

Darren worked on implementing the SIMD accelerated version of Smith-Waterman, using our non-SIMD version as a starting point. He wrote implementations to handle both protein and DNA sequences. These programs were written in C++. He also conducted our benchmarking experiments of all 4 of the Smith-Waterman versions on protein sequences.

Ishan implemented our non-SIMD version of Smith-Waterman (that was used as a benchmark point for our tests). This was written in C++, and two versions were written, one for DNA sequences and one for protein sequences. He also implemented programs for WaveFront Alignment (WFA), conventional edit distance calculation, and a program to generate mutated DNA sequences for input to the WFA benchmarking experiment. He (along with Kiron) conducted the benchmarking experiments on WaveFront Alignment and edit distance algorithms.

Kiron implemented optimizations on the existing Striped Smith-Waterman SIMD-accelerated project to generate improvements in speed. Specifically, he implemented Query Profile Optimization, which included aligned memory allocation, OpenMP parallelization, and more efficient vectorization. He also wrote a script to compare CPU time speedup from the Striped Smith-Waterman Github to our optimized version over 100 runs (benchmark.sh). He (along with Ishan) conducted the benchmarking experiments on WaveFront Alignment and edit distance algorithms.

William also implemented optimizations on the existing Striped Smith-Waterman SIMD-accelerated project to generate improvements in speed. Specifically, he added backward trace optimizations, which included replacing scalar comparisons with SIMD vectorization, and mask-based filtering for branch reduction. He also conducted our benchmarking experiments of all 4 of the Smith-Waterman versions on DNA sequences.