaram (S/Y) and the sequence of Sedgewick that was used by S/Y. Table 1 shows a representative set of data on several files of sizes 500000 and 1000000.

Table 1: Best/Median/Worst Sorting Times (ms)

FILE	OURS	S/Y
500000.0	721/724/737	749/750/752
500000.1	722/724/726	749/750/751
500000.2	721/724/725	749/751/752
1000000.0	1585/1606/1610	1677/1678/1678
1000000.1	1602/1603/1614	1678/1680/1681
1000000.2	1610/1613/1616	1678/1680/1682

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References

Sedgewick, R. (1996). Analysis of shellsort and related algorithms. In *Algorithms—ESA '96, Fourth Annual European Symposium, Barcelona, Spain.* Lecture Notes in Computer Science 1136, Springer-Verlag, 1–11.

Simpson, R., and Yachavaram, S. (1999). Faster shellsort sequences: a genetic algorithm application. *Proceedings of the International Society for Computers and Their Applications(ISCA), April 7-9, 1999.* (First author's home page: `http://cs.mwsu.edu/%7Esimpson/`)