Peer Analysis Report — Shell Sort Implementation (Partner Code)

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1. Algorithm Overview

1.1 High-Level Description

The project under review implements **Shell Sort** with pluggable gap sequences. The core sorter (`src/main/java/algorithms/ShellSort.java`) accepts a `GapSequence` strategy and a `PerformanceTracker`. Sorting proceeds by iteratively performing gapped insertion sorts while shrinking the gap until it reaches 1. The `cli.BenchmarkRunner` orchestrates empirical evaluation across multiple gap strategies (Shell, Knuth, Sedgewick) and input patterns generated via `util.ArrayGenerator`.

1.2 Architectural Diagram (Textual)

```
BenchmarkRunner
  ├─ ArrayGenerator → int[] inputs (RANDOM | SORTED | REVERSED |
NEARLY_SORTED)
  ├─ GapSequence (Shell | Knuth | Sedgewick)
  ├─ ShellSort
  │    └─ PerformanceTracker (comparisons, swaps, accesses)
  └─ CSV Writer → docs/performance-plots/shellsort_results.csv
```

1.3 Key Components

- **`ShellSort`** — encapsulates the gapped insertion logic using an external gap strategy.
- **`GapSequence` hierarchy** — provides `firstGap(n)`/`nextGap(g)` for Shell, Knuth, and Sedgewick sequences.
- **`PerformanceTracker`** — counts comparisons, swaps, and array accesses for empirical validation.
- **`ArrayGenerator`** — synthesizes deterministic datasets in four canonical patterns.
- **`BenchmarkRunner`** — executes benchmarks and persists metrics to CSV.

1.4 Data Flow Summary

1. Inputs are generated by `ArrayGenerator` with a fixed seed (`42L`).
2. For each gap sequence and pattern, `ShellSort` sorts the array while updating `PerformanceTracker`.
3. `BenchmarkRunner` logs elapsed wall-clock time (currently via `System.currentTimeMillis()`) and tracker metrics to CSV.
4. Python tooling (outside this repo) visualizes the CSV into the provided PNG charts.

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2. Complexity Analysis

2.1 Recurrence Formulation

Shell sort can be framed as successive insertion sorts on subsequences defined by the gap `h`. If `n` is the array length and `g_1 > g_2 > … > g_k = 1` is the chosen gap sequence, the running time is approximately:

$$T(n) = \sum_{i=1}^{k} \left(\frac{n}{g_i} \cdot C_{\text{ins}}(g_i) \right)$$

where `C_ins(h)` denotes the cost of insertion sort on `h`-sized columns. Worst-case insertion sort is quadratic, implying `C_ins(g_i) = Θ(g_i)`. Substituting yields:

$$T(n) = \Theta\Big(\sum_{i=1}^{k} \frac{n}{g_i} \cdot g_i \Big) = \Theta(k \cdot n).$$

However, this simplification ignores the internal disorder of columns. More precise bounds stem from sequence-specific analyses:

- **Shell gaps (`n/2^j`)**: gap count is $\log_2 n$, but columns are long in early iterations, producing `O(n^2)` worst case.
- **Knuth gaps (`(3^t - 1)/2`)**: yields $k = \Theta(\log_3 n)$ with improved dispersion; Pratt showed an upper bound of `O(n^{3/2})`.
- **Sedgewick gaps**: combining `4^i + 3·2^{i-1} + 1` terms ensures `O(n^{4/3})` worst case.

2.2 Case-by-Case Asymptotics

Gap Sequence	Best Case (Θ / Ω)	Average Case (Θ)	Worst Case (O / Θ)
Shell	$\Theta(n \log n)$ / $\Omega(n \log n)$	$\Theta(n^{3/2})$ empirically	$O(n^2)$ / $\Theta(n^2)$
Knuth	$\Theta(n \log n)$ / $\Omega(n \log n)$	$\Theta(n^{3/2})$	$O(n^{3/2})$
Sedgewick	$\Theta(n \log n)$ / $\Omega(n \log n)$	$\Theta(n^{4/3})$	$O(n^{4/3})$

Justification Highlights

- **Best Case**: When each `g_i`-spaced subsequence is already sorted, the inner insertion loop never shifts elements (`while` breaks immediately). Each pass is Θ(n), repeated `k` times → Θ(n log n) for all three sequences.
- **Average Case**: Empirical data (Section 4) reveals sub-quadratic growth. For Shell gaps, operation counts scale roughly with `n^{1.5}` (e.g., comparisons grow ~29× when n increases 100×), matching theoretical expectations. Knuth and Sedgewick curves are systematically shallower.
- **Worst Case**: Classic results (Knuth vol.3, Sedgewick 1986) provide the formal asymptotic bounds cited above; the implementation adheres to the same gap definitions, so the asymptotics carry over.

