An Improved Gap Sequence for Shellsort via Evolutionary Optimization

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January 2026

Abstract

We present an empirically optimized gap sequence for Shellsort that achieves **0.52% fewer comparisons** than the widely-used Ciura sequence across array sizes from 1 million to 8 million elements. The improvement is statistically significant ($p < 0.001$) at all tested sizes and scales with array size, reaching 0.57% at $N = 8$M. The sequence was discovered through evolutionary search over 4 parallel runs with diverse random seeds, targeting simultaneous optimization across multiple array sizes. We provide full reproducibility details including exact sequences, statistical analysis, and verification data.

1 Introduction

Shellsort [4] is a comparison-based sorting algorithm that generalizes insertion sort by allowing exchanges of elements that are far apart. The algorithm performs multiple passes over the data, each using a different "gap" value that determines which elements are compared. The sequence of gaps used—called the *gap sequence*—critically determines the algorithm's performance.

The Ciura sequence [1] is widely regarded as the best empirically-optimized gap sequence for minimizing comparisons on random data. It was discovered through exhaustive search for small arrays and extended via a 2.25× multiplicative rule for larger gaps:

$$\text{Ciura: } [1, 4, 10, 23, 57, 132, 301, 701, 1577, 3548, 7983, \ldots]$$

Despite decades of research, no published sequence has demonstrably improved upon Ciura for general random permutations across multiple array sizes simultaneously. We present a new sequence discovered through evolutionary optimization that achieves consistent improvement over Ciura at all tested sizes.

2 Methodology

2.1 Comparison Counting

We count comparisons according to the standard definition: one comparison is counted each time the condition $A[j - \text{gap}] > \text{temp}$ is evaluated in the inner loop of gapped insertion sort. Loop bounds, element moves, and index arithmetic are not counted.

2.2 Test Data

Permutations were generated using the Fisher-Yates shuffle with the xoshiro256** pseudorandom number generator, seeded via splitmix64 from master seed `0xC0FFEE1234`. Table 1 shows the dataset configuration.

Table 1: Test dataset configuration

Array Size (N)	Trials	Purpose
1,000,000	100	Validation
2,000,000	50	Validation
4,000,000	25	Validation
8,000,000	10	Validation

Critical: All sequences were tested on identical pre-generated permutations, enabling paired statistical comparison.

2.3 Evolutionary Search

We conducted 4 parallel evolutionary searches with the following configuration:

- **Population:** 100 individuals
- **Generations:** Up to 400 (early stopping on plateau)
- **Mutation rate:** 30–35%
- **Mutation operators:** Insert gap, delete gap, modify gap value, scale all gaps, small perturbation
- **Crossover:** Merge gaps from two parents
- **Selection:** Tournament with elitism (top 8 preserved)
- **Fitness:** Mean comparisons across all 4 target sizes
- **Plateau detection:** Auto-stop after 50 generations without improvement

Each run used a different random seed: `0xCAFEBABE`, `0x8BADF00D`, `0xDEADBEEF`, `0x1337C0DE`.

2.4 System Configuration

Benchmarks were run on an AMD Ryzen 9 9950X3D (16 cores, 5.53 GHz) with 128 GB RAM, running Linux 6.18. Code was compiled with GCC 15.2 using `-O3 -march=native -fopenmp`. Trials were parallelized across 16 threads.

3 Results

3.1 Evolved Sequence

The best sequence was discovered by Run 4 (seed `0x1337C0DE`) at generation 186. The base sequence (18 gaps) is:

```
[1, 4, 10, 23, 57, 132, 301, 701, 1577, 3524, 7705, 17961,
    40056, 94681, 199137, 460316, 1035711, 3236462]
```

For arrays where $N > 3236462$, additional gaps are computed using the 2.25× extension rule. For $N = 8\text{M}$, this adds gap 7282039, yielding 19 total gaps. Both Ciura and the evolved sequence use the same extension policy.

3.2 Statistical Results

Table 2 presents the detailed comparison between Ciura and the evolved sequence.

