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| Accelerating genome sequence alignment on a RISC-V many core cluster |
| Group No: 28 |
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| Summary  This project explores accelerating genome sequencing, specifically read mapping, on the MemPool many-core architecture. Read mapping is a crucial step in genome sequencing, involving aligning short DNA sequences (reads) to a reference genome.  Key Aspects:   * Platform: MemPool, a scalable many-core architecture with low-latency shared memory. * Algorithm: Smith-Waterman algorithm, a dynamic programming approach for sequence alignment. * Parallelism Approaches:   + Anti-diagonal: Exploits parallelism across elements within the same diagonal of the dynamic programming matrix.   + Row-parallel: Computes entire rows of the matrix concurrently using techniques like prefix sum. * Roofline Analysis: Roofline analysis was used to understand the performance limitations of the system and identify potential optimizations.   Observations:   * Initial results with anti-diagonal parallelism showed limited speedup due to inherent data dependencies and a limited number of elements per diagonal for typical read lengths. * Row-parallel implementation demonstrated significant performance improvements by reducing data dependencies and enabling more efficient utilization of the many-core resources * We achieve significant increase in throughput in the rowparallel method for a loss in arithmetic intensity but still remain in the compute bound region |
| KEY DIAGRAMS : |