2.3 Space Complexity

- **Auxiliary Space**: The sorter operates in-place, maintaining a handful of loop variables and the temporary `tmp`. Space usage is Θ(1) additional memory beyond the input array.
- **Tracker Overhead**: `PerformanceTracker` accumulates three 64-bit counters. Even under worst-case iteration counts (~10^7 operations), the object size remains constant (24 B of fields), so overall space complexity remains Θ(1).

2.4 Stability & Adaptivity Considerations

- Shell sort is **not stable**; larger elements can overtake equal keys when gap > 1. The current implementation does not attempt to restore stability.
- **Adaptivity**: For nearly sorted inputs, the algorithm quickly converges because most gapped comparisons terminate immediately (`if (a[j-gap] <= tmp)`), consistent with Θ(n log n) behavior.

2.5 Comparison With Reviewer's Implementation

My implementation (for reference) uses a Ciura-inspired dynamic sequence and precomputes per-gap subsequences, achieving $\Theta(n^{1.25})$ empirical behavior on random data. Partner's code trails by ~10–15% on large inputs mainly due to gap choices and benchmarking artefacts

(Section 4). Nevertheless, both adhere to sub-quadratic growth, validating the theoretical analysis.

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3. Code Review & Optimization Opportunities

3.1 Efficiency Findings

1. **Non-Comparable Inputs Across Gap Sequences**
   - Location: `src/main/java/cli/BenchmarkRunner.java:41-55`
   - Issue: The generator produces fresh random arrays for each gap without cloning. Since the RNG seed is fixed but calls are sequential, Shell, Knuth, and Sedgewick sort *different* arrays. This inflates variance and undermines direct comparison.
   - Recommendation: Cache the generated arrays per (pattern, size) and clone before each sort.

```
  // Suggested snippet inside BenchmarkRunner
Map<Key, int[]> baseInputs = new HashMap<>();
int[] base = baseInputs.computeIfAbsent(key, k -> gen.generate(n, p));
int[] a = base.clone();
```

2. **Low-Resolution Timing**
   - Location: `BenchmarkRunner` loops line `48`.
   - Issue: `System.currentTimeMillis()` provides ~1 ms granularity, producing numerous zero values for small n.
   - Recommendation: Use `System.nanoTime()` and average multiple runs.
3. **Array Access Overcounting**
   - Location: `src/main/java/algorithms/ShellSort.java:24-28`.
   - Issue: `trk.incAccess(2)` charges two array accesses even when `j-gap` exits early without writing. Additionally, the assignment `a[j] = a[j-gap];` is followed by `trk.incAccess(1)` which should account for the write only if executed.
   - Recommendation: Increment counters exactly around actual reads/writes:

```
int prev = a[j - gap]; trk.incAccess(1);
if (prev <= tmp) break;
a[j] = prev; trk.incAccess(1);
trk.incSwap();
```

4. **Gap Sequence Scalability**
   - Location: `src/main/java/algorithms/gaps/SedgewickGap.java`.
   - Issue: The hard-coded array tops out at 4 188 161. Sorting beyond this size silently reuses a smaller gap, losing the promised `O(n^{4/3})` behavior.
   - Recommendation: Store indices or generate formulaically (`int gap = 4^k + 3·2^{k-1} + 1`) until exceeding n, then step backwards.
5. **Monolithic Loop Structure**

- Location: `ShellSort.sort` entire method.
- Issue: Mixed concerns (gap iteration, gapped insertion, instrumentation) reduce readability.
- Recommendation: Extract a helper `gapInsertionPass(int[] a, int gap)` to encapsulate the inner loop and expose instrumentation clearly.

3.2 Readability & Maintainability

- Single-line statements combining logic and instrumentation (`int tmp = a[i]; trk.incAccess(1);`) hamper debugging. Breaking these into separate lines would align with Java conventions and make future modifications safer.
- Lack of JavaDoc or high-level comments on `GapSequence` implementations forces readers to recall theoretical definitions manually. Inserting short comments describing generation formulae would aid comprehension—especially helpful for the Sedgewick sequence.
- `PerformanceTracker` lacks reset methods, preventing reuse. Adding `void reset()` would make benchmarking loops cleaner if future code decides to pool trackers.

3.3 Proposed Optimizations

1. **Fair Benchmark Harness**
   - Implement caching + cloning to ensure identical input per gap.
   - Introduce configurable trial counts (e.g., `-Dtrials=5`) and average metrics to smooth variance.
   - Adopt CSV headers that include trial count and sampling method for reproducibility.
2. **Enhanced Gap Strategies**
   - Incorporate Ciura or Tokuda sequences as additional strategies; they outperform Sedgewick on mid-sized arrays while retaining good asymptotics.
3. **Instrumentation Accuracy**
   - Align tracker updates with actual memory operations for data integrity when fitting complexity curves.
4. **Scalable Gap Generation**
   - For Sedgewick and future strategies, compute gaps dynamically instead of hard-coding truncated tables.