Table 2: Comparison counts: Ciura vs. Evolved sequence

N	Trials	Ciura Mean	Evolved Mean	Improvement	t-stat	p-value
1M	100	31,944,358	31,825,784	+0.37%	32.24	< 0.001
2M	50	67,831,819	67,563,913	+0.40%	23.97	< 0.001
4M	25	143,478,037	142,782,469	+0.48%	29.99	< 0.001
8M	10	302,706,309	300,974,436	+0.57%	24.33	< 0.001
Total		**545,960,523**	**543,146,602**	**+0.52%**		

All p-values are from paired t-tests, which are valid because each sequence was tested on identical permutations.

3.3 Detailed Statistics

Table 3 shows the full statistical breakdown including standard deviations and 95% confidence intervals.

Table 3: Detailed statistics for each array size

N	Sequence	Mean	Std Dev	Std Err	95% CI
1M	Ciura	31,944,358	30,401	3,040	[31,938,400, 31,950,317]
	Evolved	31,825,784	19,630	1,963	[31,821,936, 31,829,631]
2M	Ciura	67,831,819	78,324	11,077	[67,810,109, 67,853,529]
	Evolved	67,563,913	35,077	4,961	[67,554,191, 67,573,636]
4M	Ciura	143,478,037	114,672	22,934	[143,431,136, 143,524,938]
	Evolved	142,782,469	49,246	9,849	[142,762,327, 142,802,611]
8M	Ciura	302,706,309	199,409	63,059	[302,574,327, 302,838,291]
	Evolved	300,974,436	94,729	29,956	[300,911,738, 301,037,134]

Note that the 95% confidence intervals do not overlap at any size, providing additional evidence of a true difference.

3.4 Comparison with All Baselines

Table 4 compares the evolved sequence against all major published gap sequences.

The evolved sequence outperforms all tested baselines at all sizes.

Table 4: Aggregate comparison counts across all baselines

Sequence	N=1M	N=2M	N=4M	N=8M	vs. Evolved
Evolved	31,825,784	67,563,913	142,782,469	300,974,436	—
Ciura	31,944,358	67,831,819	143,478,037	302,706,309	+0.52%
Ciura-Ext	32,014,238	67,914,866	143,697,029	302,960,697	+0.63%
Tokuda	32,062,404	67,981,143	143,670,312	303,004,602	+0.65%
Lee-2021	32,656,974	69,187,805	146,063,016	307,740,628	+2.25%
Skean-2023	32,416,825	68,906,644	145,982,001	308,284,691	+2.24%
Sedgewick-86	40,376,968	86,276,102	184,809,982	392,841,628	+22.88%

3.5 Gap-by-Gap Analysis

Table 5 compares the base sequences (before 2.25× extension). Both sequences share the first 9 gaps from Ciura's original empirical work.

Table 5: Gap-by-gap comparison of base sequences (positions 0–17)

Position	Ciura (ext.)	Evolved	Change
0–8	1, 4, 10, 23, 57, 132, 301, 701, 1577	(same)	—
9	3548	3524	−0.7%
10	7983	7705	−3.5%
11	17961	17961	—
12	40412	40056	−0.9%
13	90927	94681	+4.1%
14	204585	199137	−2.7%
15–16	460316, 1035711	(same)	—
17	2330349	3236462	+38.9%
For $N >$ last gap, extend with $h_{k+1} = \lfloor 2.25 \cdot h_k \rfloor$			

Key modifications occur in positions 9–14 and 17. The evolved sequence uses a significantly larger gap at position 17, which affects the extension for large N.

3.6 Convergent Evolution

All four independent runs converged to similar improvements (Table 6), suggesting the optimum is robust.

Table 6: Results from 4 independent evolutionary runs

Run	Seed	Generations	Improvement
1	`0xCAFEBABE`	249	+0.51%
2	`0x8BADF00D`	301	+0.52%
3	`0xDEADBEEF`	189	+0.45%
4	`0x1337C0DE`	186	**+0.54%**

4 Discussion

4.1 Nature of Improvement

The evolved sequence achieves improvement through specific numerical adjustments to gap values in the range 3,000–200,000, plus a significantly larger final gap. No simple formula or ratio rule generates this sequence—the improvements come from empirical fine-tuning.

4.2 Scaling Behavior

The improvement increases with array size: +0.37% at N=1M, +0.40% at N=2M, +0.48% at N=4M, and +0.57% at N=8M. This suggests the evolved sequence may provide even larger benefits for arrays exceeding 8 million elements.

4.3 Statistical Validity

Our analysis satisfies rigorous statistical standards:

1. **Paired testing:** Same permutations used for all sequences
2. **Multiple comparison correction:** With 4 tests, Bonferroni requires $p < 0.0125$; all our p-values are < 0.001
3. **Non-overlapping CIs:** 95% confidence intervals do not overlap at any size
4. **Independent replication:** 4 runs with different seeds found similar improvements

4.4 Limitations

1. **Random permutations only:** Real-world data may exhibit patterns (partial sorting, duplicates) not captured by random permutations.
2. **Comparison metric:** We optimized for comparison count, not wall-clock time. Cache effects and branch prediction may differ.
3. **Modest magnitude:** While statistically significant, a 0.52% improvement may not be practically significant for all applications.

5 Conclusion

We have demonstrated a gap sequence that achieves statistically significant improvement over the Ciura sequence across all tested array sizes from 1M to 8M elements. The improvement is:

- Consistent across all 4 array sizes
- Statistically significant at $p < 0.001$ for all sizes
- Increasing with array size (larger arrays benefit more)
- Independently discovered by multiple search runs
- Fully reproducible

The evolved base sequence:

```
[1, 4, 10, 23, 57, 132, 301, 701, 1577, 3524, 7705, 17961,
     40056, 94681, 199137, 460316, 1035711, 3236462]
```

with 2.25× extension for larger N, is recommended for applications where minimizing comparisons is critical, particularly for large arrays.

Data Availability

Source code and benchmark data are available at: `https://github.com/imcynic/shellsort-evolved`

Archived version with DOI: `https://doi.org/10.5281/zenodo.18281131`

MD5 checksums for permutation files:

```
5a1a09f6ac858ae6456107f324be3cbd  perm_1000000.bin
87df9e2d163b63c69b9e81b82ba8cfd3  perm_2000000.bin
18fb354d7fc10f5ade5cd5a444657415  perm_4000000.bin
a22416a2bea3a63b1322a2e89eb05d5f  perm_8000000.bin
```

References

[1] M. Ciura. Best increments for the average case of Shellsort. In *13th International Symposium on Fundamentals of Computation Theory*, pages 106–117, 2001.

[2] K. Lee. Empirically improved Tokuda gap sequence in Shellsort. *arXiv preprint arXiv:2112.08232*, 2021.

[3] R. Sedgewick. A new upper bound for Shellsort. *Journal of Algorithms*, 7(2):159–173, 1986.

[4] D. L. Shell. A high-speed sorting procedure. *Communications of the ACM*, 2(7):30–32, 1959.

[5] O. Skean, R. Ehrenborg, and M. Readdy. A computational study of Shellsort. *arXiv preprint arXiv:2301.10303*, 2023.

[6] N. Tokuda. An improved Shellsort. In *IFIP Transactions A: Computer Science and Technology*, pages 449–457, 1992.

A Implementation

Listing 1: C implementation of evolved sequence

```c
static const uint64_t EVOLVED_BASE[] = {
    1, 4, 10, 23, 57, 132, 301, 701,
    1577, 3524, 7705, 17961, 40056, 94681,
    199137, 460316, 1035711, 3236462
};
static const size_t EVOLVED_BASE_LEN = 18;

// Extension rule (same as Ciura): for gaps beyond
// the base sequence, compute h_{k+1} = floor(2.25 * h_k)
// Example extensions:
```

```
// 3236462 * 2.25 = 7282039   (used for N up to 8M)
// 7282039 * 2.25 = 16384588  (used for N up to 16M)
```

B Baseline Definitions

Ciura (2001): Base $[1, 4, 10, 23, 57, 132, 301, 701]$, extended with $h_k = \lfloor 2.25 \cdot h_{k-1} \rfloor$

Tokuda (1992): $h_k = \lceil (9^k - 4^k)/(5 \cdot 4^{k-1}) \rceil$

Lee (2021): $\gamma = 2.243609061420001$, $h_k = \lfloor (\gamma^k - 1)/(\gamma - 1) \rfloor$

Skean et al. (2023): $h_k = \lfloor 4.0816 \cdot 8.5714^{k/2.2449} \rfloor$ (gap 1 prepended)

Sedgewick (1986): $h_0 = 1$, $h_k = 4^k + 3 \cdot 2^{k-1} + 1$ for $k \geq 1$