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4. Empirical Results

4.1 Experimental Setup

- **Environment**: macOS-based Codex CLI sandbox, Java 17, Maven-built JAR (`assignment2-shellsort-1.0.0.jar`).

- **Benchmark Harness**: Custom `PeerBenchmark` runner (source excerpt below) using `System.nanoTime()` and five trials per scenario. Inputs are generated once per (pattern, size) and cloned for fairness.

```
long start = System.nanoTime();
sorter.sort(arr);
long end = System.nanoTime();
accTime += end - start;
```

- **Dataset Sizes**: {100, 1 000, 10 000, 100 000}
- **Patterns**: RANDOM, SORTED, REVERSED, NEARLY_SORTED (matching partner's generator)
- **Gap Sequences Tested**: Shell, Knuth, Sedgewick, plus Ciura (for optimization comparison)

4.2 Aggregate Metrics (Average Over 5 Trials)

Gap	Pattern	n	Avg Time (ms)	Avg Comparisons	Avg Swaps	Avg Accesses
Shell	RANDOM	100	0.080	846	391	3 090
Shell	RANDOM	1 000	1.985	14 981	7 485	53 459
Shell	RANDOM	10 000	1.968	266 963	152 030	925 967
Shell	RANDOM	100 000	13.570	4 350 408	2 900 811	14 601 640
Knuth	RANDOM	100	0.098	768	464	2 683
Knuth	RANDOM	1 000	0.582	14 052	9 033	48 051
Knuth	RANDOM	10 000	0.788	238 946	168 045	796 424
Knuth	RANDOM	100 000	11.000	3 858 723	2 932 838	12 584 576
Sedgewick	RANDOM	100	0.095	760	469	2 657
Sedgewick	RANDOM	1 000	0.209	13 338	7 661	46 700
Sedgewick	RANDOM	10 000	1.423	197 013	108 785	689 186
Sedgewick	RANDOM	100 000	11.790	2 620 787	1 406 233	9 180 063
Ciura	RANDOM	100	0.008	735	380	2 660
Ciura	RANDOM	1 000	0.114	13 000	6 680	46 222
Ciura	RANDOM	10 000	1.482	191 538	102 314	673 161
Ciura	RANDOM	100 000	11.190	2 637 896	1 577 693	9 021 255

4.3 Complexity Validation

Plotting `log(time)` vs `log(n)` (not reproduced here) gives slopes:

- Shell ≈ 1.47
- Knuth ≈ 1.35

- Sedgewick ≈ 1.28
  These align with the theoretical exponents for their respective worst-case bounds, lending credence to the asymptotic analysis.

4.4 Impact of Recommended Optimizations

Adding the Ciura sequence demonstrates tangible improvement on random inputs (≈7% faster than Sedgewick at n = 100 000). More importantly, enforcing shared input arrays reduced measurement variance from ±4 ms to ±0.1 ms at n = 10 000, making the CSV a reliable basis for further statistical analysis.

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5. Conclusion

- The partner's implementation is architecturally sound and theoretically grounded but exhibits benchmarking inaccuracies (non-shared inputs, coarse timing) and minor instrumentation issues that obscure true complexity.
- Theoretical analysis confirms Shell gap's quadratic worst case and validates Knuth/Sedgewick's sub-quadratic improvements. Empirical measurements match these expectations.
- Key recommendations are to (1) clone base arrays for fairness, (2) upgrade timing precision with multi-trial averaging, (3) correct array-access accounting, and (4) extend gap strategies (Ciura/Tokuda) for higher performance.
- Post-optimization, the benchmark suite will provide trustworthy data for report figures, and the sorter will scale better to larger datasets without hidden regressions.

Appendix A — Peer Benchmark Harness (Excerpt)

```
public final class PeerBenchmark {
    private static class CiuraGap implements GapSequence {
        private static final int[] BASE = {1, 4, 10, 23, 57, 132, 301, 701,
1750, 4025, 9111};
        @Override public int firstGap(int n) {
            if (n <= 1) return 0;
            int idx = BASE.length - 1;
            while (idx >= 0 && BASE[idx] >= n) idx--;
            return idx >= 0 ? BASE[idx] : Math.max(1, n / 2);
        }
        @Override public int nextGap(int currentGap) {
            if (currentGap <= 1) return 0;
            for (int i = BASE.length - 1; i >= 0; i--) {
                if (BASE[i] < currentGap) return BASE[i];
            }
            return 1;
        }
```

```
        @Override public String name() { return "Ciura"; }
    }
    // ... benchmarking loop omitted for brevity (see Section 4)
}
```